

SUPPLEMENTARY MATERIAL

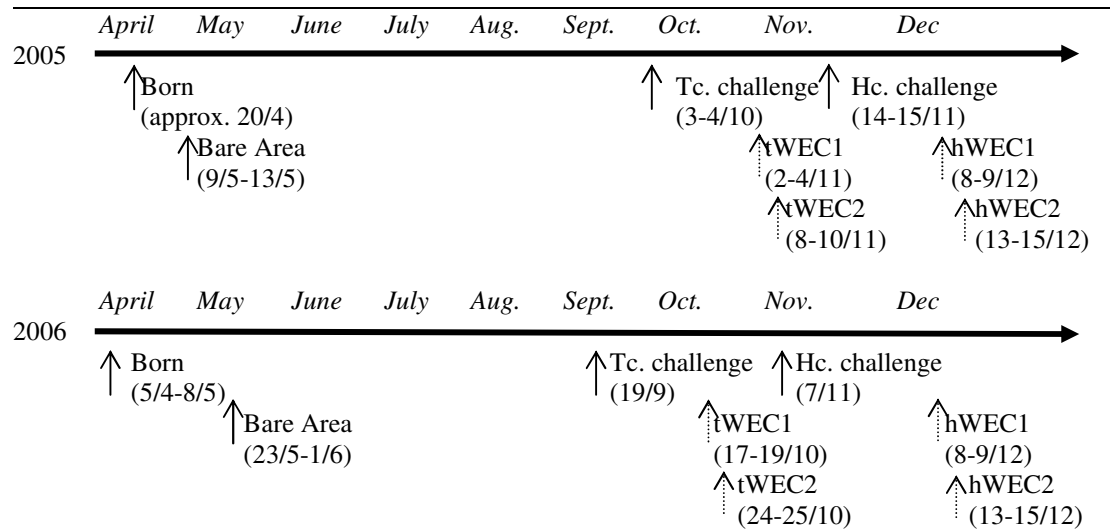


Figure S1.—A timeline of the phenotypic measurements taken on reference population. Shown are the dates of measurement for bare breech area, the challenge dates for *Trichostrongylus colubriformis* (Tc.) and *Haemonchus contortus* (Hc.), and the dates of faecal collection for faecal worm egg counts (WEC).

