USING ABATTOIR GENERATED DATA AND BCMS RECORDS FOR CARCASE TRAIT EVALUATIONS (Carcase trait evaluations)

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Final Project Report For Circulation

Executive summary

- At the start of the project over 3.9 million carcass records from 2001 to 2014 were available from six different abattoirs. At the completion of the project, seven abattoirs are supplying data – in some cases records are transferred routinely (i.e. weekly) via an automated email and data upload system – with 4.8 million carcass records available.
- It is thought that this data represents about 31% of the national slaughter population, this varies across years but is higher in recent years where we have more data provided.
- Systems to clean, validate and consolidate data have been put in place to maximise the available data.
- Investigations were undertaken to develop appropriate statistical models, in particular methods of accounting for hybrid vigour given the cross bred nature of the carcass data.
- Genetic parameters have been estimated for five carcass traits. In all cases the traits were found to be heritable. The moderate to high heritability's estimated show that the traits are highly suitable for genetic selection. Heritability estimates for net weight, conformation, fat, and age at slaughter were 0.40, 0.41, 0.45, and 0.63, respectively.
- EBVs were produced for nearly 3 million UK beef and dairy animals.
- Comparing the EBVs across different breeds show that while there are some small differences in ranking, in general there is much more variation within a breed than across the breeds. This demonstrates that the most progress will be made by selecting animals with favourable EBVs within the breed you currently have than by substituting breeds, as no one breed is better than another.
- Genetic trends show little change in recent years. This is not surprising given that until now the tools did not exist to directly select for these carcass traits. Using proxy traits the pedigree sector have made significant genetic improvements but with a poor penetration rate and uptake of performance recorded bulls in the commercial sector the impact has not been observed.
- Now that EBVs are available for the traits of direct interest to the commercial sector clear market signals can occur and hopefully will stimulate commercial finishers to source bulls with favourable carcass trait genetics and we will start to see an improvement in the commercial animals with more animals having the right genetics to better meet and respond to market specifications.
- In particular, age at slaughter has been identified as a very valuable trait to select for as this has a huge impact on the profitability of the beef enterprises.

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Introduction

This project is a continuation of a previous project funded to look at if abattoir data could be used to produce Estimated Breeding Values (EBVs) for abattoir carcass traits. This Phase 1 project concluded that the data was sufficient, which led to the current Phase 2 project to develop the EBVs as part of a routine genetic evaluation system, which at the end was ready to produce regular routine genetic evaluations for abattoir carcass traits.

Description of data

The carcase data was supplied by six abattoirs, namely ABP, Dovecote Park, Stoddart's, McIntosh Donald, Morrisons, and Dunbia, and were collated into a single database. In February 2014, the database consisted of 3,926,064 rows of data, of which 374 animal records were duplicated. After removing the duplicates the initial dataset consisted of 3,925,690 records. For confidentiality Individual abattoirs will be kept anonymous, and the individual abattoirs contributed 2,255,228, 871,958, 399,171, 13,295, 111,794 and 274,244 of the records. It is this data that is described further in the following sections.

However, at the end of the project (October 2016) there were almost a million more abattoir records available (n= 4,803,702) 7 different abattoirs. Several abattoirs are transferring records on a regular (usually monthly) basis using automated data transfers and we are endeavouring to do the same with the remaining abattoirs.

The records grouped by year and abattoir are shown in Table 1. The reported data was collected up until June 2014.

Table 1 Records grouped by year of kill and abattoir from 2001 through to 2014

Year	Combined	Source					
		A	B	C	D	E	F
Null	1		1				
2001	27,108		27,108				
2002	33,792		33,792				
2003	41,562		41,562				
2004	52,029		52,029				
2005	62,302		62,302				
2006	122,474		71,204	51,270			
2007	125,819		74,419	51,400			
2008	452,346	329,013	73,756	49,577			
2009	432,822	310,462	74,754	47,606			
2010	475,641	344,462	82,760	48,419			
2011	503,028	367,493	86,466	49,069			
2012	571,432	438,498	82,240	50,694			
2013	826,128	428,948	80,243	51,136		95,748	170,053
2014	199,206	36,352	29,322		13,295	16,046	104,191
Total	**3,925,690**	**2,255,228**	**871,958**	**399,171**	**13,295**	**111,794**	**274,244**

Matching abattoir data to BCMS

The animal identity given in the abattoir data was the UK eartag and this was reformatted if necessary (i.e. spaces, slashes removed) and matched to BCMS data. However, not all identities could be matched to BCMS and Table 2 shows the percentage of records that were not matched from each abattoir company. Two companies had a considerable number of animals that do not match to BCMS and thus the data would not be used. For one abattoir, these animals that had not matched were due to the fact supplied data also came from their Northern Ireland abattoir whilst the other abattoir is largely based in Ireland had supplied cattle identities including animals that originated from Ireland (country code prefix IE) or Northern Ireland (Country and region code prefix UK 9).

Table 2 Percentage of animals not matched to BCMS grouped by source

Source	Total count	Count not matched to BCMS (%)
A	2255228	359148 (15.9)
B	871958	3159 (0.4)
C	399171	1353 (0.3)
D	13295	33 (0.2)
E	111794	1277 (1.1)
F	274244	74547 (27.2)

Abattoir data

Breeds

From the abattoir data there were 621 different entries for breed. Some entries could be grouped as there were different ways of recording the same breed type. For example, there were numerous different entries for a Limousin cross, such as LIMX, LIX, LIM X, LMX, LIXX, LIMRX, LIMBX. There were some animals which had no record for Breed (74,786) in addition some date entries were entered by mistake. The 30 most recorded breed codes are shown in Table 3. It can be seen that the top five breed codes were Limousin cross (LIMX), Aberdeen Angus cross (AAX), Charolais cross (CHX), Holstein Friesian (HF) and Simmental cross (SMX). The ten most common breed codes for each abattoir are shown in Table 4. It can be seen that there are differences among abattoirs with the breeds of cattle slaughtered and the ranking of breeds.

Table 3 Most common breed codes obtained from abattoir data from 2001 through to 2014

	Breed code	Count		Breed code	Count
1	LIMX	601,924	16	HE	36,671
2	AAX	545,121	17	SM	36,476
3	CHX	382,510	18	BB	35,071
4	HF	342,195	19	HFX	25,378
5	LIM	236,839	20	BRB	24,238
6	SMX	234,869	21	SAX	17,842
7	HEX	224,085	22	SIM	17,306
8	CH	146,393	23	BFX	16,481
9	AA	139,172	24	HOL	14,129
10	BBX	117,000	25	SDX	13,377
11	BRBX	94,306	26	WB	12,789
12	BF	90,113	27	MOX	11,377
13	FR	72,123	28	SD	10,863
14	BAX	71,890	29	SHOX	10,644
15	HO	50,597	30	STX	10,047

Table 4 Ten most common breed codes (and percentage of total animals) by abattoir

Abattoir company	A	B	C	D	E	F
1	LIMX (18.0)	AAX (40.5)	AAX (22.1)	LIMX (29.7)	LIMX (33.1)	LIM (20.9)
2	HF (11.8)	HEX (17.1)	LIMX (21.9)	CHX (29.0)	CHX (23.4)	HF (16.4)
3	CHX (10.8)	LIMX (7.7)	CHX (17.2)	SMX (16.5)	BRBX (8.1)	HEX (7.2)
4	LIM (7.1)	AA (7.5)	SMX (9.5)	AAX (5.4)	SMX (7.6)	CH (7.0)
5	SMX (6.6)	CHX (3.4)	HF (5.5)	HF (3.6)	LIM (4.5)	BRB (5.9)
6	CH (5.3)	SMX (3.2)	AA (5.3)	BRBX (3.0)	AAX (3.8)	FR (4.8)
7	AAX (4.1)	HE (2.4)	BBX (2.7)	SAX (1.8)	CH (2.4)	BF (3.8)
8	BBX (3.9)	BBX (1.8)	BF (1.8)	LIM (1.4)	BAX (2.0)	HO (3.8)
9	BRBX (3.1)	BAX (1.2)	LIM (1.4)	SM (1.1)	BSHX (1.8)	CHX (3.7)
10	BF (3.0)	BRBX (1.2)	BAX (1.1)	BAX (1.0)	SHOX (1.6)	SMX (3.5)
Other breeds	26.2	13.8	11.5	7.4	11.8	23.0

Sex

A range of codes existed to describe sex as shown in Table 5. Not all animals had a record for sex (320 animals) or it was coded wrongly. H would indicate a heifer, C a cow, S a steer (bullock), YB a young bull, MB a mature bull, and V would denote a veal calf.

Table 5 Codes available to describe sex from data recorded 2001 through to 2014

	Sex code	Count		Sex code	Count		Sex code	Count
1	S	1,828,569	21	V	1,268	41	#	19
2	H	983,345	21	SB	1,212	42	AB	19
3	YB	382,939	23	YBA	1,169	43	VH	13
4	C	321,680	24	YBO	805	44	ES	7
5	Steer	108,310	25	HB	659	45	]	6
6	Cow	67,782	26	YBV	442	46	2	3
7	Heifer	63,437	27	HF	314	47	B16	2
8	SS	35,850	28	H36	246	48	CON	2
9	YBull	31,574	29	OS	231	49		1
10	HS	27,603	30	YBB	229	50	wenlockom	1
11	SA	14,273	31	OH	200	51	SBONNERC145	1
12	MB	10,336	32	HV	179	52	.	1
13	B	10333	33	SF	176	53	6	1
14	YBS	8838	34	AAS	139	54	t	1
15	HA	6472	35	AAH	103	55	CL	1
16	CLF	6119	36	OTS	54	56	F	1
17	CF	5048	37	S36	51	57	NULL	320
18	Bull	3132	38	VS	47			
19	S V	1677	39	OTH	45			
20	V	1268	40	EH	23			

Conformation

There are five main classes for conformation: E, U, R, O, and P (where E=excellent and P=poor). In the EUROP scale in the UK classes P, O, and U are further sub-divided into – and +. The 15 point scale however, divides each letter class into 3 subclasses e.g. +E, =E, -E. It appears that both the EUROP and 15 point scale and a combination of the two scales were used by the six data sources (Table 6). It appears that all abattoirs used the 15 point scale with some categories having been written in alternative ways e.g. –O and O-. Overall the percentage of animals in each of the five main conformation classes E, U, R, O, and P 0.7%, 16.0%, 38.5%, 39.9%, and 4.9% respectively. Table 7 gives the numbers of animals contributed by each abattoir for each of the main conformation classes.

Table 6 Summary of conformation classes from data recorded 2001 through to 2014

Conformation class given by abattoir	Converted to numerical value	Count	Conformation class given by abattoir	Converted to numerical value	Count
E+	45	43	0+	18	1
E=	42	256	O+	18	974779
E	42	26919	O	15	129335
E'	42	20	O'	15	908
E-	39	1433	0	15	1
U+	36	105679	O=	15	17775
U=	33	11670	-O	12	393132
U	33	59669	O-	12	49096
U'	33	877	P+	9	123077
-U	30	409251	P=	6	12042
U-	30	40501	P	6	3442
R+	27	65597	P'	6	711
R	24	1261360	-P	3	39092
R'	24	1538	P-	3	13087
R=	24	30242		NULL	248
-R	21	6	H	NULL	1
R-	21	153504	NC	NULL	10
			NULL	NULL	4
			U3	NULL	2

Table 7 Distribution of carcases for conformation class categorised as E, U, R, O, and P from data recorded 2001 through to 2014 (with NULL categories removed)

	Number contributed by abattoir (Percentage of grade within abattoir)					
	Abattoir A	Abattoir B	Abattoir C	Abattoir D	Abattoir E	Abattoir F
E	240,99	1,112	492	54	1,251	1,663
	(1.1)	(0.1)	(0.1)	(0.4)	(1.1)	(0.6)
U	452,571	30,325	65,316	5,594	40,752	33,091
	(20.1)	(3.5)	(16.4)	(42.1)	(36.5)	(12.1)
R	798,183	345,447	226,398	6,312	56,565	79,342
	(35.4)	(39.6)	(56.8)	(47.5)	(50.6)	(28.9)
O	832,622	491,995	95,918	936	13,123	130,433
	(36.9)	(56.4)	(24.1)	(7.0)	(11.7)	(47.6)
P	147,512	3,061	10,686	399	91	29,702
	(6.5)	(0.4)	(2.7)	(3.0)	(0.1)	(10.8)

Fatness

There are five main fatness classes ranging from 1 (very lean) to 5 (very fat). In the EUROP scale, classes 4 and 5 are sub-divided into L (leaner) and H (fatter). However, there were several forms of a single class as shown in Table 8 which indicates the use of the 15 point scale. Unlike conformation, ABP have used the EUROP scale for fat class up until 2010 with the additional class '5,' and in following years the 15 point scale has been used. Dovecote has used the EUROP scale prior to 2005 and from 2005 onwards has used the 15 point scale. The EUROP scale was used by Stoddart, McIntosh Donald and Morrisons over the entire extraction period. Both the EUROP and the 15 point scale were used by Dunbia. Dunbia data were taken from 3 abattoirs, one of which used the 15 point scale and 2 used the

EUROP scale. In Table 9 the classes were collapsed and it can be seen that 71% of carcases fall into the desired categories 3 and 4L.

Table 8 Summary of fat classes from data recorded 2001 through to 2014

Fat class given by abattoir	Converted to numerical value	Count	Fat class given by abattoir	Converted to numerical value	Count
NULL	NULL	2264	-4	30	11278
0	NULL	3	4-	30	248035
	NULL	318	4L	30	1229916
-1	3	831	4	33	207760
1-	3	3439	4'	33	583
1	6	69237	4M	33	2
1'	6	277	4=	33	17196
1=	6	3758	4+	36	68624
1+	9	6632	4H	36	330814
-2	12	3349	-5	39	907
2-	12	9524	5-	39	12648
2	15	323583	5L	39	32414
2'	15	1060	5	42	5811
2=	15	14508	5'	42	26
2+	18	29839	5=	42	576
-3	21	13053	5H	45	5511
3-	21	34859	5+	45	1048
3	24	1079641			
3'	24	2046			
3=	24	37839			
3+	27	116099			

Table 9 Distribution of carcases for fat class from data recorded 2001 through to 2014 (with NULL categories removed).

Fat class	Number contributed by abattoir (Percentage of grade within abattoir)					
	Abattoir A	Abattoir B	Abattoir C	Abattoir D	Abattoir E	Abattoir F
1	66572 (3.0)	2871 (0.3)	4133 (1.0)	9 (0.1)	138 (0.1)	10451 (3.8)
2	313242 (13.9)	19805 (2.3)	6852 (1.7)	321 (2.4)	3810 (3.4)	37833 (13.8)
3	873975 (38.8)	164839 (19.0)	105527 (26.5)	2014 (15.1)	21318 (19.1)	115864 (42.3)
4L	779170 (34.6)	551193 (63.4)	226734 (56.9)	7804 (58.7)	63873 (57.1)	85996 (31.4)
4H	195157 (8.7)	108253 (12.4)	50399 (12.6)	3076 (23.1)	21922 (19.6)	20631 (7.5)
5L	22473 (1.0)	21331 (2.5)	4648 (1.2)	69 (0.5)	693 (0.6)	3168 (1.2)
5H	4323 (0.2)	1400 (0.2)	517 (0.1)	2 (0.0)	28 (0.0)	289 (0.1)

Net Carcase Weight

There were 2,223 records (including negative values and zero values) that were less than 5 kg which were assumed either to be mistakes when recording or due to deductions from condemnations. In total 4,099 weight records which were less than 100kg were excluded from the below calculations and figures as they were thought to be recording errors or veal calves passing through the abattoir. Thus editing of weights, taking account of animal age, will be required prior to genetic analysis to establish suitable ranges. The weight data item is referred to as net carcase weight. Figure 1 shows a normal distribution for net weight with the largest proportion of carcases weighing between 280 and 350 kg. Table 10 shows that the mean weight was 329 kg, which depending upon data source ranged from 314 to 373 kg. Four out of the six abattoir companies recorded date of birth. From date of birth and kill date columns the age at slaughter could be calculated. A wide range of slaughter ages exist (from 0 to 214 months), which includes mature cattle as well as prime beef and veal.

Table 10 Descriptive statistics for net carcase weight grouped by source from data recorded 2001 through to 2014.

	Min weight (kg)	Max weight (kg)	Average weight (kg)	St.dev weight (kg)	Count
Overall	100	904	328.5	55.96	3,921,209
Abattoir A	100	904	332.5	59.26	2,252,651
Abattoir B	100	791.2	314.1	48.44	870,828
Abattoir C	109	658	326.2	44.85	398,452
Abattoir D	172.9	552	349.2	52.99	13,293
Abattoir E	153.9	564.5	373.4	49.91	111,763
Abattoir F	100	745.98	325.9	52.49	274,222

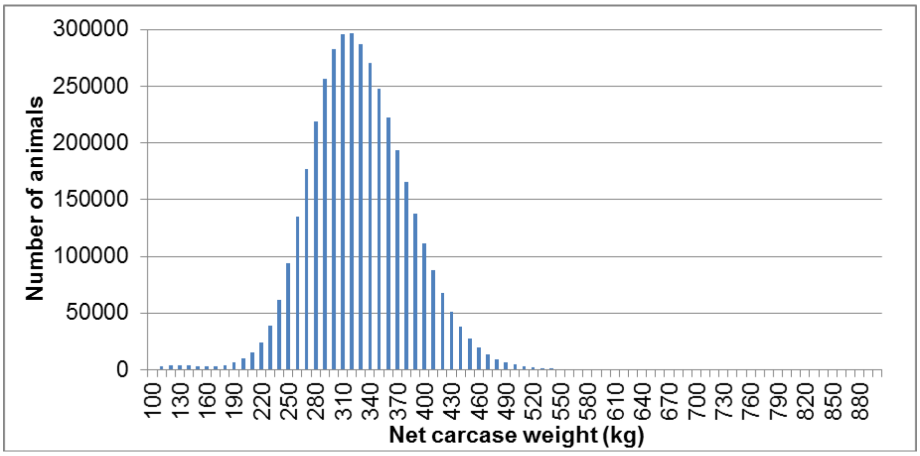

Figure 1 Distribution of net carcase weight at slaughter from data recorded 2001 through to 2014. (Bars in graph = 10 kg groupings 100-109 kg, 110-119 kg, 120-129 kg ….)