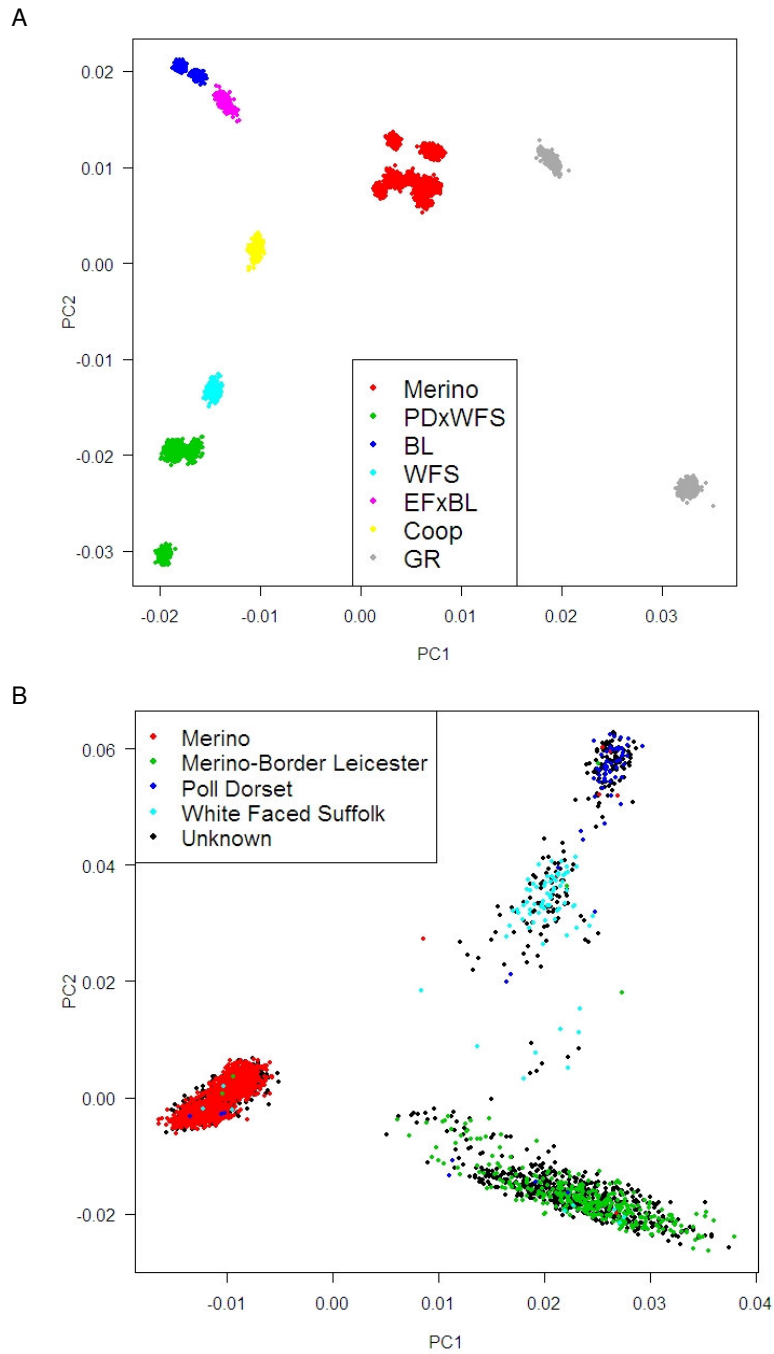


Figure S2.—The first and second principal components when the genomic relationship matrix is built with only the paternal (A) or maternal (B) haplotypes. Each animal is represented by a single point, and the points are coloured according to the recorded sire (A) or dam (B) pedigree. Animals with incorrect recorded dam pedigree can be seen by incorrect clustering, i.e. a green or blue dot in the red cluster of Merino dams. Sire breeds are Merino, Poll Dorset (PD), White Face Suffolk (WFS), Border Leicester (BL), East Frisian (EF), Coopworth (Coop), the Golden Ram selection line [GR, see Marshall *et al.* (2009)] and their crosses.

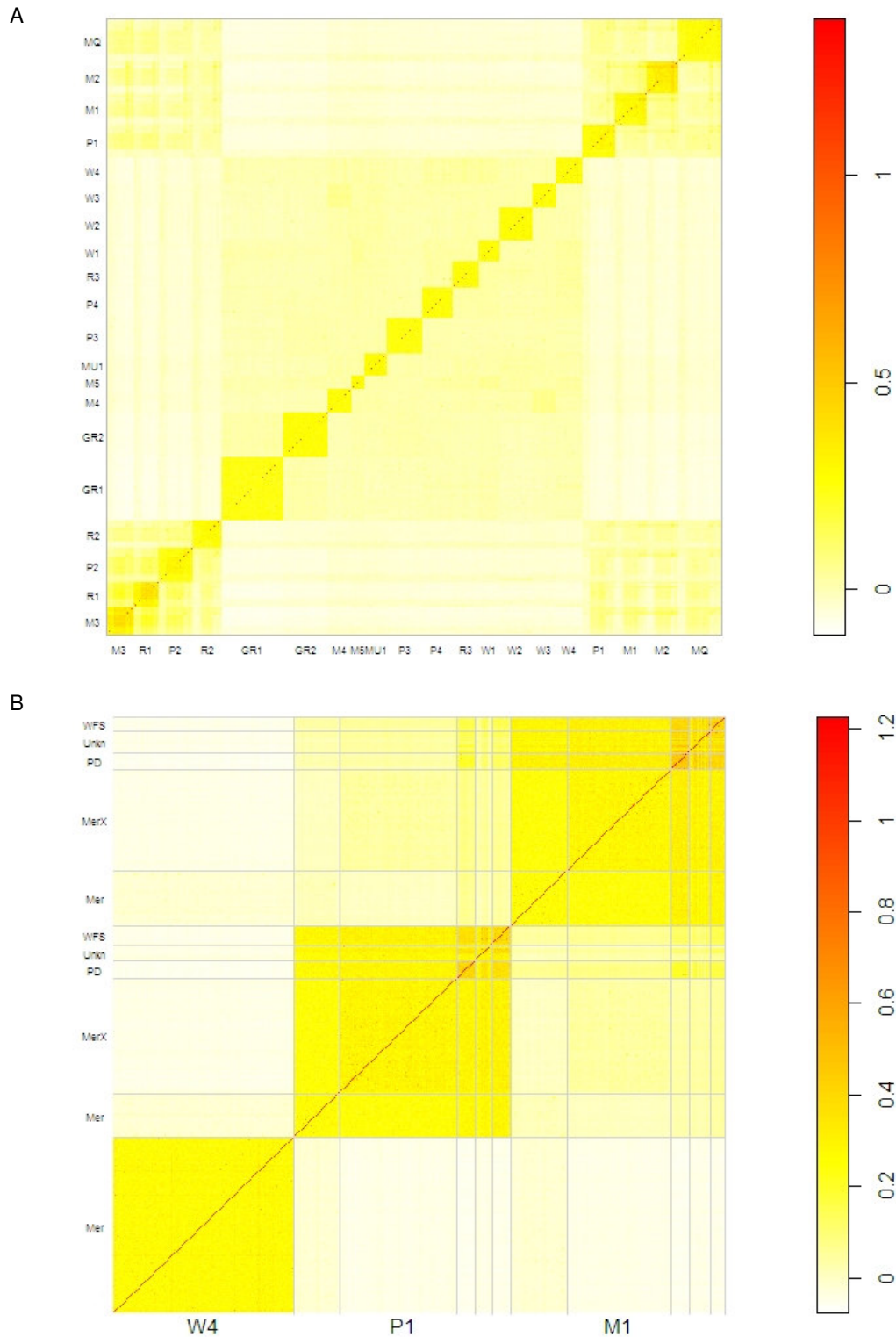
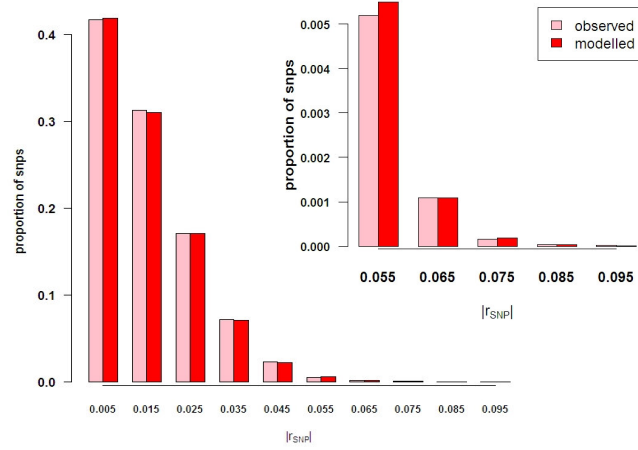
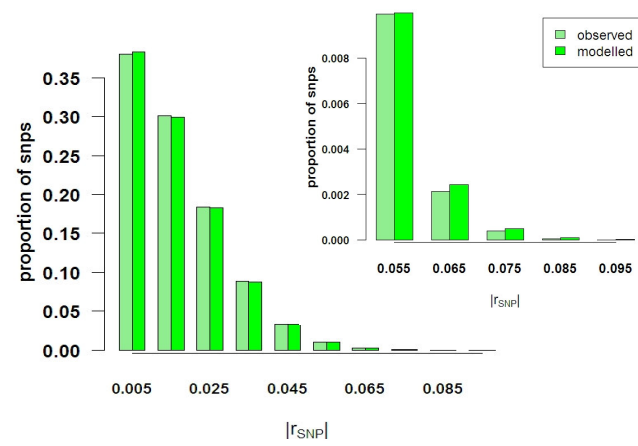