Age at slaughter

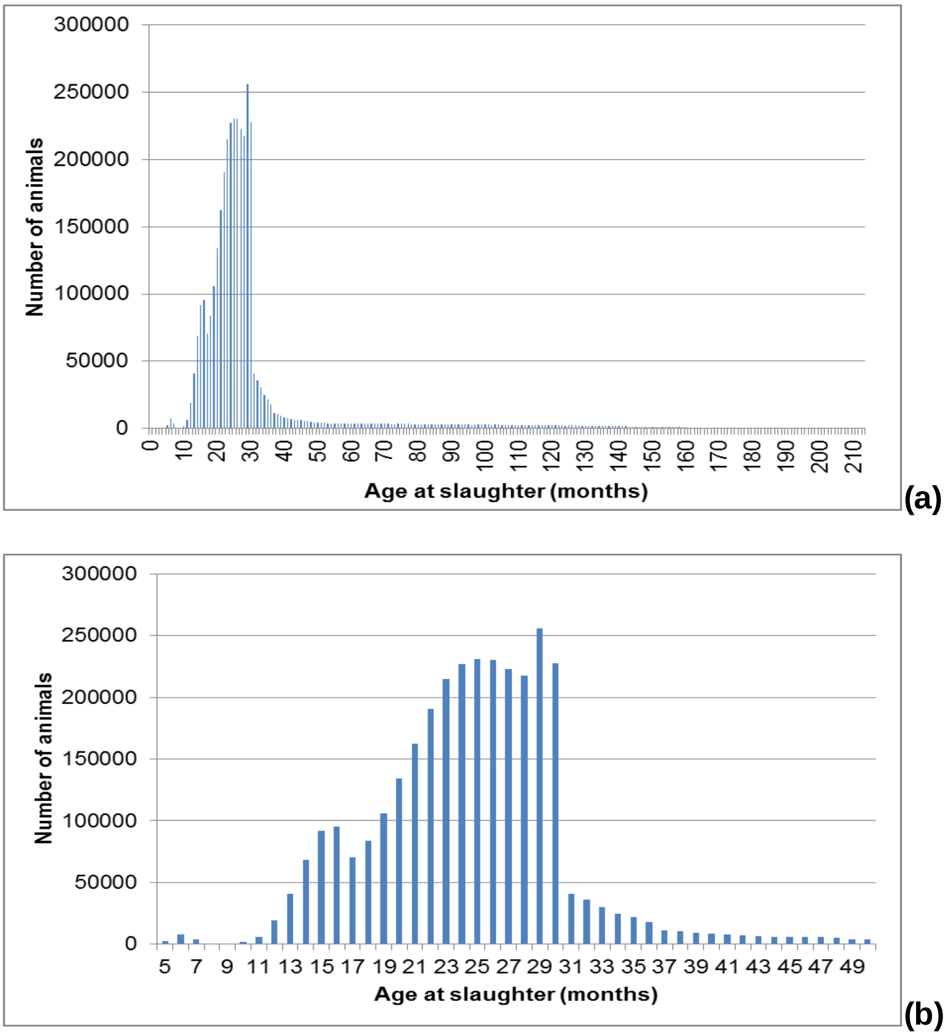

Figure 2 Distribution of age at slaughter from 2001 through to 2014 (a) all ages and (b) restricted to 5 to 50 months for a closer look.

Comparison of sample abattoir data with UK national beef slaughter statistics

To give an idea whether the sample of abattoir data obtained here is representative of the national population means and percentages are compared and given in Tables 11 to 15. The data came from six abattoir companies from various years between 2001 and 2014 (Table 1). Table 11 gives the total numbers of UK cattle slaughtered nationally and the overall numbers provided from abattoirs from 2001 to 2014. With each year there is an increased percentage of abattoir data from the national population. The year with the most data was in 2011, but the year with the largest percentage of national data was in 2013, which was 31.5% (as shown in Table 11) .

Table 11 Total numbers of cattle slaughtered in the UK and the number cattle available from abattoir data (thousand head)

Year	National data	Sample abattoir data	Percentage in abattoir data
2001	2164.2	27.1	1.3
2002	2282.2	33.8	1.5
2003	2275.0	41.6	1.8
2004	2393.2	52.0	2.2
2005	2412.6	62.3	2.6
2006	2644.5	122.5	4.6
2007	2661.3	125.8	4.7
2008	2631.8	452.3	17.2
2009	2512.9	432.8	17.2
2010	2759.5	475.6	17.2
2011	2837.9	503.0	17.7
2012	2680.7	571.4	21.3
2013	2625.0	826.1	31.5

Source: DEFRA for national slaughter statistics

Table 12 Comparison of percentage distribution of prime beef carcases 2009 – 2013 for national population (N) and abattoir sample (S)

	National statistics			Abattoir sample			Abattoir sample (Prime[†])		
%	Steer	Heifer	Young Bull	Steer	Heifer	Young Bull	Steer	Heifer	Young Bull
2009	55	34	11	55	31	14	56	31	13
2010	54	32	14	56	29	15	56	31	13
2011	54	33	13	56	31	13	57	31	12
2012	56	32	12	55	31	15	58	29	13
2013	55	33	12	55	32	14	57	30	13

[†] Prime cattle included steers, heifers, and young bulls greater than 12 months but less or equal to 36 months of age
Source: AHDB UK Yearbook 2014 Cattle

Table 13 Comparison of prime cattle average carcase weights 2009 – 2013 for national population (N) and overall abattoir sample (S)

	National statistics				Abattoir sample			
Kg deadweight	Steers	Heifers	Young Bulls	Prime (overall)	Steers	Heifers	Young Bulls	Prime (overall)
2009	361.7	313.7	351.6	341.8	343.5	300.4	342.5	330.3
2010	368.3	321.5	345.8	347.7	351.4	307.5	329.5	335.9
2011	364.6	319.1	344.4	344.7	347.2	304.9	330.4	332.1
2012	367.1	320.3	346.4	347.0	351.4	306.6	338.6	335.9
2013	360.7	315.9	338.8	340.6	353.2	310.9	332.2	337.4

Source: AHDB UK Yearbook 2014 Cattle

The composition of prime cattle with steers, heifers, and young bulls in abattoir data is similar to national statistics as shown in Table 12. It would be recommended that prime cattle are edited for age at slaughter because the sex/category code could not be solely relied upon. The mean weights for prime slaughter cattle are lighter in the abattoir data than those taken from national statistics as shown in Table 13. Slight differences could be due to if hot carcase weight is used in national statistics rather than cold carcase weight. Also, net weights provided here may include losses through condemnations. Edited abattoir data to include prime cattle only has very similar percentages of each conformation or fat class to those reported in national statistics as shown in Tables 14 and 15. Differences between the abattoir sample and national statistics could be due to different proportions of breeds that comprise the data in the two datasets. Abattoirs in different locations around the UK are likely to have varying proportions of cattle breeds depending on what breeds are reared in the particular region as well as different preferences of the different abattoirs (as shown in Table 4).The abattoir data might be slightly bias towards Scottish abattoirs and less influence from Welsh abattoirs. However, more and more abattoir companies are being approached about supplying data, therefore, a more representative sample taken throughout the UK should transpire.

Table 14 Comparison of conformation class in 2013 from abattoir sample and national statistics

%	E	U	R	O	P
Abattoir sample 2013	1.1	19.3	36.9	36.0	6.6
Abattoir sample 2013 Prime	1.2	21.9	40.4	34.9	1.5
National 2013	1.0	21.1	41.4	34.2	2.1

Source: AHDB UK Yearbook 2014 Cattle

Table 15 Comparison of Fat class in 2013 from abattoir sample and national records

%	1 and 2	3	4	5
Abattoir sample 2013	15.8	35.3	47.7	1.2
Abattoir sample 2013 Prime	10.7	34.0	54.3	1.0
National 2013	13.1	33.2	52.8	0.9

Source: AHDB UK Yearbook 2014 Cattle

Summary of abattoir data

- Over 3.9 million records obtained from the three data providers
- The three most common breed types were Limousin Cross, Aberdeen Angus Cross, and Charolais Cross.
- Slight differences in the scales used for classifying carcase conformation and fat across years and between data providers. Therefore, it would be suitable to add the effects of abattoir (location of death (individual abattoir) or source (Abattoir A, Abattoir B, Abattoir C, Abattoir D, Abattoir E, Abattoir F) and the year-season of death for genetic analysis.
- Means for net carcase weight were similar between data providers but editing will be required to remove outliers/erroneous data.
- Data has been obtained from younger animals (specifically reared for beef) and mature animals (cull dairy cows, bulls that have been bred from). These animals should be treated separately.
- The year with most data was 2013 which represented about 31 % of the national slaughter population.
- The sample of abattoir data obtained here had similar distributions to national slaughter statistics for animal type (steer, heifer, young bull), fat and conformation classes. Mean weights were lower in this data than national slaughter statistics, which could be due to the breeds that comprise the slaughter cattle in the particular abattoirs used in this study.

Preparation of a data set for genetic parameter estimation of carcase traits

Genetic parameter estimation and model development is required to produce Estimated Breeding Values (EBVs). While all animals are included to compute EBVs, only a very clean subset of the data is used to estimate genetic parameters and develop models. Further to this the size of the data set is limited by the computing power of the statistical software (SAS and ASReml) used to estimate genetic parameters and develop models. This is routine practice for the calculation of genetic parameters and subsequent EBVs.

Clean up of data prior to editing

Over 3.9 million slaughter records from six individual abattoirs were available (full details available in the previous data description section). Prior to applying edits to this data set to render it suitable for genetic parameter estimation some simple restrictions were applied to clean the data. These restrictions and the number of animals remaining after each restriction are shown in Table 16. These initial cleaning procedures resulted in just fewer than 2.8 million records remaining.

Table 16 Summary of restrictions to clean raw data

	Restriction	Rows lost	Rows remaining
	Original count		3,925,669
1	Remove duplicates (eartag)	4 (2 duplicates)	3,925,665
2	Remove where difference between kill date (abattoir) and death date (bcms) > 10 days	1,566	3,924,099
3	Removed animals without sex recorded	40	3,924,059
4	Removed where age at slaughter <=365 (1 year)	465,740	3,458,319
5	Removed where age at slaughter >1095 days (3 years)	407,050	3,051,269
6	Removed where age at slaughter is null	755	3,050,514
7	Removed where conformation class was null and did not appear in Table 2	3	3,050,511
8	Removed where fat class was null, blank and zero	2,205	3,048,306
9	Removed where not prime slaughter animal (slaughter code does not appear in Table 3)	258,882	2,789,424
10	Removed where sex was non male/female and incorrect with respect to slaughter type	0	2,789,424

Explanation of cleaning edits Age at slaughter was accepted when it was between 12 months and 36 months of age and for animals recorded as heifers, steers, or young bulls as these were animals expected to be produced for prime beef production (slaughter codes as in Table 18). Veal calves were not included in this study (with calves defined as being less than 12 months of age). The majority of bulls produced for prime beef tend to be slaughtered prior to 16 months of age due to price penalties however there was no edit for maximum age other than 36 months of age. In the earlier feasibility carcase trait study it was found that kill date from abattoir data and death date from BCMS were not always the same. It was thought some of these records may indicate a mismatch, but for the majority the differences were minor, with most differences being only one day, indicating that the animal was matched correctly between both sources. The majority of differences were no more than 10 days therefore this was accepted as a suitable cut-off. Abattoirs differed slightly in their recording of conformation and fat classes, however sometimes there were erroneous inputs in these columns. The classes allowed for conformation are shown in Table 17.

Table 17 Conformation classes accepted in data set

Conformation class
E, E-, -E, E+, E=, E’
U, -U, U-, U+ U=, U’
R, -R, R-, R+, R=, R’
O, -O, O-, O+, O=, O’
P, -P, P-, P+, P=, P’

Table 18 Slaughter types accepted in data set

Slaughter type code	Slaughter type
YB	Young bull
H	Heifer
S	Steer

Trait definitions for genetic parameter estimation

Net carcase weight (kg) is the weight of the body of an animal, after the removal of the animal’s head, hide, feet/legs, thoracic organs, internal fats, and abdominal organs, dressed according to a defined specification (three specifications exist in the UK namely Standard Specification, EC Reference Specification and UK Specification) followed by chilling (thus also known as cold carcase weight). Cold carcase weight is approximately 2% less than hot carcase weight.

Conformation of the carcase is graded under the EUROP system, defined by 5 main classes E, U, R, O, and P. which through European Union regulations allow for 3 further subdivisions (e.g. E+, E, E-) of each conformation, thus 15 classes in total. These classes were converted to numerical values 1 to 15 as shown in Table 19, and multiplied by three to be line with a conversion table supplied by Signet (scale 3 to 45). A 15 point scale with values 1 to 15 as used by Hickey et al (2007[1]) would result the same as the values 3 to 45.

Fat class is graded under the EUROP scale with the five main classes (1, 2 ,3 ,4 ,5) but abattoirs differed by the use of both the 7 point and 15 point scale. The 15 point scale was used and converted to a numerical value 1 to 15 and the 7 point and 15 point scales were applied to this as shown in Table 19. The values 1 to 15 were multiplied by three as explained for conformation above.

Age at slaughter (days) is the interval between birth and slaughter.

Average daily carcase gain (kg/day) was calculated from net carcase weight divided by age at slaughter in days. For analysis the value was multiplied by 100 as the variance estimates were very small. But then for reporting of the final EBVs it is expressed as kg/day.

Limitations It is unknown whether some measurements for net carcase weight may include further losses due to condemnation. Some condemnation data had been provided recently from some abattoirs for preliminary analysis but the timeframes rarely overlapped with the current data set. Net carcase weight would be lower than

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[1] Hickey, J.M., Keane, M.G., Kenny, D.A., Cromie, A.R., and Veerkamp, R.F. 2007. Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. Journal of Animal Science 85:314-321.

expected in cases where part of an animal's carcase has been condemned. Those animals that have had part or their entire carcase condemned are largely unknown and this is where further work to obtain condemnation data would be advantageous. It should be noted that average daily carcase gain includes the initial birth weight of the animal because birthweight is not commonly known.

Table 19 Numerical values on a 15 point scale given to conformation and fat classes

Conformation class scale					Fat class scale		
Numerical value[†]	EUROP 5-point	EUROP 15-point			Numerical scale[†]	EUROP 7-point	EUROP 15-point
15 (45)		+E			1 (3)		-1
14 (42)	E	E	Decreased conformation		2 (6)	1	1
13 (39)		-E			3 (9)		+1
12 (36)		+U			4 (12)		-2
11 (33)	U	U		Increased fatness	5 (15)	2	2
10 (30)		-U			6 (18)		+2
9 (27)		+R			7 (21)		-3
8 (24)	R	R			8 (24)	3	3
7 (21)		-R			9 (27)		+3
6 (18)		+O			10 (30)	4L	-4
5 (15)	O	O			11 (33)		4
4 (12)		-O			12 (36)	4H	+4
3 (9)		+P			13 (39)	5L	-5
2 (6)	P	P			14 (42)		5
1 (3)		-P			15 (45)	5H	+5

[†] Numerical values were multiplied by 3 in final genetic parameter estimation to be consistent with conversion table provided by Signet

Editing data for across breed genetic parameter estimation

The edits listed in Table 16 and 20 were carried out to create a file for genetic parameter estimation and the number of animals remaining after each edit is shown. The purpose of the edits was to clean the data to produce a high quality data set, but also to reduce the data set to a size suitable for the analysis software available. The edited data set for genetic parameter estimation consisted of 43,272 animals (1.1 % of the original combined data set) with carcase measurements, which were from a total of 1,708 sires. The pedigree was extracted from the super-pedigree (a pedigree combining all available pedigree sources allowing for a much richer pedigree) for 3 generations and consisted of 109,719 animals. The final data set was sufficiently big for parameter estimates. However, it was too large for software such as SAS that was used to test for effects to be considered in the model. Therefore, there were further edits carried out to produce a data set for fixed effects analysis.

Whilst the primary aim was to produce genetic parameters applicable to an across breed scenario, a series of breed specific data sets were also formed following similar logic as that applied for the across breed data set. For these within breed data sets the restriction of kill records between 2010 and 2013 were widened to include records from 2002 to 2014, a minimum number of progeny per sire was reduced from 25 to 15 for numerically larger sire breeds (Aberdeen Angus, Limousin, Charolais, Simmental, Hereford) and 10 for numerically smaller sire breeds, contemporary group size was reduced from 10 to 5 for numerically smaller sire breeds, and the restriction that sires had to appear in 3 or more years of data was removed. Table 20 describes the data sets that were formed as part of this project. Table 21 summarises the counts for individual breeds.

Table 20 Summary of edits (in order) to create data sets for genetic parameter estimation

	Edits	Rows lost	Rows remaining
			2,789,424
11	Removed if dam missing birth date or <540 days (~18 months) at calving	74,627	2,714,797
12	Remove if record does not have a BCMS id	2,393	2,712,404
13	Remove if sire and/or dam unknown	1,963,633	748,771
14	Remove if sire breed percentage of a single breed is not >=87.5	14,715	734,056
15	Removed records outside +/-3sd for carcase weight for age group category, slaughter type, and sire breed	4,044	730,012
16	Removed records outside +/-3sd for average daily carcase gain for age group category, slaughter type, and sire breed	2,137	727,875
17	Removed records that did not have a proper birth on herd	6,962	720,913
18	Removed records which died in their birth herd	0	720,913
19	Removed records with no off record from birth herd	0	720,913
20	Removed records which moved more than 3 times including move to abattoir (must be on site for >13 days to be classed as a move)	49,200	671,713
21	Removed records where the herd was unknown	0	671,713
22	Removed records whose last off movement was not death	278	671,435
23	Removed records which spent <14 days in their finishing herd	26,751	644,684
24	Removed records where kill location is not ‘SH’ (slaughter house)	103	644,581
27	Removed records whose birth season herd only used one sire	231,025	413,556
28	Removed records killed before 2010 and after 2013	135,852	277,704
29	Removed records of sires who appeared in <3 kill years	27,422	250,282
30	Removed records (and sires) whose sire had <25 progeny	130,620	119,662
31	Capped the number of records per sire to a maximum of 50 (taking 1st 50 progeny born)	35,329	84,333
32	Removed records where less than 10 animals per birth herd-year-season	25,950	58,383
33	Removed records where less than 10 animals per kill herd-year-season	14,743	43,640
34	Removed records from a breed group containing <150 progeny	364	43,272

Net carcase weight and average daily carcase gain were edited to include those animals which had measurements within three standard deviations of the mean of the two traits. Due to known differences for growth between slaughter categories (heifer, steer, young bull), age and breed the above edits were made per slaughter category / age / sire breed group. Month at slaughter was divided into four age groups for both heifers and steers; these were 12-17 months, 18–23 months, 24–29 months, and 30–36 months. For young bulls one age group which spanned 12-36 months was used. Young bulls were mainly within the age range of 12 to 16 months, group sizes per breed were generally small, and relatively few were available at later ages. The breed of the sire was obtained from the calculated breed proportion rather than using BCMS breed and the sire was required to be at least 87.5 % (i.e. purebred) of one breed for the progeny to remain in the data set.

Table 21 Number of animals and sires per sire breed in edited data set for genetic parameter estimation

Sire breed	Number of animals	Number of sires	Sire breed	Number of animals	Number of sires
Aberdeen Angus	18,666	645	British Blue	792	38
Charolais	6,357	239	Salers	747	30
Limousin	5,348	232	South Devon	719	31
Simmental	5,342	191	Beef Shorthorn	398	16
Hereford	1,720	75	Lincoln Red	223	12
Stabiliser	891	33	Luing	163	6
British Blonde	886	38	Sussex	151	5
Holstein Friesian	869	117	Total	43,272	1,708

Table 22 Summary details of the different data sets used for genetic parameter estimation

Breed	**Number of animals**	**Number of sires**	**Number in pedigree**
Across-Breed	43,272	1,708	109,719
Across-Breed (edited)	26,678	1,141	73,793
Aberdeen Angus	41,271	1,185	93,020
Beef Shorthorn	2,352	169	6,892
British Blonde	4,954	321	13,388
British Blue	3,216	234	8,953
Charolais	10,149	339	25,389
Hereford	8,170	367	19,107
Holstein Friesian	9,403	855	28,983
Limousin	10,477	392	26,472
Luing	1,045	76	2,774
Salers	2,198	134	5,940
Simmental	9,059	367	21,707
South Devon	3,592	233	9,308
Stabiliser	4,205	191	10,109
Welsh Black	1,994	149	5,081

Fifteen sire-breeds remained in the final data set with counts ranging from 151 to 18,666 animals as shown in Table 21. A summary of counts for the separate data sets of individual breed analysis for the numerically larger sire breeds (with over 1000 animals after individual breed edits) are given in Table 22.