Figure S3.—Plots of the genomic relationship matrix. Shown is the matrix for all sheep (A) and the matrix magnified for offspring from sires W4, P1 and M1 (B). The colour of each square indicates the relationship between each pair of animals, as defined by the colour bar. To make the matrix, animals were sorted according to sire breed, sire and dam breed. Labels indicate the sire (x-axis) and dam breed (Y-axis), where dam breeds were Merino (Mer.), Merino cross Border Leicester (MerX), Poll Dorset (PD), Unknown (Unkn) or White Faced Suffolk (WFS).

A



B



C

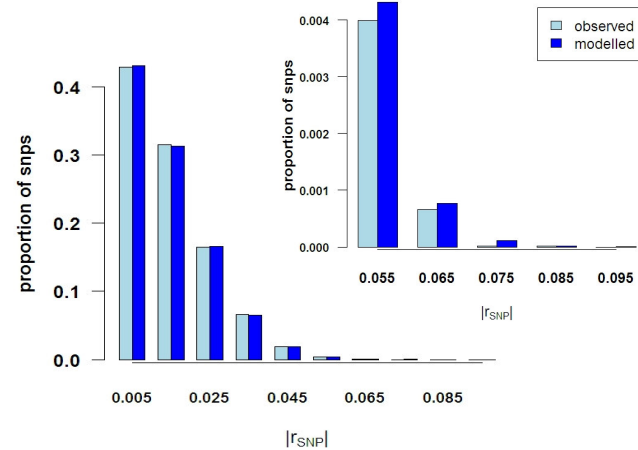


Figure S4.—The observed (left column) and modelled (right column) distribution of correlations between markers and the traits under investigation ($|r_{SNP}|$), where the sampling error N has been added to the back to the modelled distributions. Traits are *Trichostrongylus colubriformis* (A) or *Haemonchus contortus* (B) faecal worm egg count (tWEC, hWEC) and bare breech area (C). The tails for each of the distributions are shown in the insert for each plot.