Heterosis and recombination estimates

To take account of hybrid vigour, heterosis and recombination coefficients calculated from four breed types were included in the model for genetic parameter estimation. To calculate heterosis and recombination coefficients between every breed group available would be extremely complex; hence the method deemed most suitable was to assign the many different breed groups to 4 different breed types; dairy (1), native beef (2), continental beef (3), and indicus/other breeds (4). The heterosis/recombination coefficients (In this case 6 different coefficients for each animal) were included in the model as covariates. Details of the current breed groups are shown in Appendix A.

Heterosis and Recombination coefficients were calculated from the breed type proportions of the animal's sire and dam and the formulae are as follows:

$$heterosis_{ij} = \frac{\left(sire_i * \ dam_j\right) + \left(sire_j * \ dam_i\right)}{100}$$

$$recombination_{ij} = \frac{\left(sire_i * \ sire_j\right) + (dam_i * \ dam_j)}{100}$$

where *i* and *j* correspond to two different breed types

Each row of data (one row per animal) therefore has twelve coefficient columns for heterosis (6 columns) and recombination (6 columns) which are given for the following breed type combinations:

Het 1 and Rec 1 = breed types 1 and 2

Het 2 and Rec 2 = breed types 1 and 3

Het 3 and Rec 3 = breed types 1 and 4

Het 4 and Rec 4 = breed types 2 and 3

Het 5 and Rec 5 = breed types 2 and 4

Het 6 and Rec 6 = breed types 3 and 4

In some cases the breed type of the parents were unknown thus three assumptions were made based upon the breed type proportions of the animal and are as follows

1. If an animal is 100 % of one breed type then both the sire and dam is assumed to be 100 % of the same breed type of the animal.
2. If an animal is 50:50 for two breeds and both parents are unknown then we assume that the sire is 100% of one breed and the dam is 100% of the other breed. The heterosis and recombination calculations of the animal are not affected by the way around the breed types of the sire and dam are chosen.
3. If an animal does not conform to breed type proportions as in assumptions 1 and 2 (e.g. animal is 75:25 for two breed type proportions) then both parents are given the same breed type proportions of the animal.

These assumtions may not be true but they are deemed the most appropriate in the situation when breed proportions of the parents are unknown.

Later in the project, additional methods of accounting for hybrid vigour were tested. The three methods tested were;

Method 1 (breed types) – Breeds are collapsed into 4 breed types; dairy, continental beef, native beef and other and PEB per breed type is calculated, for example a Hereford x Angus cross would be 100% native beef. The het/rec coefficients are worked out for each combination of breed type; dairy*continental, dairy*native etc with in total 6 combinations for both het and rec to be modelled – 12 effects. The assumption is that there is little to no hybrid vigour within breed types.

Method 2 (Single effect) – Rather than collapse breeds into breed types the heterosis and recombination effects are calculated for each individual breed cross, but then summed together into a single het and a single rec effect to be modelled. The assumption is that the hybrid vigour expressed is the same for all breed crosses.

Method 3 (single effect plus) – This expands on method 2 but allows dairy and beef animals to be treated separately. Like method 2, it will calculate the het/rec values per individual breed cross but instead of summing into a single term they will be summed into 3 terms; dairy (dairy*dairy crosses), beef (beef*beef crosses) and dairy-beef (dairy*beef crosses). The assumption here is that the hybrid vigour effects are different for dairy and beef, but within the 3 classes the hybrid vigour expressed is the same. In total 3 het and 3 rec effects are modelled.

Method 1 was the same as that used in the initial work. The results of these comparisons (not shown) indicated that there were little difference between methods 1 and 3, a small effect on the Conformation trait when method 2 was used. Method 3 was chosen for the final set of EBVs as although it had little effect compared to method1, it was felt this was easier to explain and more acceptable to industry.

Statistical Model Development

In order to estimate genetic parameters appropriate statistical models are required. The statistical package SAS was used to test fixed effects for significance, and to aid the construction of appropriate statistical models. For all traits the following terms were tested for significance (using Proc Mixed in SAS).

- Category – this is inclusive of sex; steer, heifer or young bull
- Birth-Herd-Year-Season (birthHYS) – a birth contemporary group; Year and season of animal birth. Season was defined as 3 four month periods; February – May, June – September and October – January.
- Source – abattoir company
- Kill site – Uses the abattoir site given as location of death in BCMS. Some companies have animals killed at more than one site.
- Kill-Herd-Year-Season (killHYS)* – a kill contemporary group; Year and season of animal death. Season was defined as 3 four month periods; February – May, June – September and October – January
- Kill date* – to test if there were differences associated with a days kill (i.e. operator effects)
- Age at slaughter in days (linear and quadratic)
- Sire breed (all sires purebred)
- Dam age at calving grouped into 4 categories; 1 – 3 years, 3 – 6 years, 6 – 9 years and 9 or older years.
- Dam percentage of dairy; 0-100% of the primary dairy breeds (evaluated by dairyco)
- Heterosis and Recombination coefficients (using proportion of each breed values calculated by EGENES on the bovine super-pedigree)

*Both these terms were nested within kill site. This is because a kill date is specific to site in the context that we want to account for day to day differences on a particular site (i.e. the person who trims the carcase etc.) and for the kill contemporary to avoid confounding as in most cases the whole contemporary group go to the same site consistently.

First order interactions of the above terms were also considered. However, due to size constraints not all could be fitted at once. Therefore, interactions were fitted one at a time and the terms where the P value was less than 0.2 were added to the full model for consideration.

Maternal effects

The edited data set consisted of 34,124 dams, which gives a mean of 1.3 offspring per dam. There were 7,773 dams with more than 1 offspring and up to a maximum of 6 offspring. Maternal effects (genetic and environmental) are generally considered to be low among carcase traits as development of carcase tissues occur in later development when the diet relies less upon the dam's milk. In some breeds and systems it is also likely that maternal effects are non-existent, for example in dairy breeds where the calf is removed from its dam within days of its birth. However, models including maternal effects were studied in preliminary univariate analyses to investigate their importance. Maternal effects did appear to exist in some traits (results not shown). However, it was realised that the maternal effect was largely due to the dam breed effect which could not be disentangled; therefore the effect was not included in any of the final models.

Models

For all traits an animal model was chosen i.e. animal was included as a random effect and linked to the animal's pedigree. The fixed effects are shown below where '/' means an effect is nested within another and '.' means an interaction between traits.

Category, dam age class, source, dam percentage dairy, kill site/kill date het1 het2 het3 het4 het5 het6 rec1 rec2 rec3 rec4 rec5 rec6, Category.killHYS, birthHYS kill site/killHYS

For all models, regardless of if they were significant or not, heterosis and recombination coefficients were included in the models. For net weight and ADCG age (linear and quadratic) was a significant covariate, whereas age quadratic was not significant for fat and age linear and quadratic were not significant for conformation. Dam percentage dairy was not significant for age.

In the literature it is common for carcase traits to be adjusted either by weight or age. Therefore the traits examined here were also analysed with various adjustments using another trait as a (co)variable in the model.

Net weight, conformation, fat, and ADCG (adjusted for age at slaughter) also included age linear, age quadratic, age.category, and age.kill site in the model

Conformation, fat, days at slaughter (weight adjusted) included net weight in the model

Net weight, Conformation, days at slaughter (fat adjusted) included fat class in the model

Net weight, fat, days at slaughter (conformation adjusted) included conformation class in the model

Genetic Parameter Estimation

Univariate analysis

ASReml was used to estimate genetic parameters. Table 23 shows the genetic parameters estimated from univariate models for the across-breed data set. Alternative models were evaluated where the traits were adjusted for weight, age at slaughter, conformation or fat. Heritability estimates were fairly robust across the different models fitted with the various adjustments. The heritability estimates for weight, conformation, fat, age, and ADCG ranged from 0.36 to 0.42, 0.38 to 0.42, 0.43 to 0.46, 0.62 to 0.64, and 0.43 to 0.48 respectively. ADCG tends to decrease with age so it would make sense to include age in the model. It would be expected that a multivariate analysis that makes use of phenotypic and genetic correlations between the traits would be a good option, which means that adjustments using other traits as (co)variables would not be necessary. Firstly, bivariate analyses were carried out between all pairwise combinations of the traits in order to obtain starting values to build up the model.

Table 23 The genetic parameter estimates (standard errors) from univariate analysis of an across-breed data set including adjustments

Trait /Adjustment	Additive variance (V_A)	Residual variance (V_E)	Phenotypic variance (V_P)	Heritability (h^2)
Carcase weight				
No adjustment	250.1 (14.97)	347.3 (11.51)	597.4 (5.87)	0.42 (0.022)
Age	246.3 (14.98)	362.7 (11.57)	609.0 (5.92)	0.40 (0.022)
Conformation	194.3 (12.80)	339.7 (10.01)	534.0 (5.11)	0.36 (0.022)
Fat	253.5 (15.17)	356.6 (11.68)	610.1 (5.97)	0.42 (0.022)
Age, Conformation, Fat	202.3 (12.90)	320.4 (10.01)	522.7 (5.08)	0.39 (0.022)
Conformation[†]				
No adjustment	0.40 (0.024)	0.57 (0.019)	0.97 (0.010)	0.42 (0.022)
Weight	0.32 (0.021)	0.53 (0.016)	0.85 (0.008)	0.38 (0.022)
Age	0.40 (0.024)	0.57 (0.019)	0.97 (0.010)	0.42 (0.022)
Fat	0.38 (0.024)	0.58 (0.018)	0.96 (0.009)	0.39 (0.022)
Fat[†]				
No adjustment	0.63 (0.036)	0.76 (0.027)	1.39 (0.014)	0.45 (0.023)
Weight	0.64 (0.036)	0.75 (0.027)	1.39 (0.014)	0.46 (0.023)
Age	0.63 (0.036)	0.76 (0.027)	1.38 (0.014)	0.45 (0.023)
Conformation	0.59 (0.035)	0.78 (0.027)	1.37 (0.014)	0.43 (0.023)
Age				
No adjustment	277.7 (13.93)	171.2 (10.24)	448.9 (4.99)	0.62 (0.026)
Weight	283.1 (13.91)	159.3 (10.18)	442.5 (4.98)	0.64 (0.026)
Conformation	278.4 (13.94)	170.6 (10.24)	449.0 (4.99)	0.62 (0.026)
Fat	278.9 (13.94)	169.8 (10.24)	448.8 (4.99)	0.62 (0.026)
Weight, Conformation, Fat	282.9 (13.94)	162.1 (10.21)	445.0 (4.99)	0.64 (0.026)
ADCG[†]				
No adjustment	0.0009 (0.00005)	0.001 (0.00004)	0.0018 (0.00002)	0.48 (0.023)
Age	0.0007 (0.00004)	0.0009 (0.00003)	0.0017 (0.00002)	0.43 (0.022)

[†] Prior to scaling up: Conformation and Fat were multiplied by 3 in final analyses, and ADCG was multiplied by 100.

Bivariate analysis

Pairwise combinations of traits net weight, conformation, fat and age was carried out and the results for heritability estimates, genetic correlations, residual correlations and phenotypic correlations are shown in Tables 24 and 25. The heritability estimates from the four-way combinations for each trait were very similar. Heritability estimates for net weight, conformation, fat, age at slaughter, and average daily carcase gain **(ADCG)** ranged from 0.40–0.41, 0.41–0.42, 0.45–0.46, 0.62–0.63, and 0.48–0.50, respectively. ADCG is a function of net weight and age and it was found to be strongly genetically correlated with net weight and its relationship with conformation and fat class is also similar to those estimates with net weight. The genetic correlation between ADCG and age was moderate and negative (-0.42) dissimilar to the relationship between age and net weight. It could be argued that ADCG is not essential to analyse in a multivariate analysis together with net weight and age as it is a function of both those traits.

Table 24 Heritability estimates† obtained from bivariate combinations of net weight, conformation, fat, age, and average daily carcase gain (ADCG)

	Bivariate trait				
	Net weight	Conformation	Fat	Age	ADCG
Net weight		0.40 (0.022)	0.40 (0.021)	0.41 (0.022)	0.40 (0.022)
Conformation	0.41 (0.022)		0.41 (0.022)	0.42 (0.022)	0.41 (0.022)
Fat	0.45 (0.022)	0.46 (0.022)		0.45 (0.023)	0.45 (0.022)
Age	0.63 (0.026)	0.62 (0.026)	0.62 (0.026)		0.62 (0.026)
ADCG	0.48 (0.023)	0.47 (0.023)	0.47 (0.022)	0.50 (0.023)	

† For heritability estimates of a trait results are shown on the horizontal (row) together with the trait it was analysed on the vertical (column). For instance heritability estimates for net weight were 0.40, 0.40, 0.42, and 0.40 when analysed with conformation, fat, age, and ADCG.

Table 25 Genetic, residual, and phenotypic correlations from bivariate combinations of net weight, fat, age, and average daily carcase gain (ADCG)

	Net weight	Conformation	Fat	Age
Genetic correlations				
Net weight				
Conformation	0.49 (0.035)			
Fat	-0.38 (0.040)	-0.51 (0.036)		
Age	0.03 (0.039)	-0.10 (0.039)	-0.04 (0.038)	
ADCG	0.86 (0.011)	0.49 (0.033)	-0.36 (0.038)	-0.42 (0.031)
Residual correlations				
Net weight				
Conformation	0.26 (0.021)			
Fat	0.27 (0.025)	0.19 (0.026)		
Age	0.24 (0.032)	0.10 (0.032)	0.10 (0.033)	
ADCG	0.88 (0.006)	0.23 (0.023)	0.26 (0.027)	-0.08 (0.035)
Phenotypic correlations				
Net weight				
Conformation	0.35 (0.006)			
Fat	-0.01 (0.006)	-0.11 (0.007)		
Age	0.13 (0.007)	-0.003 (0.007)	0.03 (0.008)	
ADCG	0.87 (0.002)	0.34 (0.006)	-0.02 (0.007)	-0.27 (0.007)

These estimates are in line with the review by Ríos Utrera and Van Vleck (2004[2]) with average heritability estimates from literature of 0.40, 0.36, and 0.40 for similar traits carcase weight, backfat thickness, and longissimus muscle area, respectively. However, it was found in their study that there was a wide range in heritability estimates, and one reason could be due to differences between breeds. Literature on age at slaughter as a trait, rather than being used as a covariate in models of other carcase traits, have not been found and if any exist there would be few. The heritability of age at slaughter is high and possibly this is because the industry has paid little attention for it to be a measure for selection. Wide variation exists for age at slaughter within sire progeny (with standard deviations of a single sire's progeny ranging from 1.87 to 176.6 days (sires with at least 10 steer progeny)) and between sires (with an overall mean age at slaughter of 697.7 days and a standard deviation of 102.1 days).

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[2] Ríos Utrera, A. and Van Vleck, L.D. 2004. Heritability estimates for carcass traits of cattle: a review. Genetics and Molecular Research 3:380-394.

Multivariate analysis: Three and four traits

Both a three-trait analysis (net carcase weight, conformation class, and fat class) and a four-trait analysis (net carcase weight, conformation class, fat class, and age at slaughter) were carried out (results not shown) and found similar estimates as those from the bi-variate evaluations.

Within breed genetic parameter estimates

Univariate models (results not shown) and four-trait multivariate models were run and genetic parameters estimated within sire breeds. In some cases the within breed data sets were too small to obtain sensible results. Six sire breeds, namely Aberdeen Angus, Charolais, Hereford, Holstein Friesian, Limousin, and Simmental were probably large enough numerically to obtain reasonable results. Heritability estimates for these six breeds ranged from 0.12 (Holstein Friesian) to 0.30 (Aberdeen Angus), 0.11 (Simmental) to 0.28 (Limousin), 0.15 (Holstein Friesian) to 0.36 (Hereford), and 0.44 (Charolais) to 0.75 (Hereford) for net weight, conformation class, fat class and age at slaughter, respectively.

Genetic parameter estimates for within-breed analyses are given in Tables 26 and 27. Similar to the across-breed analysis the genetic correlations for the above five beef breeds were positive between net weight and conformation class, and negative between fat class with net weight and conformation class. Similarly, for the Holstein Friesian sired subset the genetic correlation between net weight and conformation class was positive, however different to beef sired breeds, the genetic correlation between conformation class and fat class was positive, and the relationship between net weight and fat was not different to zero (Table 26). Genetic correlations between age at slaughter and the three other traits were not significant in any of the within breed analyses.

These differences in genetic correlation trends for beef and dairy sired animals is not surprising since breeding goals differ for the two breed types and selection has gone in different directions. Since, Holstein Friesian sired animals contributed only 2 % of the across-breed data set it is not surprising that the trends are not similar in the two data sets. These differences between beef and dairy breeds have been reported in other studies. Hickey et al. (2007[3]) found all genetic correlations between net weight, conformation, and fat as positive in dairy animals. Whereas, the study of Kause et al. (2015[4]) on beef breeds found that the genetic correlation between conformation and fat was close to zero in Angus, Hereford, and Simmental, but negative in Charolais and Limousin breeds. Altarriba et al. (2009[5]) also found in the Pirenaica beef breed in Spain a negative genetic correlation between conformation and fat (-0.35) but the relationship between weight and fat was not different to zero.

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[3] Hickey, J.M., Keane, M.G., Kenny, D.A., Cromie, A.R., and Veerkamp, R.F. 2007. Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. Journal of Animal Science 85:314-321.

[4] Kause, A., Mikkola, L., Strandén, I., and Sirkko, K. 2015. Genetic parameters for carcass weight, conformation and fat in five beef cattle breeds. Animal 9:35-42.

[5] Altarriba, J., Yagüe, G., Moreno, C., and Varona, L. 2009. Exploring the possibilities of genetic improvement from traceability data: An example in the Pirenaica beef cattle. Livestock Production Science 125:115-120.

Table 26 Heritability estimates (highlighted on diagonal) and genetic correlations (below diagonal) from within-breed four-trait analyses

	Net weight	Conformation	Fat	Age
Aberdeen Angus				
Net weight	**0.30 (0.021)**			
Conformation	0.11 (0.061)	**0.21 (0.019)**		
Fat	**-0.26 (0.056)**	-0.06 (0.065)	**0.26 (0.021)**	
Age	0.05 (0.046)	-0.02 (0.054)	0.07 (0.049)	**0.54 (0.025)**
Charolais				
Net weight	**0.22 (0.042)**			
Conformation	**0.54 (0.118)**	**0.17 (0.039)**		
Fat	**-0.34 (0.139)**	-0.11 (0.155)	**0.23 (0.044)**	
Age	0.17 (0.119)	**0.39 (0.130)**	-0.02 (0.122)	**0.44 (0.054)**
Hereford				
Net weight	**0.29 (0.05)**			
Conformation	0.13 (0.132)	**0.20 (0.042)**		
Fat	-0.15 (0.111)	**-0.25 (0.126)**	**0.36 (0.047)**	
Age	0.003 (0.091)	0.14 (0.091)	0.07 (0.083)	**0.75 (0.053)**
Holstein Friesian[†]				
Net weight	**0.12 (0.045)**			
Conformation	**0.56 (0.191)**	**0.19 (0.051)**		
Fat	-0.09 (0.282)	**0.71 (0.175)**	**0.13 (0.045)**	
Age	0.20 (0.169)	-0.23 (0.144)	-0.09 (0.168)	**0.54 (0.066)**
Limousin				
Net weight	**0.23 (0.052)**			
Conformation	**0.32 (0.145)**	**0.28 (0.057)**		
Fat	**-0.44 (0.145)**	-0.55 (0.117)	**0.33 (0.058)**	
Age	0.21 (0.121)	-0.00 (0.119)	0.05 (0.110)	**0.58 (0.06)**
Simmental				
Net weight	**0.23 (0.039)**			
Conformation	0.21 (0.158)	**0.11 (0.032)**		
Fat	**-0.25 (0.121)**	-0.39 (0.151)	**0.30 (0.045)**	
Age	-0.10 (0.102)	-0.16 (0.138)	0.02 (0.094)	**0.73 (0.057)**

[†] Initially analysis did not converge. Analyses were run again to convergence but variances liable to change from P to B.

Table 27 Estimates for additive, residual, and phenotypic variances from within-breed four trait analyses

	Additive variance	Residual variance	Phenotypic variance
Aberdeen Angus			
Net weight	158.3 (12.09)	376.5 (9.57)	534.8 (5.23)
Conformation	1.3 (0.13)	5.2 (0.11)	6.5 (0.06)
Fat	2.4 (0.20)	6.7 (0.16)	9.1 (0.09)
Age	258.6 (14.17)	219.2 (10.37)	477.8 (5.41)
Charolais			
Net weight	122.7 (24.60)	427.8 (20.52)	550.5 (10.82)
Conformation	1.5 (0.36)	7.3 (0.31)	8.8 (0.17)
Fat	3.0 (0.63)	10.5 (0.52)	13.5 (0.27)
Age	167.8 (23.41)	216.7 (18.03)	384.5 (8.63)
Hereford			
Net weight	139.7 (23.47)	336.4 (18.83)	476.1 (10.20)
Conformation	1.2 (0.25)	4.5 (0.21)	5.7 (0.12)
Fat	3.3 (0.47)	5.7 (0.37)	9.0 (0.20)
Age	424.7 (38.93)	144.9 (27.46)	569.5 (14.92)
Holstein Friesian			
Net weight	55.3 (23.15)	401.0 (20.89)	456.4 (11.15)
Conformation	1.3 (0.37)	4.7 (0.31)	6.01 (0.16)
Fat	2.3 (0.82)	13.1 (0.72)	15.5 (0.38)
Age	349.7 (59.08)	341.1 (45.51)	690.8 (20.66)
Limousin			
Net weight	139.5 (33.90)	478.0 (27.31)	617.4 (13.16)
Conformation	3.2 (0.70)	8.3 (0.56)	11.5 (0.26)
Fat	5.4 (1.04)	11.2 (0.81)	16.5 (0.38)
Age	320.2 (39.81)	231.2 (29.5)	551.4 (13.94)
Simmental			
Net weight	137.7 (25.19)	465.5 (21.19)	603.2 (12.11)
Conformation	0.8 (0.27)	7.2 (0.25)	8.1 (0.15)
Fat	4.1 (0.66)	9.5 (0.53)	13.6 (0.29)
Age	223.8 (22.44)	83.6 (16.05)	307.4 (8.20)

The parameters estimated within-breeds tended to be comparable with those estimated from the across-breed data. The estimates for net weight tended to be lower from individual breed analyses than the across breed analyses. However, if sire breed was included in the across-breed analysis as an effect then results were more comparable. What is different is the phenotypic variances between sire breeds. This will need to be considered when producing the EBVs so that the top animals are not just the top animals of the breed with the biggest variance.

Genetic Parameter Estimation Summary

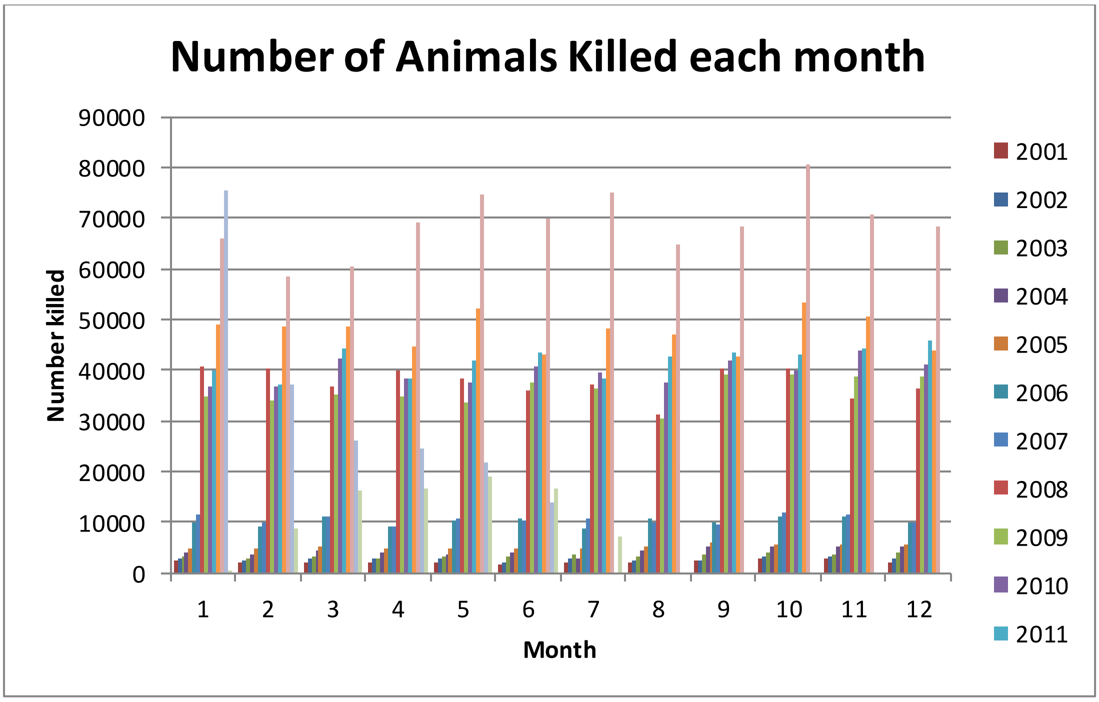
- Genetic parameters were estimated using a multivariate model with the traits net weight, conformation, fat, and age at slaughter to provide additive genetic and residual (co)variances for production of EBV's.
- All traits were moderate to highly heritable with sufficient genetic variation indicating that they are highly suitable traits for genetic improvement programs.
- Heritability estimates for net weight, conformation, fat, and age at slaughter were 0.40, 0.41, 0.45, and 0.63, respectively.
- Genetic parameter estimates differed among individual breeds, particularly between beef and dairy breeds. The proportions of different breeds in the across breed analysis do not mirror the national data due to differing levels of recording sire ID among breeds.

Preparation of a dataset for production of EBVs for carcass traits

Using the estimated genetic parameters and statistical models developed in previous section, Estimated Breeding Values (EBVs) were produced on an across breed dataset. The software package MiX99 (used for all national evaluations undertaken by EGENEs) was used to calculate the EBVs along with reliability/accuracy values. These EBVs have been developed such that systematic evaluations can be routinely undertaken post the current project. As such there is batch ids associated with each run and logging of all the relevant information. In October 2015, all the data was refreshed and the new Dawn Meats data included into the analyses. The EBVs and data presented in this report is based on this version of data. So the numbers reported will vary from those reported in previous sections of this report.

Data preparation for the production of EBVs was similar – but with limits relaxed - to that applied to estimate genetic parameters. The raw data file for EBV estimation contained 4,040,725 carcase records with the last abattoir data 11th September 2015.

The figure below shows that the number of animals slaughtered each calendar month is relatively stable, and this is also seen with in abattoirs (graphs not shown).



The number of records per abattoir varied as the size of the processing plants and the range of data varied.

Abattoir	A	B	C	D	E	F	G
N records	2,255,228	871,958	399,171	274,237	111,780	85,056	13,295

Animals have many breed codes and these are collapsed into breed groups where the breed codes relate to similar breeds. E.g. LIM, LIMX, LM, LMX, BLM are all collapsed into LIM. Where possible the data in the raw abattoir file was enriched and checked against other sources like BCMS for accuracy. For example a small number of abattoir dates suggested the animal was less than 0 at slaughter, these dates were updated with BCMS dates which gave sensible ages at slaughter. A series of data edits were undertaken and these are described in table 28.

Table 28 Summary of edits/deletions (in order of application) to create a dataset for genetic evaluation

Edits	Count
Duplicate eartags in abattoir data	2
More than 10 days difference in kill date in BCMS and abattoir	1,603
Sex information missing	40
Age at slaughter < 0 or missing	44
Age at slaughter < 365 days (12m)	463,493
Age at slaughter > 1095 days (36m)	446,393
Carcase weight <0 kg	786
Conformation class missing or not in the allowed values	4
Fat class was null, missing or 0	2,206
Not a prime slaughter animal (H, S or YB)	15,165
Dam <540 days (18m) at calving	52,320
No BCMS id	1,185
Dam missing birth date	31,585
Unknown dam	1,428
Unknown sire AND maternal grand sire unknown	1,538,102
Outside +/-3sd for carcase weight (within sire breed, category and age group)	8,690
Outside +/-3sd for ADCG (within sire breed, category and age group)	3,052
No bcms birth record	10,678
Died in their birth herd	0
No off record from birth herd	0
Last BCMS movement was not death (and animal not killed in 2015)	11,722
Finish herd was unable to be assigned as death herd (for 2015 killed animals)	133
Spent <14 days in their finishing herd	132,632
Kill Location not a slaughter house	122
Animals not spent at least 60 days in finishing herd	91
Birth herd-year-season with less than 3 animals	225,582
Finishing herd-year-season with less than 3 animals	31,651

After edits 1,032,191 records remained. A three generation pedigree was built using combined data from all available sources and this resulted in a pedigree file with 2,416,966 animals.

The number of records per abattoir after edits is below, note sorted by size so the Abattoir letter may not be the same as previously reported.

Abattoir	**A**	**B**	**C**	**D**	**E**	**F**	**G**
N records	463,784	336,106	134,485	47,041	34,340	11,415	5,020

Of the edited carcase data, 412,052 had a missing sire (but must have had a known maternal grand sire to remain in the analysis. The breeds that had the highest number of missing sires were Angus, Holstein, Limousin, Belgian Blue, Hereford, Charolais and Simmental; basically the main breeds represented in the data.

Table 29 summarises the number of records (with known sires) and the number of sires represented for each breed with 100+ records. In total there are 43,413 different sires from 34 different breed groups. There is a much higher representation of Angus and Hereford than you would expect. This is due to the abattoirs participating and the markets they target, and because sires are generally recorded more in native breeds due to incentives such as the native breed schemes.

Table 29 Summary of the number of animals and sires in the dataset for genetic evaluation grouped by sire breed

Sire Breed	Breed Grp ID	No. Animals	No. Sires	Sire Breed	Breed Grp ID	No. Animals	No. Sires
Aberdeen Angus	1	300677	9425	Ayrshire	6	2533	136
Limousin	55	158095	8837	Brown Swiss	21	1449	74
Holstein Friesian	12	134825	4631	Lincoln Red	56	1423	109
Charolais	29	99863	4904	Galloway	42	1242	192
Hereford	49	97296	3689	Swedish Red & White	82	1171	27
Simmental	80	74139	3904	dairy shorthorn	27	1137	71
Belgian Blue	98	63358	1264	Highland Luing	50	1086	170
Blonde D'Aquitaine	7	19741	1149	Norwegian Red	66	955	11
British Friesian	13	12344	508	Meuse Rhine Issel	63	896	58
South Devon	77	9844	901	Longhorn	54	890	94
Stabilisers	83	8232	520	Red Poll	74	566	64
beef shorthorn	26	8285	841	Gelbvieh	46	536	49
Salers	75	7585	490	Jersey	52	460	69
Welsh Black	90	5721	469	Piemontese	69	422	48
Montbeliarde	62	3332	140	British White White Park	24	365	45
Sussex	84	3159	219	Murray Grey	61	233	27
Devon	35	2749	262	Gloucester	47	122	16

Scaling phenotypic variances

While it is expected that there will be breed differences due to the genetics of different breeds the variation within breeds should be similar as we know that often there is as much variation within breeds as there are across breeds. In order for the resulting EBVs not to be influenced due to differences in variances the phenotypes were scaled such that the phenotypic variances for all breeds are the same as native beef breeds. In order for this adjustment to be based on robust data, adjustments were done within breed type and category.

The following table shows the raw summary of the data before scaling.

Breed type*	Cat	N	A(wt)	S(wt)	A(age)	S(age)	A(con)	S(con)	A(fat)	S(fat)
1	H	6845	289	41.9	847	136.1	13	4.2	27	6
2	H	132576	281	31	727	118.5	19	3.6	31	4.1
3	H	157383	314	37.1	733	127.7	24	4.6	28	4.7
4	H	790	308	34.8	770	114.4	21	3.9	28	5.4
1	S	89593	320	39.3	800	128.8	13	3.2	25	4.8
2	S	294580	326	37.2	749	115.5	20	3.8	30	3.9
3	S	214143	367	44.8	763	120.5	25	4.8	27	5
4	S	509	348	40	776	117.3	21	4.7	27	5.1
1	YB	63956	281	33.6	472	64.1	13	3.2	20	5.9
2	YB	17813	326	45.2	464	70.9	24	4.9	26	5.4
3	YB	53860	362	50.6	473	63.7	28	6.1	22	6
4	YB	143	314	44.9	458	63.6	20	7	22	5.7

*** breed type 1 (dairy), 2 (native beef), 3 (continental beef) and 4 (other)**

Records were scaled on an individual basis for each trait using the following formula where i is the appropriate breed and category and j is the appropriate category but breed type=2

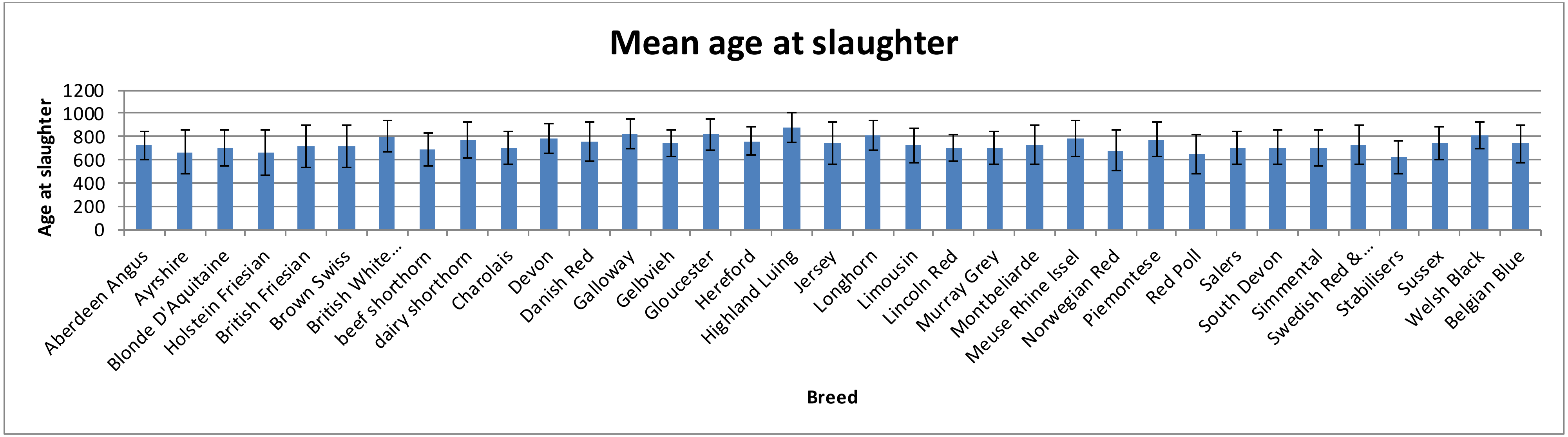
Scaled phenotype = Average(i) + [(phenotype – average(i)) * (std(j)/std(i))]

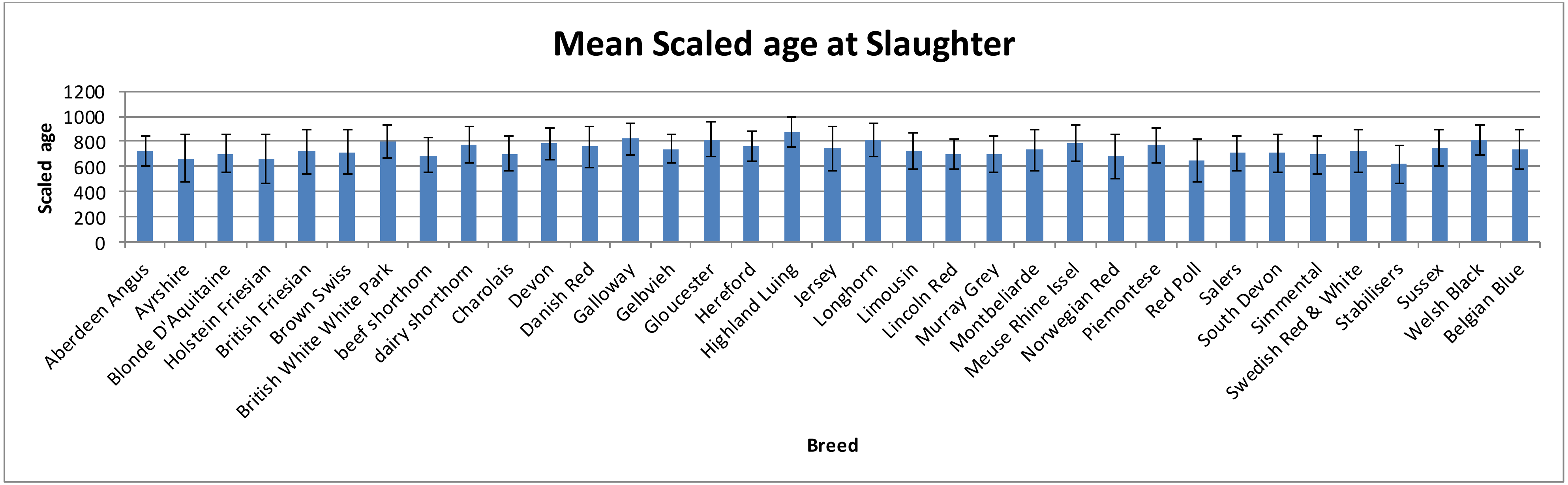
The following table shows the summary stats after scaling has occurred