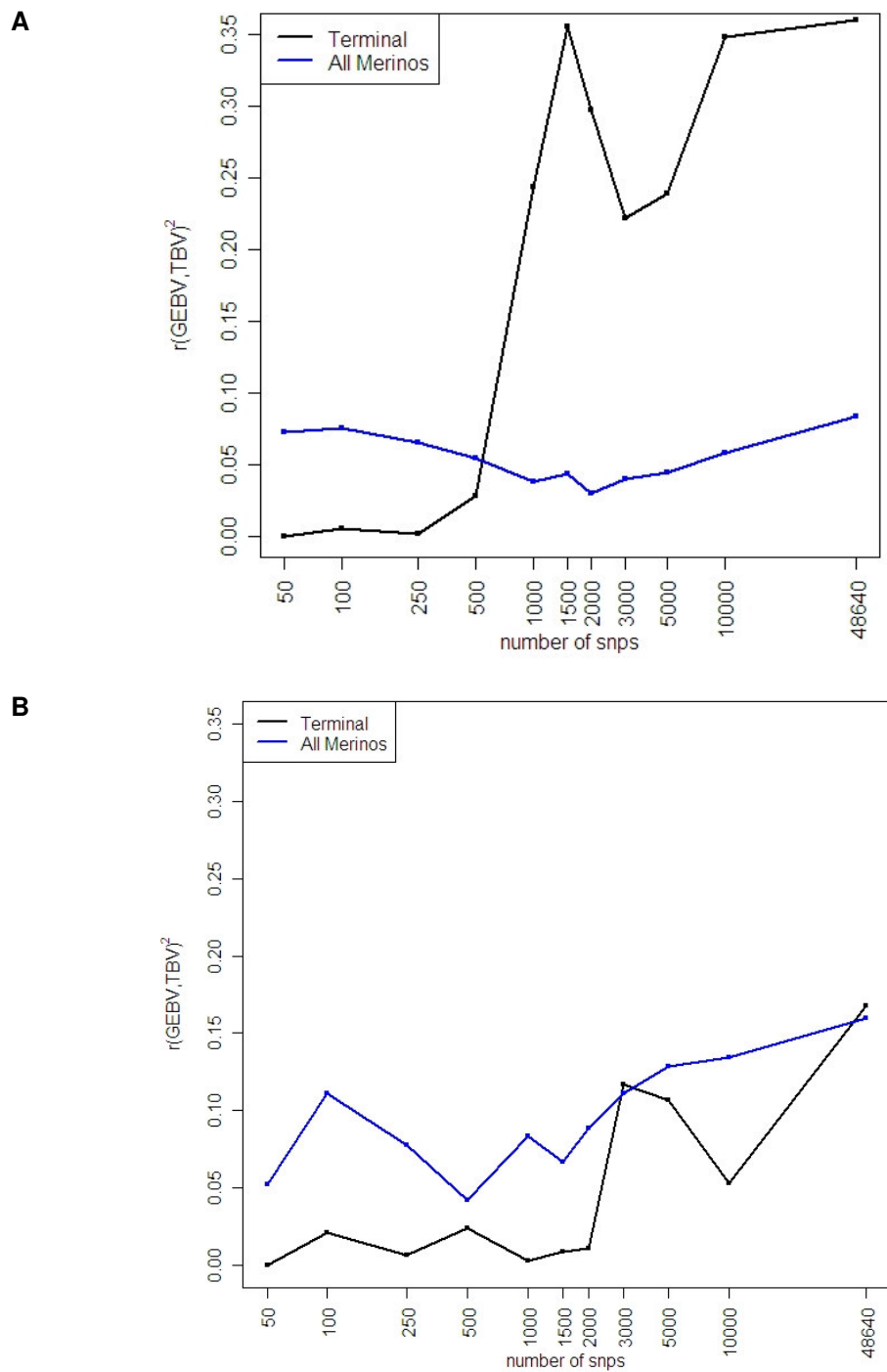


FIGURE S5.—The proportion of genetic variance explained, $r(\text{GEBV}, \text{TBV})^2$, for Terminal or Merino validation sires with an increasing number of markers used to predict genomic breeding values (GEBV). Shown are predictions with either faecal worm egg count following *Trichostrongylus colubriformis* (tWEC, A) or *Haemonchus contortus* (hWEC, B) challenge. Note the logarithmic scale on the x-axis.