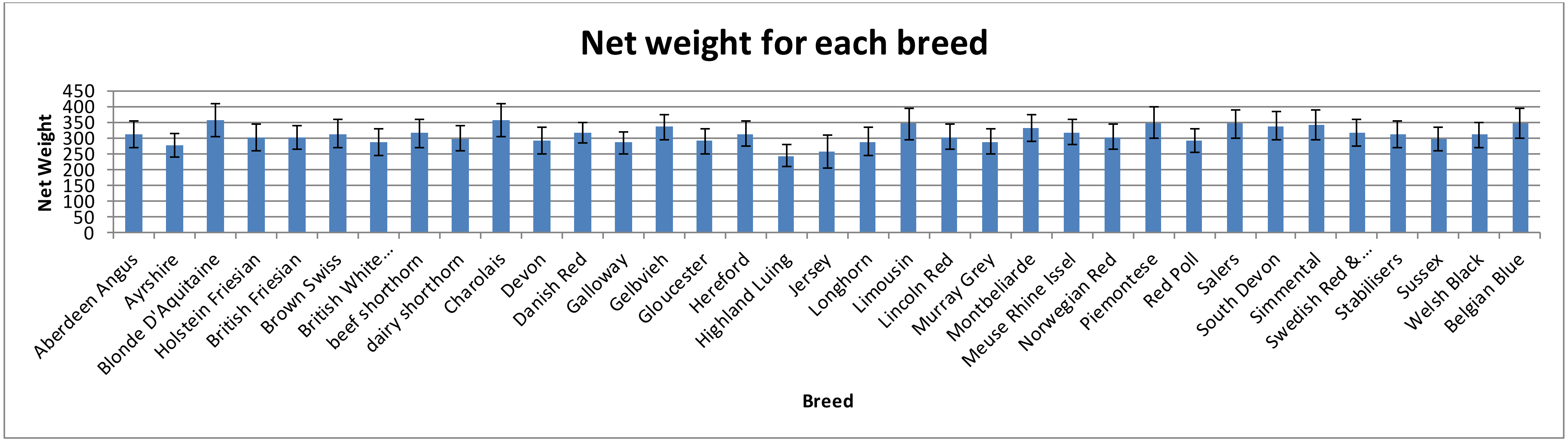
Breed type*	Cat	N	A(wt)	S(wt)	A(age)	S(age)	A(con)	S(con)	A(fat)	S(fat)
1	H	6845	288	31	846	118.5	12	3.6	26	4.4
2	H	132576	281	31	727	118.5	19	3.6	31	4.1
3	H	157383	313	31	733	118.5	23	3.5	28	4
4	H	790	308	31	769	118.5	20	3.5	27	4.2
1	S	89593	319	37.2	799	115.5	12	3.7	25	4
2	S	294580	326	37.2	749	115.5	20	3.8	30	3.9
3	S	214143	367	37.2	762	115.5	24	3.7	26	4.1
4	S	509	348	37.2	775	115.6	20	3.9	26	4
1	YB	63956	280	45.2	471	70.9	12	4.8	20	5.3
2	YB	17813	326	45.2	464	70.9	24	4.9	26	5.4
3	YB	53860	362	45.2	472	70.9	28	5	21	5.5
4	YB	143	313	45.3	458	71	20	5	21	5.3

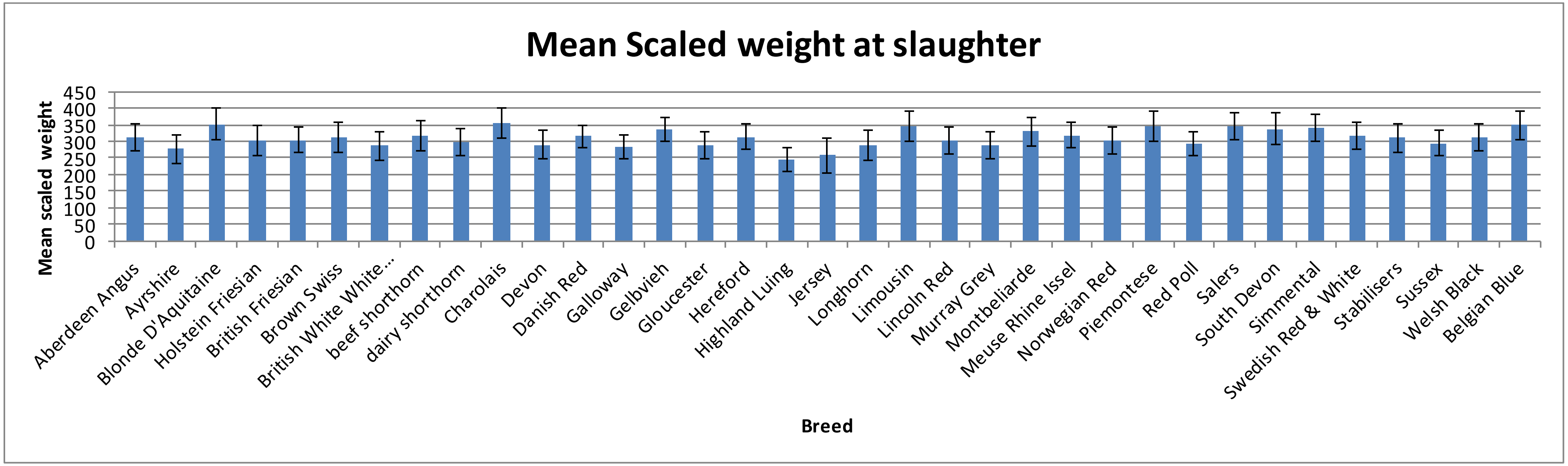
*** breed type 1 (dairy), 2 (native beef), 3 (continental beef) and 4 (other)**

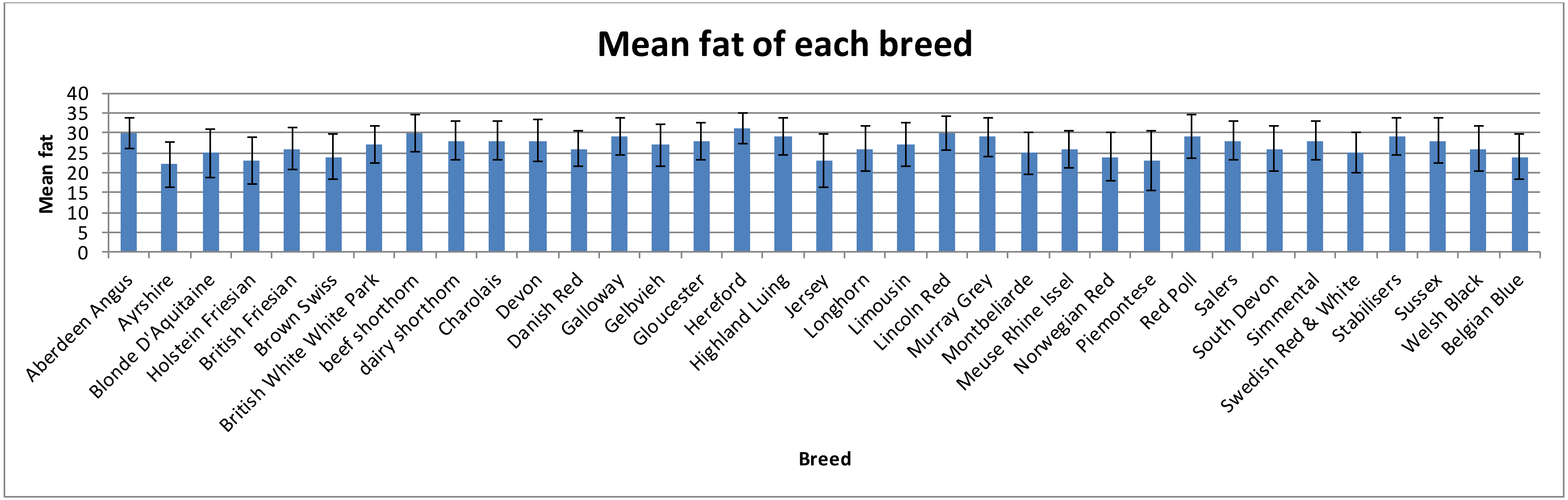
The following series of figures compare phenotypes for different breeds, the error bars are +- 1 standard deviation.

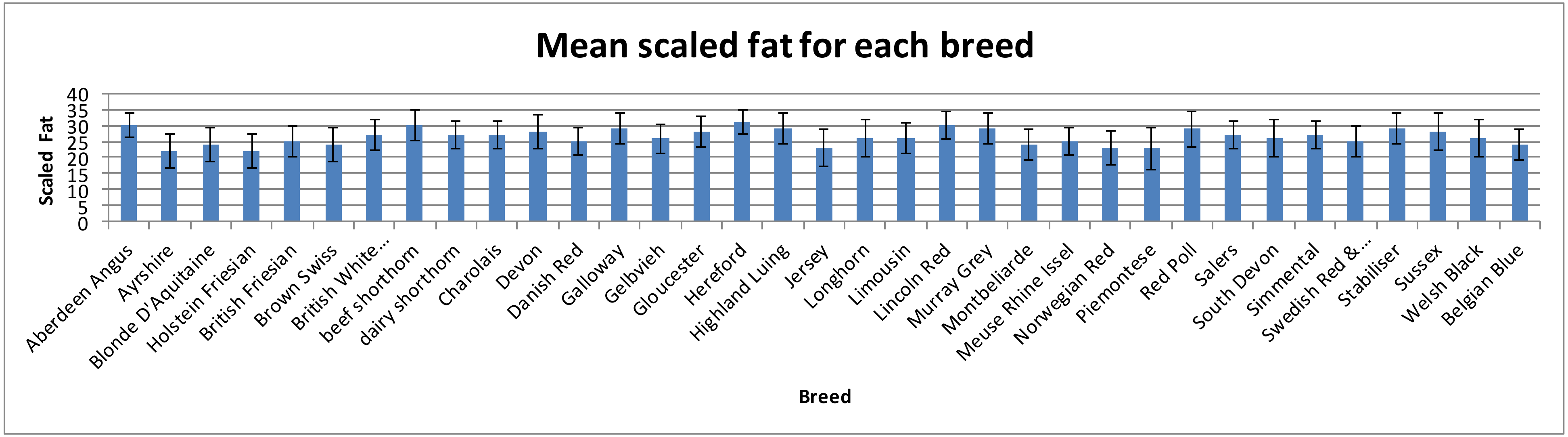

Mean age at slaughter
Age at slaughter
1200
1000
800
600
400
200
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White…
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red &…
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed

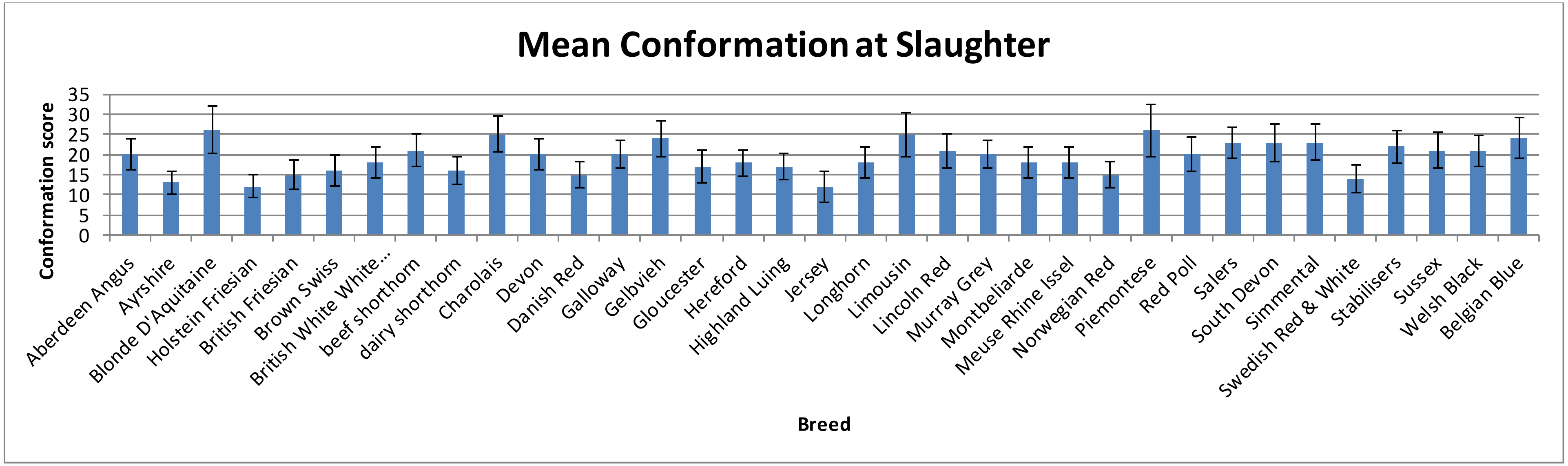

Mean Scaled age at Slaughter
Scaled age
1200
1000
800
600
400
200
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White Park
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red & White
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed

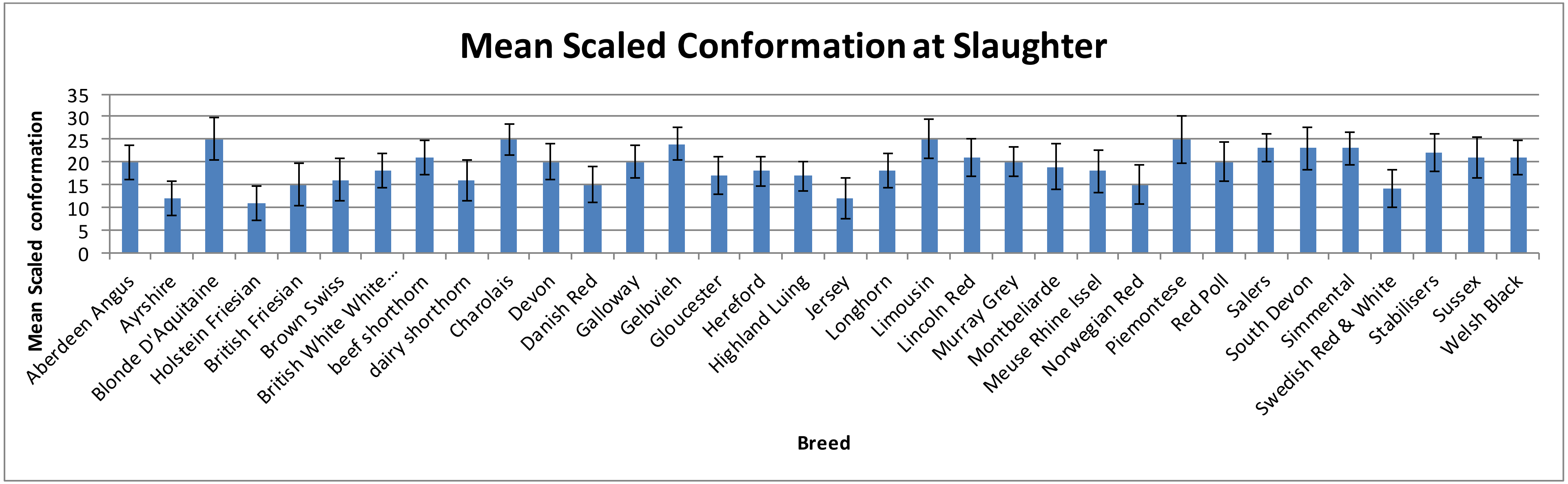

Net weight for each breed
Net Weight
450
400
350
300
250
200
150
100
50
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White…
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red &…
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed

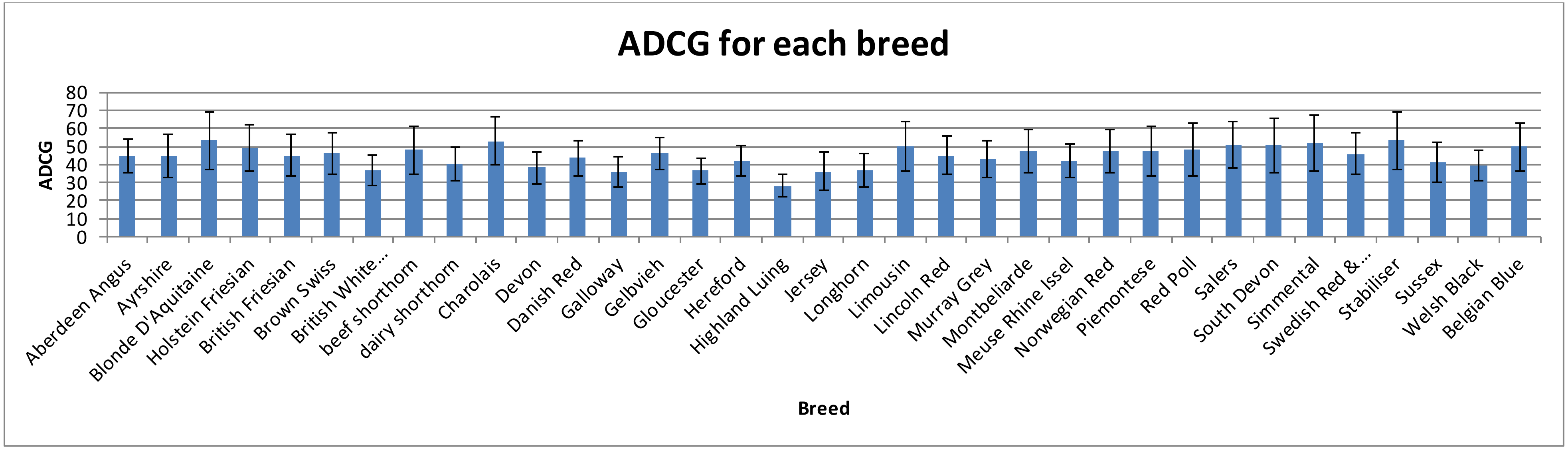

Mean Scaled weight at slaughter
Mean scaled weight
450
400
350
300
250
200
150
100
50
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White White…
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red & White
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed

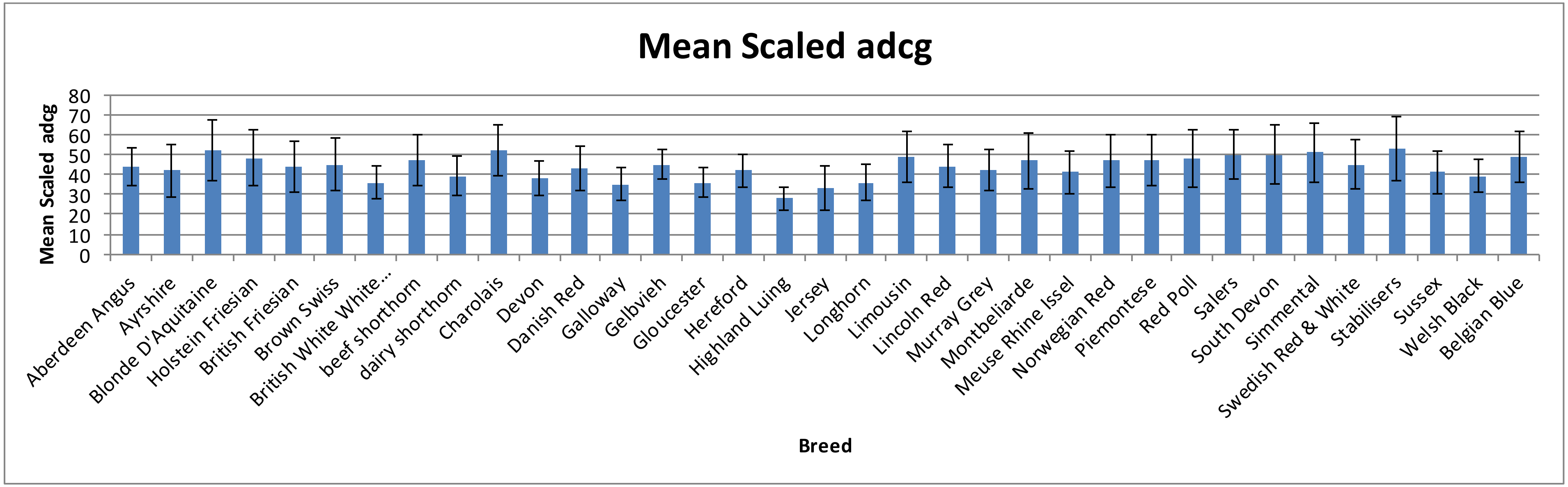

Mean fat of each breed
Mean fat
40
35
30
25
20
15
10
5
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White White Park
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red & White
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed


Mean scaled fat for each breed
Scaled Fat
40
35
30
25
20
15
10
5
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White…
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red &…
Stabiliser
Sussex
Welsh Black
Belgian Blue
Breed


Mean Conformation at Slaughter
Conformation score
35
30
25
20
15
10
5
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White White...
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red & White
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed


Mean Scaled Conformation at Slaughter
Mean Scaled conformation
35
30
25
20
15
10
5
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White White...
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red & White
Stabilisers
Sussex
Welsh Black
Breed


ADCG for each breed
ADCG
80
70
60
50
40
30
20
10
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White...
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red &...
Stabiliser
Sussex
Welsh Black
Belgian Blue
Breed


Mean Scaled adcg
Mean Scaled adcg
80
70
60
50
40
30
20
10
0
Aberdeen Angus
Ayrshire
Blonde D'Aquitaine
Holstein Friesian
British Friesian
Brown Swiss
British White White...
beef shorthorn
dairy shorthorn
Charolais
Devon
Danish Red
Galloway
Gelbvieh
Gloucester
Hereford
Highland Luing
Jersey
Longhorn
Limousin
Lincoln Red
Murray Grey
Montbeliarde
Meuse Rhine Issel
Norwegian Red
Piemontese
Red Poll
Salers
South Devon
Simmental
Swedish Red & White
Stabilisers
Sussex
Welsh Black
Belgian Blue
Breed

Statistical models and genetic parameters

The statistical models were those used for genetic parameters estimation with methodology for accounting for heterosis and recombination coefficients included. More details are in the previous sections of this report, but in brief to model heterosis, cross breed animals within dairy, beef and dairy crosses were considered as 3 separate breed types. The heterosis/recombination coefficients (In this case 3 different coefficients) were included in the model as covariates.

In addition work undertaken at the later stages of the project revised the models slightly from those developed in the earlier stages of the project. The changes were that age at slaughter would also be adjusted for carcass weight and EUROP fat class and age at slaughter added as a covariate for the weight and EUROP traits. We considered nesting some of the fixed effects within breed types but the results obtained did not yield sensible comparisons so this was not implemented.

For all traits the following model was fitted where F means it was a fixed class effect, C fitted as a co-variate effect and R as a random effect.

Trait = Category (F) +
abattoir (F) +
killdate/location (F) +
category * KillHerdYearSeason (F) +
location * KillHerdYearSeason (F) +
BirthHerdYearSeason (F) +
Dam Age Class (F) +
Once Bred heifer (F) +
Heterosis (C) + recombination (C) +
Age at slaughter (linear and quadratic)#! (C) +
percentage of dairy dam# (C) +
carcass weight at slaughter% (C) +
EUROP fat class at slaughter% (C) +
Animal (R)
= not included for age at slaughter; !=not included for average daily carcass gain; % only fitted for age at slaughter

Genetic parameters were as described it the previous section of this report, where co-variances came from the 4 way multiple trait model and variances were those from the uni-variant analysis.

Enriching the super pedigree with additional sources of information

The addition of pedigree from the purebred pedigree beef breeds performance recording with ABRI has also been built into the systems so that they can be included and enrich the depth of pedigree (and this quality of EBVs) for these breeds. To date pedigree from beef Shorthorn, Charollais and Hereford have been included and it is a relatively simple exercise to include additional breeds in the future. In addition the beef Shorthorn data has been invaluable in helping to resolve and differentiate beef and dairy Shorthorn animals recorded in BCMS where at times it is not clear which is which.

Estimated Breeding Values for Carcass traits

There have been many different sets of EBVs and for simplicity the final set, and the first official set of carcass traits EBVs produced October 2016 will be here.

Details of final set of EBVs for release to industry

General overview

EBVs were produced for 2,926,294 animals that were found in a 5 generation pedigree where the base animals were those with abattoir carcass data available for genetic evaluation. The following table shows the distributions of the EBVs and accuracies for all animals receiving EBVs.

	EBVs				**Accuracy**			
	avg	**sd**	**min**	**max**	**avg**	**sd**	**min**	**max**
SLAUGHTER AGE	1.42	14.51	-159.01	167.61	0.34	0.39	0	0.99
CARCASS WEIGHT	0.24	8.83	-73.82	73.51	0.29	0.34	0	0.99
CONFORMATION	-0.02	1.24	-9.00	9.36	0.30	0.35	0	0.99
FAT	-0.07	1.49	-11.81	9.87	0.31	0.36	0	0.99
ADCG	0.00	0.02	-0.20	0.20	0.32	0.37	0	0.99

MiX99 fixed effect solutions

The following section reports the MiX99 solutions for the different effects. These solutions all come from the final model Batch 43.

The raw un-based genetic group solutions from the analysis are shown in the table below. Compared to the beef breeds, dairy animals had groups solutions with higher ages at slaughter. Continental breeds have the higher carcase weight, conformation and average daily carcass gain. Dairy breeds were heavier than native beef, but similar conformation for the heavier weight. Native beef had the most fat cover, with continental beef the least.

Table Genetic groups solutions (un rebased) from the MiX99 analysis

Trait	**dairy**	**native**	**continental**	**other**
number	999999+	280889	356126	10785
Slaughter Age	15.88	10.20	11.20	14.98
Net Weight	0.50	-5.80	6.90	-6.02
Conformation	-0.31	-0.33	1.13	-1.09
Fat	-0.23	1.71	-0.96	0.31
ADCG	-0.52	-0.79	0.84	-1.33

We can see that young bulls (YB) are slaughtered younger but at similar weights to steers, with more muscle, less fat and a faster growth rate. Compared with Steers, heifers are slaughter 9 days older, have lighter carcasses that receive almost the same conformation class, but with great levels of fat. For dam age classes we see similar MiX99 solutions for all levels of age. Once-bred heifers are typically older at slaughter, but were slightly heavier compared to heifers but with a slight reduction in conformation, fat and ADCG.

Table Fixed effect Solutions (un rebased) from the MiX99 analysis for category

SEX	number	Slaughter Age	Net Weight	Conformation	Fat	ADCG
H	355202	102.0	5.7	1.4	5.1	3.6
S	707621	93.2	19.0	1.7	3.2	5.9
YB	147674	39.2	20.6	2.5	1.5	11.3

Table Fixed effect Solutions (un rebased) from the MiX99 analysis for dam age

DamAge Class	number	Slaughter Age	Net Weight	Conformation	Fat	ADCG
1	233588	92.8	13.3	1.5	3.7	5.3
2	510394	88.8	16.2	1.7	3.5	6.1
3	302466	87.9	16.2	1.7	3.5	6.1
4	164049	87.7	13.6	1.6	3.6	5.8

Table Fixed effect Solutions (Not rebased) from the MiX99 analysis for once bred heifer status

OBH	number	Slaughter Age	Net Weight	Conformation	Fat	ADCG
OBH	2543	118.7	10.8	1.0	1.0	3.3
H	352668	80.7	6.6	1.7	1.7	5.0
S/YB	855286	92.7	18.9	1.7	4.3	6.3

Table Fixed effect Solutions (Not rebased) from the MiX99 analysis for percent dairy in dam and slaughter age fitted as covariates

covariate	Slaughter Age	Net Weight	Conformation	Fat	ADCG
% dairy in dam		-0.13	-0.07	-0.004	-0.02
Slaughter age (l)		0.64	0.03	0.001	
Fat class	0.09				
Carcass weight	-0.02				

Biggest changers

EBVs from batch 42 were compared with batch 40 and the biggest changers were considered for each trait. In all cases the changes occurred involved sires of cross bred animals where the different ways of grouping breeds/breed types for modelling hybrid vigour had a direct impact. Any changes between batch 42 and 43 are the direct result of new carcass data.

Sires with 10+ progeny with carcass traits

In the dataset there were 53,581 distinct sires, 18,389 had more than 10 progeny. The average number of progeny with carcass records was 14 and ranged from 1 to 1,697. The bull with the most carcass progeny was '01000000059817211M' Picston Shottle with 1,697 progeny slaughtered, the next more numerous sire was '210030230730037611M' with 1,388 progeny, this is an 2007 born Angus sire 'NIGHTINGALE PLOUGHMAN G376', a bull marketed by Genus for AI.

Comparisons within breed groups

To make comparisons with different breeds, pure-bred animals with a slaughter record were considered to ensure comparisons are fair and the comparisons only include those EBVs with sufficient accuracy (0.2+ for all traits).

A summary of the average EBV for the more numerous breed groups (300+ records) are shown in the Table below.

Table Summary of EBVs for the more numerous breed groups

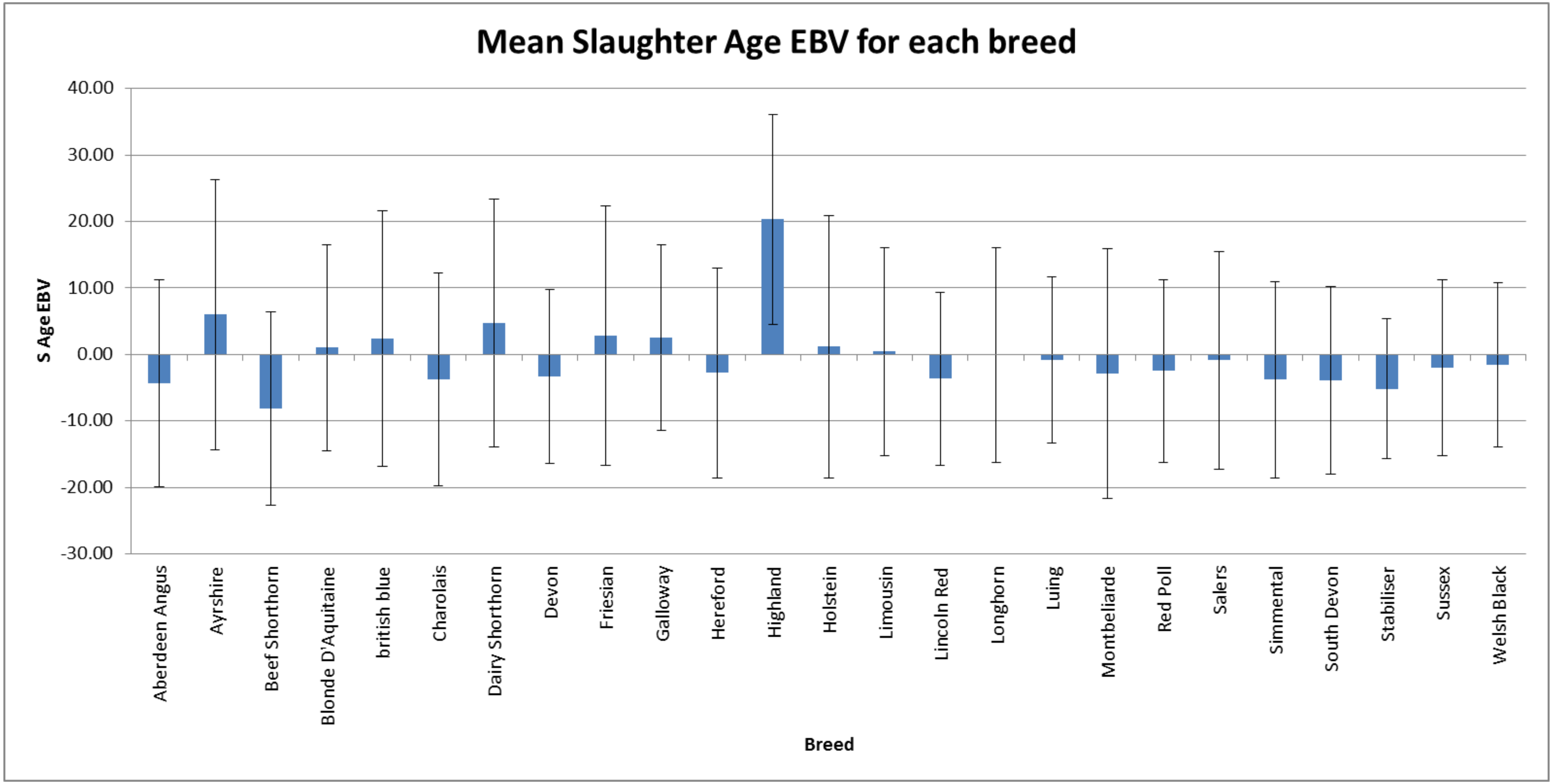
Breed Group				EBV		
	N	Sage*	Cwt*	Conf*	Fat*	ADCG*
Holstein	50107	1.15	0.92	-0.90	-0.24	0.0006
Aberdeen Angus	47429	-4.39	-7.93	-0.37	2.16	-0.0060
Limousin	32538	0.42	8.02	2.27	-1.65	0.0110
Simmental	15387	-3.80	5.25	1.12	-0.86	0.0096
Hereford	11073	-2.77	-10.68	-0.93	2.19	-0.0118
Charolais	9750	-3.80	15.13	1.61	-1.74	0.0258
South Devon	5733	-3.94	-1.38	0.08	0.42	0.0031
Welsh Black	4348	-1.55	-9.29	-0.35	1.76	-0.0106
Beef Shorthorn	3861	-8.14	-9.85	-0.85	2.24	-0.0065
Salers	2588	-0.89	4.23	0.82	-0.76	0.0062
Luing	2461	-0.86	-8.95	-0.50	1.95	-0.0107
Stabiliser	1750	-5.17	-3.69	0.28	1.49	0.0001
Blonde D'Aquitaine	1635	1.01	13.14	2.41	-3.51	0.0203
Devon	1172	-3.27	-12.76	-0.47	1.95	-0.0144
Highland	1110	20.31	-25.81	-1.41	1.86	-0.0513
Galloway	1078	2.51	-11.09	-0.44	1.71	-0.0152
Sussex	978	-2.02	-12.57	-0.24	2.08	-0.0168
Lincoln Red	924	-3.66	-12.92	-0.37	2.26	-0.0143
Ayrshire	834	6.01	-11.12	-0.45	-0.37	-0.0238
Friesian	655	2.81	-2.14	0.07	-0.01	-0.0070
Longhorn	651	-0.13	-9.85	-0.46	1.78	-0.0124
Montbeliarde	549	-2.88	2.55	1.93	-0.98	0.0075
british blue	517	2.40	10.37	2.43	-2.38	0.0129
Dairy Shorthorn	462	4.70	-7.65	-1.61	0.80	-0.0182
Red Poll	360	-2.49	-12.88	-0.57	1.97	-0.0158

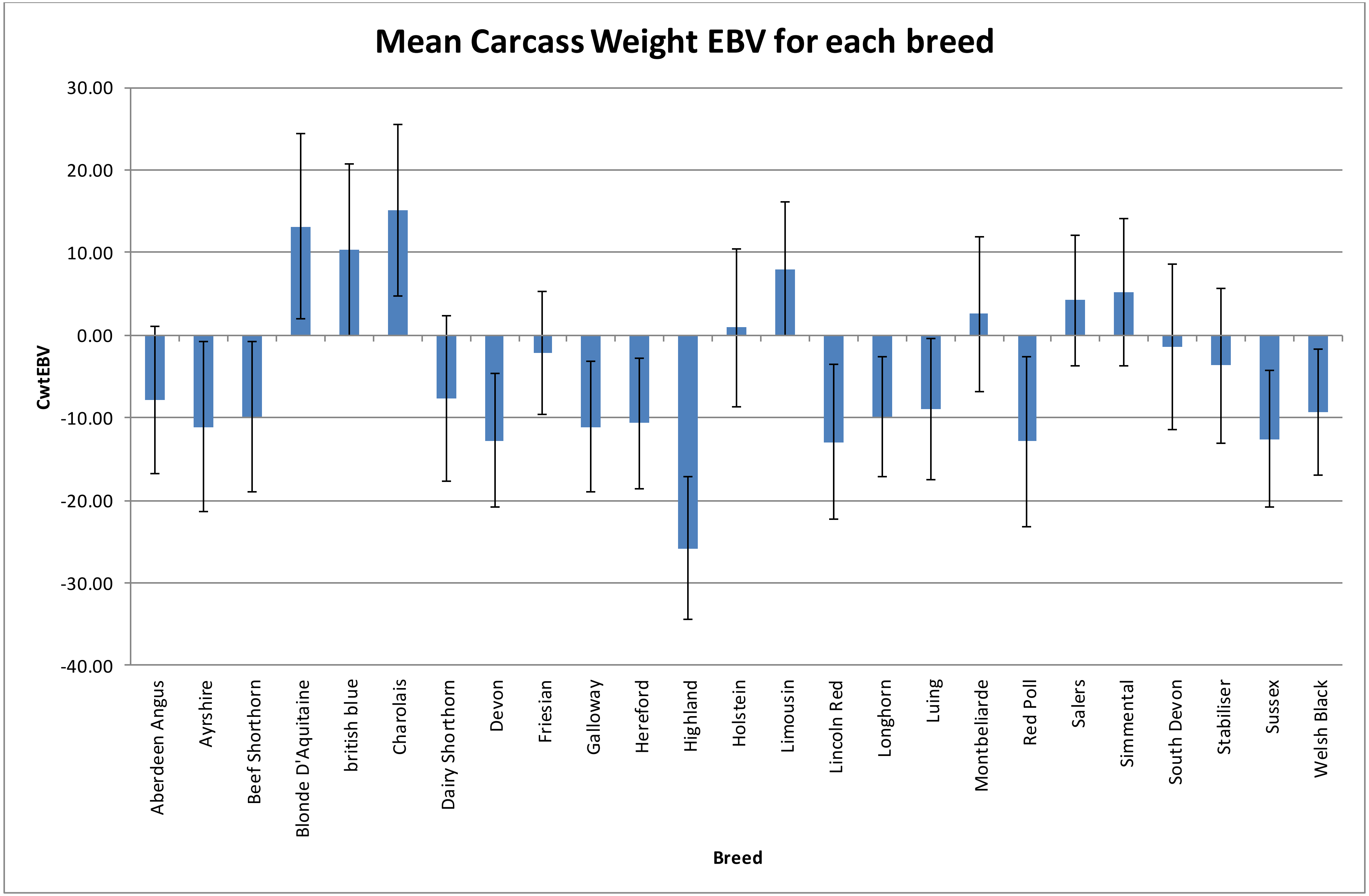
* Sage = slaughter age, cwt= carcass weight, conf= EUROP conformation, fat= EUROP fat and ADCG= average daily carcass gain. Cwt, conf and fat are adjusted for age and slaughter age has been adjusted for carcase weight and fat..