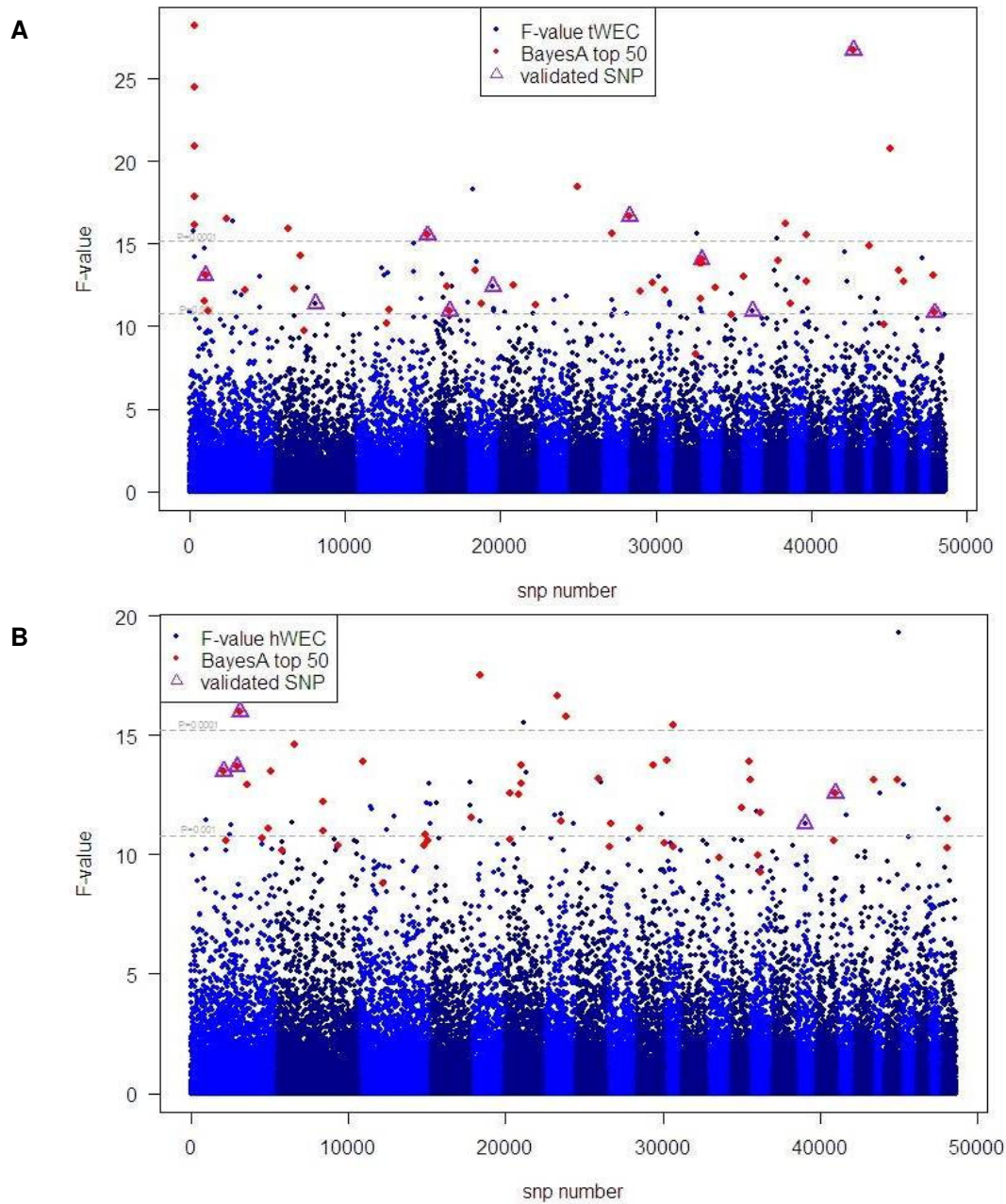


FIGURE S6.—Positions of the validated markers and the largest 50 BayesA effects following *Trichostrongylus colubriformis* (A) or *Haemonchus contortus* (B) challenge. On the x-axis is marker number and on the y-axis is the F-ratio from the single marker regressions in the reference population. Markers (SNP) are numbered sequentially across the genome and alternate chromosomes are in light and dark shades.

TABLE S1

Sire identification, breed and number of progeny genotyped from the 2005 and 2006 matings of the SheepGenomics project. Sires were chosen for inclusion in the project with reference to a particular trait, namely meat, reproduction, wool or parasite resistance.

Sire ID	Meat sires							Reproduction sires		
	M1	M2	M3	M4	M5	MQ	MU1	R1	R2	R3
Breed ^a	WSxPD	WSxPD	BL	Mer.	Mer.	WSxPD	Mer.	BL	Coop.	Mer.
2005	97	136	112	54	-	176	-	73	110	94
2006	110	74	54	73	87	101	133	91	66	82

Sire ID	Wool sires					Parasite resistance sires				
	W1	W2	W3	W4	P1	P2	P3	P4	GR1	GR2
Breed*	Mer.	Mer.	Mer.	Mer.	WFS	BLxEF	Mer.	Mer.	Mer.	Mer.
2005	82	47	86	64	107	123	82	84	145	111
2006	52	155	68	105	97	86	137	101	243	159

^aSire breeds are Mer. = Merino, WS = White Faced Suffolk, PD = Poll Dorset, BL = Border Leicester, Coop. = Coopworth, EF = East Friesian and their crosses.