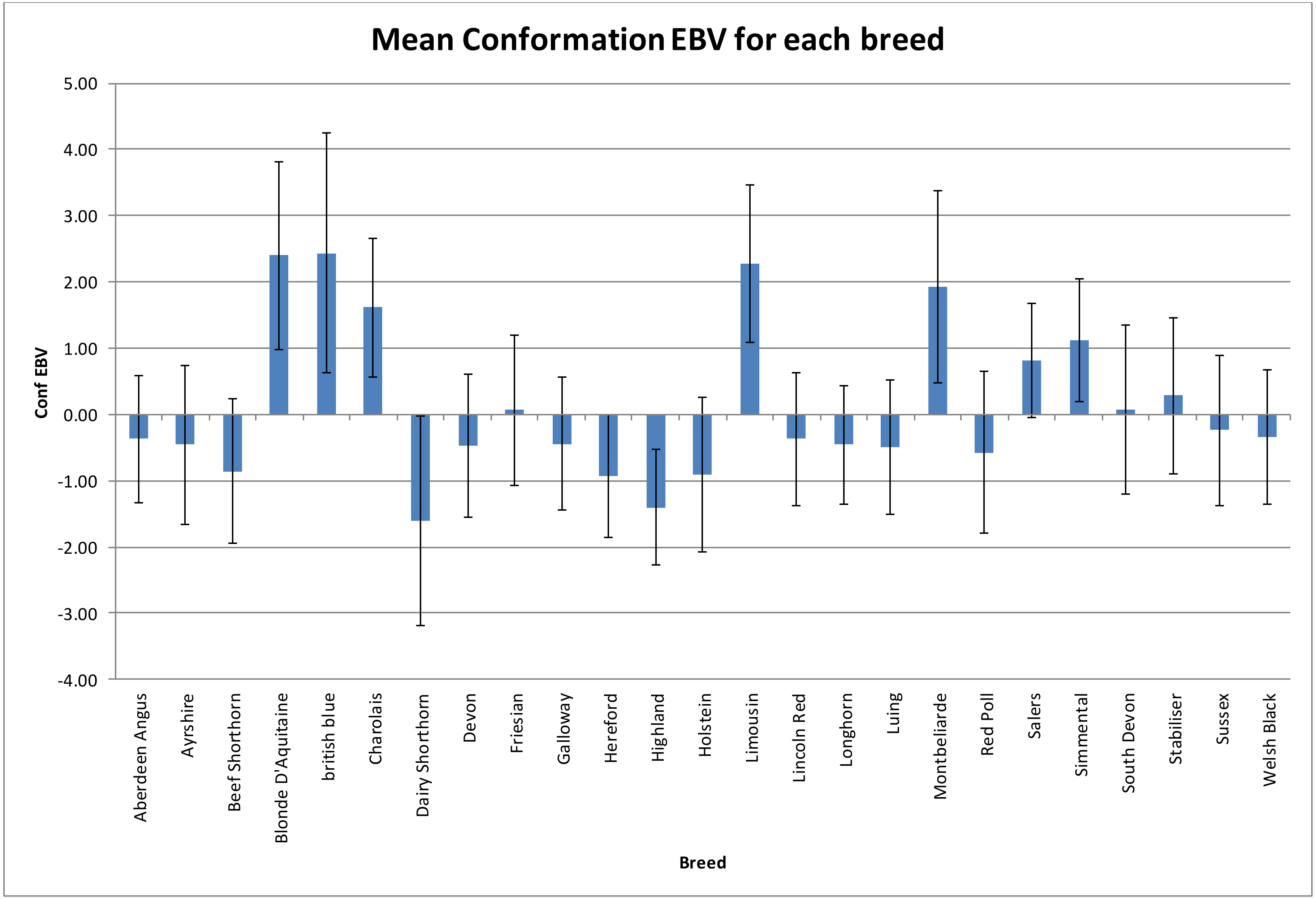
In all cases the average accuracy values were the same; 0.80, 0.68, 0.70, 0.73 and 0.74 for slaughter age, carcase weight, conformation, fat and average daily carcase gain. The reason why the average accuracy is the same for all breeds is due to the inclusion criteria; these are all animals which have their own carcase records so the same amount of information.

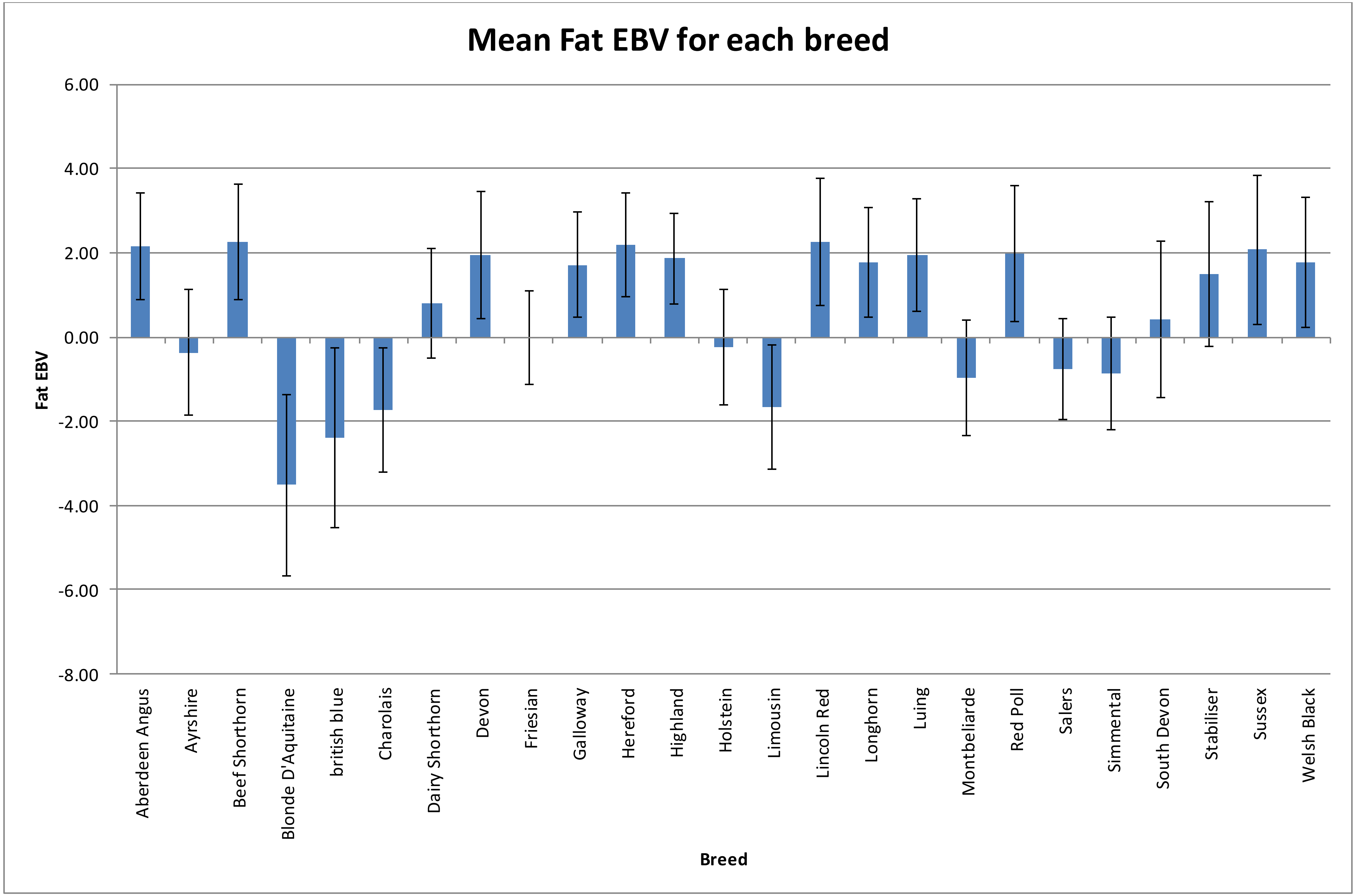
The following graphs plot the average and standard deviations (error bars represent ± one standard deviation) per sire breed for each trait (numbers as per the table above). For slaughter age generally the breeds with shorter ages to slaughter are beef breeds (i.e. Beef Shorthorn, Stabiliser, Angus, South Devon, Simmental and Charolais. Dairy breeds tended to have longer days to slaughter, although the longest age at slaughter was Highland cattle. The difference between the top and bottom breed average (ignoring Highland) was 14 days.

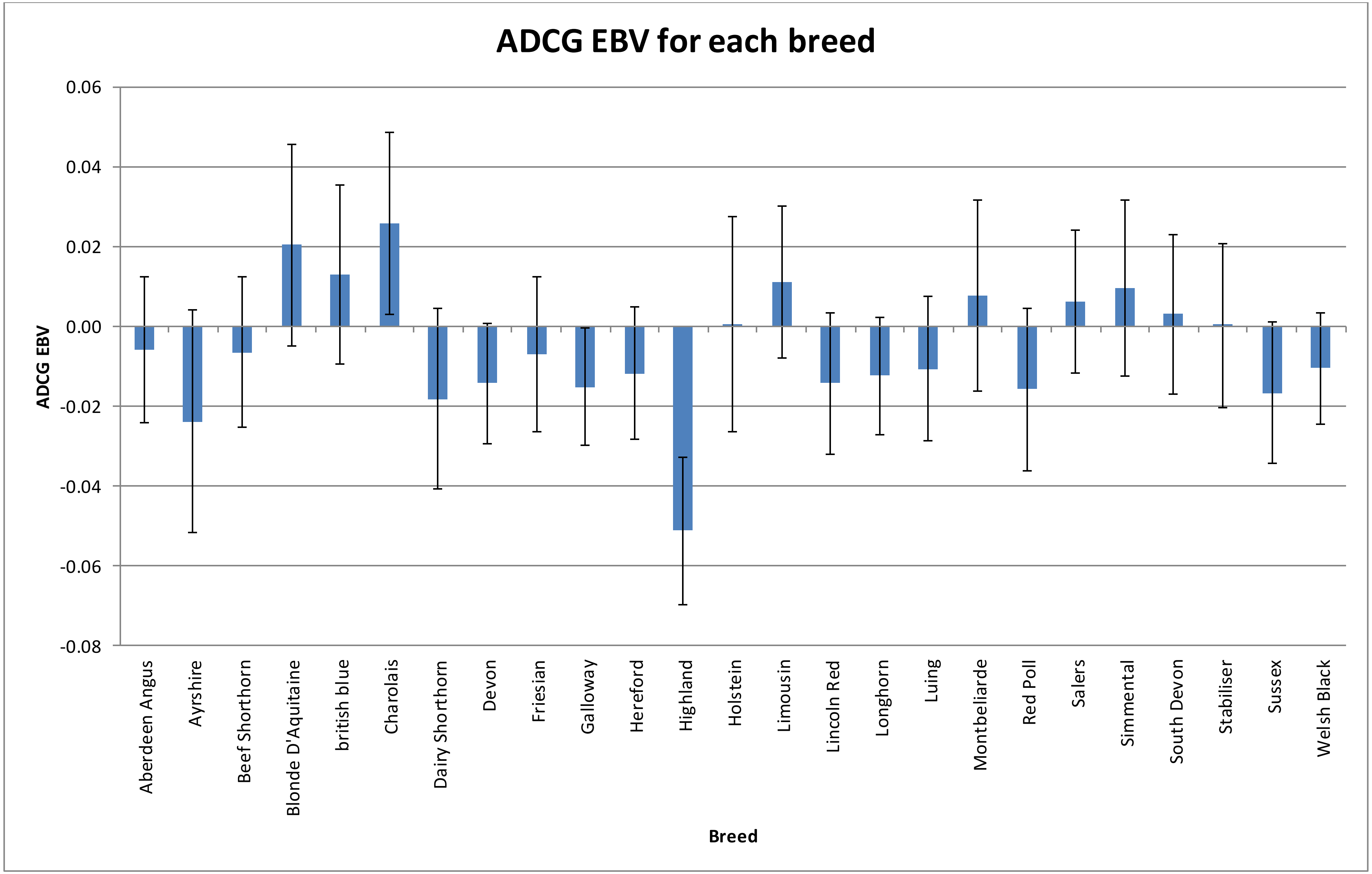
For carcase weight, continentals are have the higher EBVs, followed by dairy then native beef breeds. This was similar for conformation, although there was less of a distinction between the dairy and native beef breeds. Native beef breeds had genetics for increased fat, with continental the leanest. The continental cattle had faster growth rates compared with dairy and native beef. Native beef breeds all tended to have similar growth rates, but we do see variation in the dairy breeds with breeds like Montbeliarde ranking after the continentals and Ayrshire having some of the slowest growth rates (apart from Highland cattle).


Mean Slaughter Age EBV for each breed
S Age EBV
40.00
30.00
20.00
10.00
0.00
-10.00
-20.00
-30.00
Aberdeen Angus
Ayrshire
Beef Shorthorn
Blonde D'Aquitaine
british blue
Charolais
Dairy Shorthorn
Devon
Friesian
Galloway
Hereford
Highland
Holstein
Limousin
Lincoln Red
Longhorn
Luing
Montbeliarde
Red Poll
Salers
Simmental
South Devon
Stabiliser
Sussex
Welsh Black
Breed


Mean Carcass Weight EBV for each breed
CwtEBV
30.00
20.00
10.00
0.00
-10.00
-20.00
-30.00
-40.00
Aberdeen Angus
Ayrshire
Beef Shorthorn
Blonde D'Aquitaine
british blue
Charolais
Dairy Shorthorn
Devon
Friesian
Galloway
Hereford
Highland
Holstein
Limousin
Lincoln Red
Longhorn
Luing
Montbeliarde
Red Poll
Salers
Simmental
South Devon
Stabiliser
Sussex
Welsh Black
Breed


Mean Conformation EBV for each breed
Conf EBV
5.00
4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
Aberdeen Angus
Ayrshire
Beef Shorthorn
Blonde D'Aquitaine
british blue
Charolais
Dairy Shorthorn
Devon
Friesian
Galloway
Hereford
Highland
Holstein
Limousin
Lincoln Red
Longhorn
Luing
Montbeliarde
Red Poll
Salers
Simmental
South Devon
Stabiliser
Sussex
Welsh Black
Breed

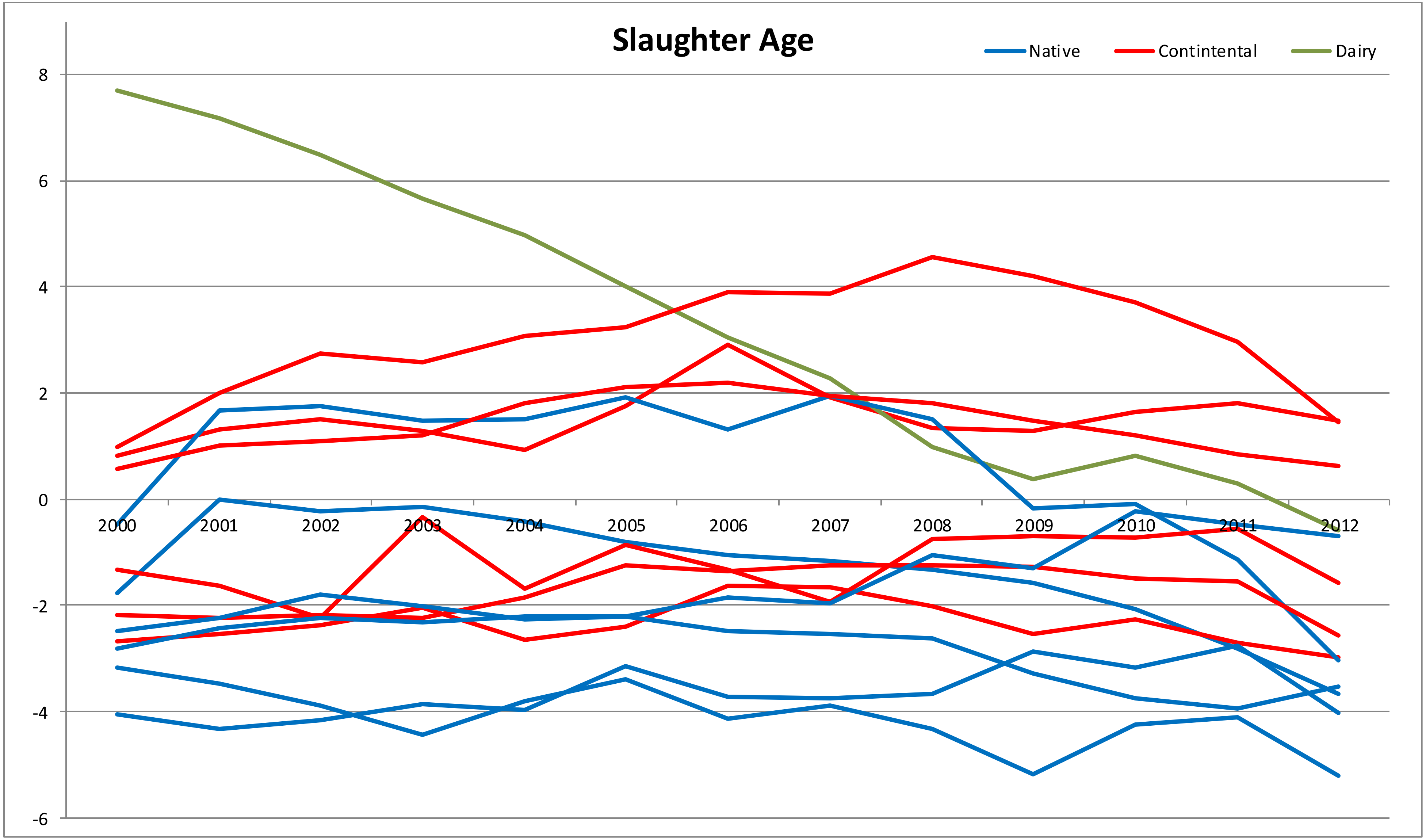

Mean Fat EBV for each breed
Fat EBV
6.00
4.00
2.00
0.00
-2.00
-4.00
-6.00
-8.00
Aberdeen Angus
Ayrshire
Beef Shorthorn
Blonde D'Aquitaine
british blue
Charolais
Dairy Shorthorn
Devon
Friesian
Galloway
Hereford
Highland
Holstein
Limousin
Lincoln Red
Longhorn
Luing
Montbeliarde
Red Poll
Salers
Simmental
South Devon
Stabiliser
Sussex
Welsh Black
Breed

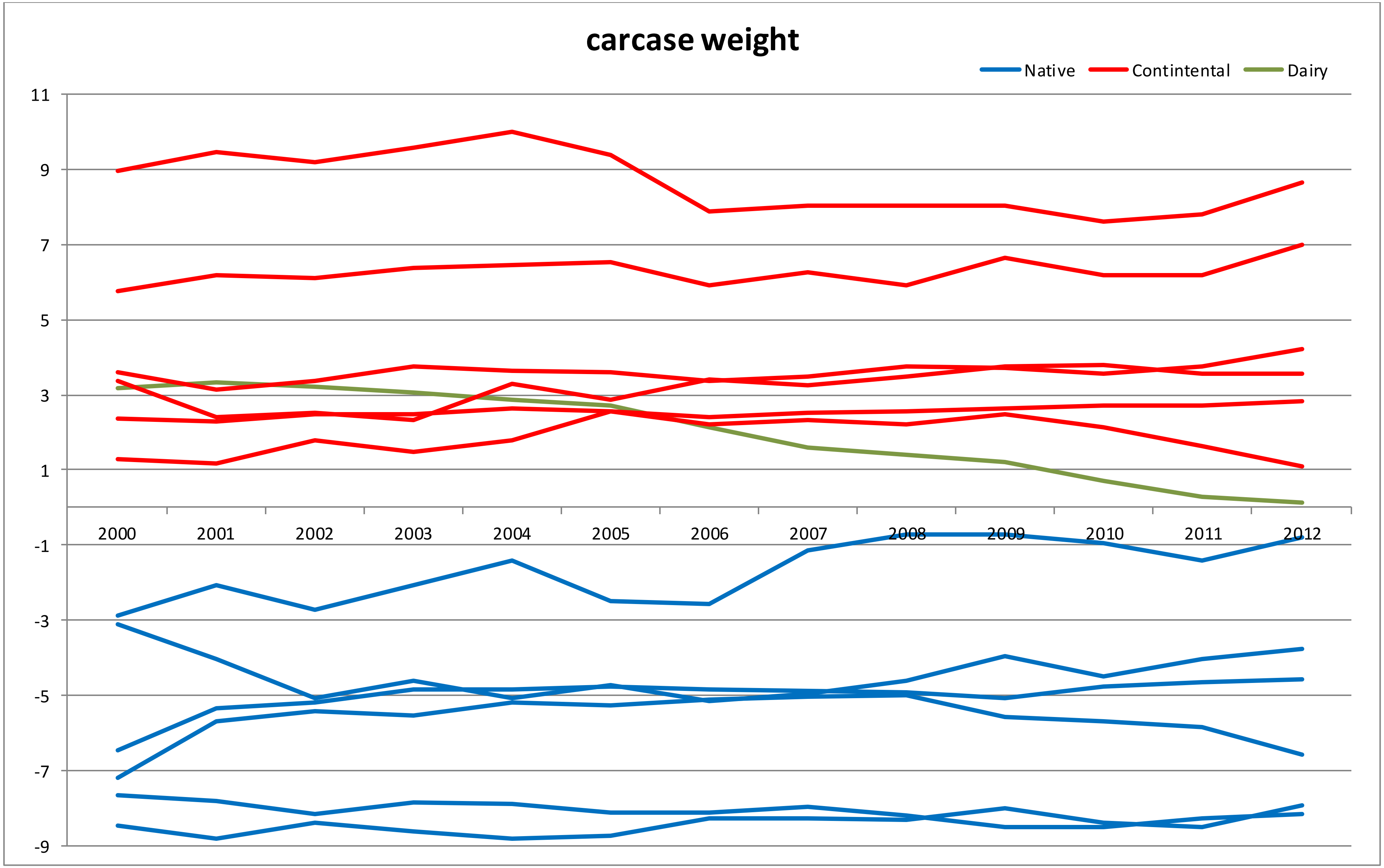

ADCG EBV for each breed
0.06
0.04
0.02
0.00
-0.02
-0.04
-0.06
-0.08
ADCG EBV
Aberdeen Angus
Ayrshire
Beef Shorthorn
Blonde D'Aquitaine
british blue
Charolais
Dairy Shorthorn
Devon
Friesian
Galloway
Hereford
Highland
Holstein
Limousin
Lincoln Red
Longhorn
Luing
Montbeliarde
Red Poll
Salers
Simmental
South Devon
Stabiliser
Sussex
Welsh Black
Breed

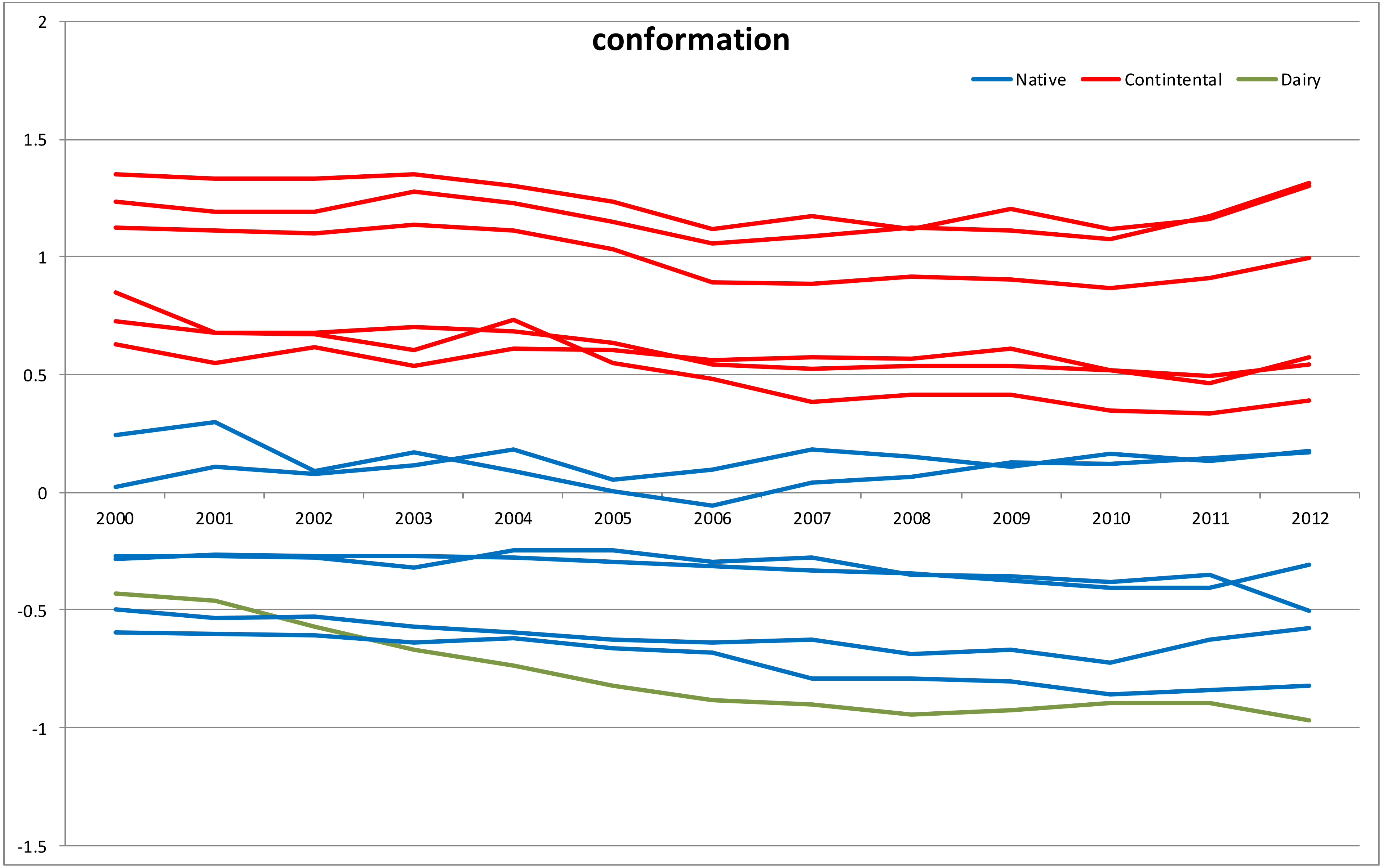
Genetic Trends

Genetic trends were produced the main breeds, based on sire breed. The number of records contributing are shown below in the table, and the trends are shown in the graphs below. Note, the breed name is only included in the table – so graphs can be shown and breeds kept anonymous – to help interpretation a N, D or C is beside the breed number to denote native, dairy or continental.

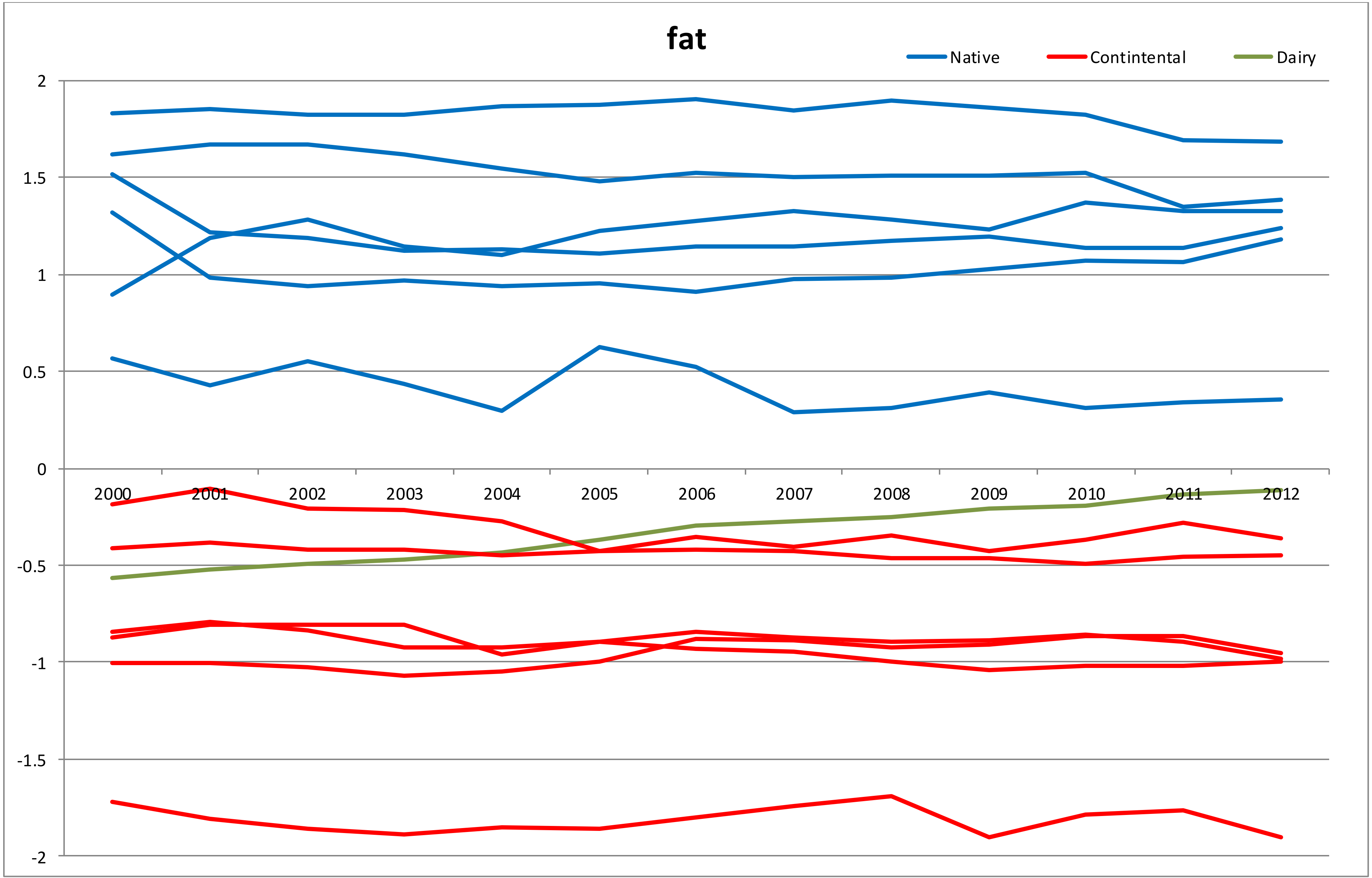
Birth year	Aberdeen Angus (1)	Blonde D'Aquitaine (7)	Holstein (12)	Beef Shorthorn (26)	Charolais (29)	Hereford (49)	Limousin (55)	Salers (75)	South Devon (77)	Simmental (80)	Stabiliser (83)	Welsh Black (90)	british blue (98)
2000	9644	1304	54763	1026	3772	3283	12859	1226	1408	6524	250	944	2780
2001	16237	1199	60458	1100	3640	6703	12868	1110	1517	6591	515	943	2511
2002	19832	1300	68995	1362	3993	8037	13339	1256	1642	7488	658	994	2909
2003	22780	1300	68534	1509	3894	9229	12837	1107	1626	7721	939	1061	3305
2004	29676	1571	67079	1762	4872	10338	15497	1381	1742	8809	1158	958	3465
2005	35402	1781	61495	2082	6605	11695	17771	1446	1823	10219	1236	933	4613
2006	36963	2663	60762	2137	10977	12552	26320	1675	2311	13411	1506	1269	6792
2007	39118	2804	59832	2213	13326	12809	27253	1612	2236	14483	2344	1358	8883
2008	40484	3042	55540	2285	14293	12994	27891	1895	2347	15474	2144	1411	9551
2009	40053	2912	49698	2160	14517	11416	25511	1653	2375	14605	2180	1431	10355
2010	43925	3951	38834	1810	16943	12435	29713	1842	2623	16010	2116	1242	13939
2011	47730	5075	36577	3268	25914	17580	42053	2170	2409	19149	2842	1228	18517
2012	21215	2743	18287	4091	17533	7372	26357	1310	1478	12008	2674	380	10418

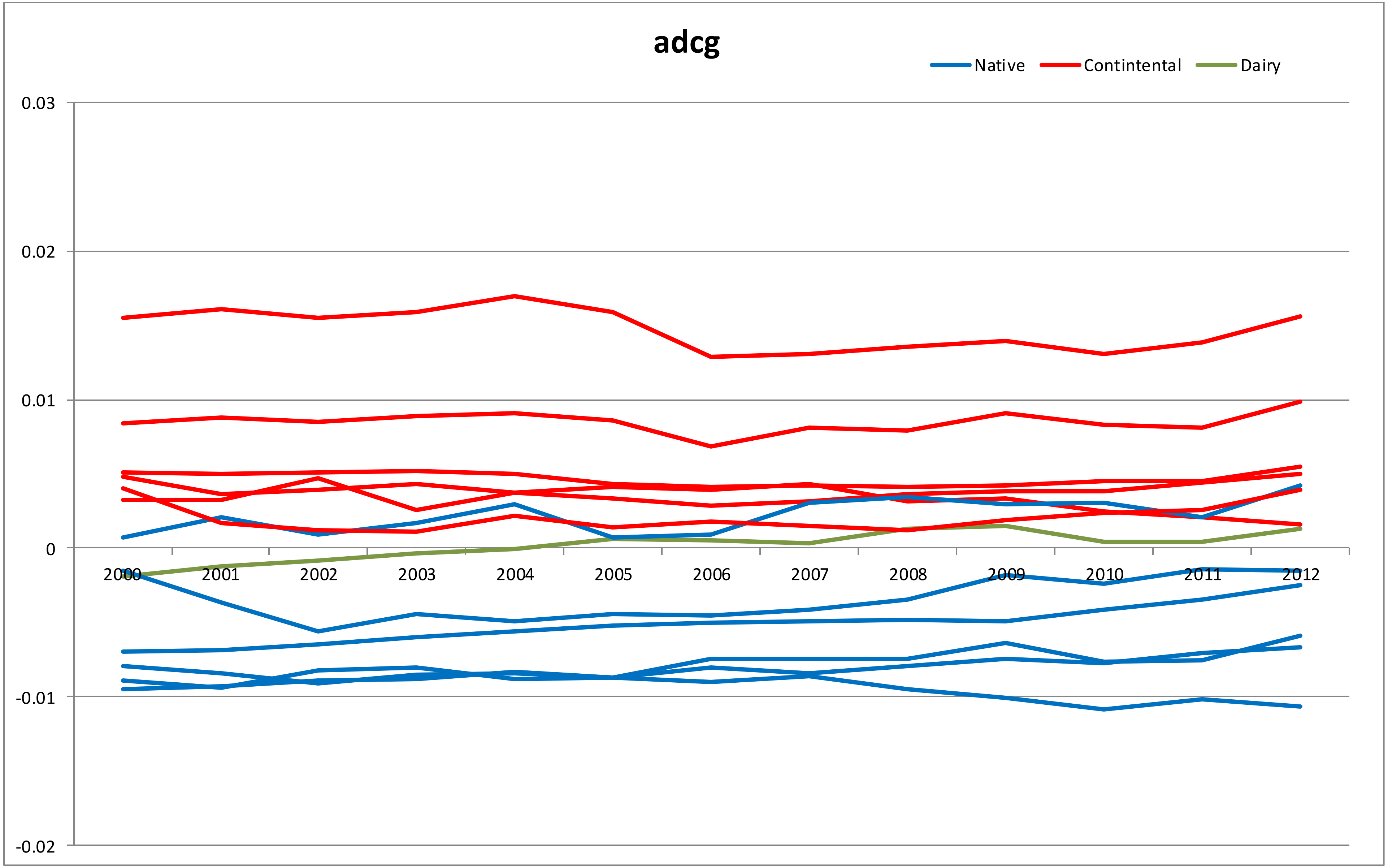

Slaughter Age
Native
Contintental
Dairy
8
6
4
2
0
-2
-4
-6
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012


carcase weight
Native
Contintental
Dairy
11
9
7
5
3
1
-1
-3
-5
-7
-9
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012


conformation
Native
Contintental
Dairy
2
1.5
1
0.5
0
-0.5
-1
-1.5
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012

Carcass Trait Evaluations




adcg
Native
Contintental
Dairy
0.03
0.02
0.01
0
-0.01
-0.02
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012

EBV Summary

Carcass trait EBVs are produced for beef and dairy beefs using a systematic system for extracting, processing, computing and post assessment of EBVs. This system gives everything batchids and stores relevant information to allow investigation into EBV changes across runs. These EBVs have been checked and are ready for distribution to the wider industry.

Appendix A: Breed groupings and breed types used to model hybrid vigour

Breed groups were categorised into four breed types which were dairy (1), native beef (2), continental beef (3), and other (4)

Table A 1 Breed type categories

Breed type	Breed Group	Description	Breed type	Breed group	Description
1	6	Ayrshire	2	57	Luing
1	12	Holstein Friesian	2	61	Murray Grey
1	21	Brown Swiss	2	67	Old English
1	37	Danish Red	2	74	Red Poll
1	48	Guernsey	2	77	South Devon
1	52	Jersey	2	79	Shetland
1	53	Kerry	2	83	Stabiliser
1	59	Malkekorthorn	2	84	Sussex
1	62	Montbeliarde	2	85	Tyrone Black
1	63	Meuse Rhine Issel	2	87	Vaynol
1	65	Normande	2	90	Welsh Black
1	66	Norwegian Red	2	92	White Park
1	73	Rotebunde	2	93	Welsh White
1	82	Swedish Red & White	2	99	coloured welsh
1	86	Tarantaise-Tarina	2	113	North Devon
1	96	Baltata Romaneasca.	3	2	Armoricaine
1	97	Belted Dutch	3	4	Angler Rotvieh
1	100	estonian red	3	5	Aubrac
1	105	SWEDISH RED.	3	7	Blonde D'Aquitaine
1	106	Abondance	3	8	Blue Albion
1	109	KIWI	3	9	Bazadaise
1	110	Lakenvelder	3	18	Bretonne Pie-Noire
1	111	Unspecified Dairy.	3	29	Charolais
2	1	Aberdeen Angus	3	30	Chianina
2	16	Blue Grey	3	33	Danish Blue
2	17	Black Poll	3	39	East Finnish Brown
2	22	Shorthorn	3	41	Frisona Espagnola
2	24	British White	3	43	Gasconne
2	25	Belted Welsh Black	3	45	Groninger Blaarkop
2	31	Chillingham	3	46	Gelbvieh
2	34	Dexter	3	55	Limousin
2	35	Devon	3	58	Maine Anjou
2	40	English Park	3	60	Marchigiana
2	42	Galloway	3	68	Parthenais
2	47	Gloucester	3	69	Piemontese
2	49	Hereford	3	70	Pinzgauer
2	50	Highland	3	71	Reggiana
2	51	Irish Moiled	3	72	Romagnola
2	54	Longhorn	3	75	Salers
2	56	Lincoln Red	3	78	Swiss Grey

Table continued

Breed type	Breed group	Description	Breed type	Breed group	Description
3	80	Simmental	4	3	Ankole
3	88	Valdostana Nera	4	11	Beefalo
3	89	Wagyu	4	15	Bison
3	98	british blue	4	19	Brahman
3	101	fleckvieh	4	23	Water Buffalo
3	102	heck	4	38	Zebu
3	103	Hungarian Steppe	4	44	Gayal
3	107	Unspecified Continental.	4	94	Yak
			4	95	Australian Lowline
			4	104	Speckle Park
			4	108	Unspecified Beef.
			4	112	Unknown.