**Supplementary Table S1.** Construction of(Co)variance matrices assuming all phenotypic variances (P1, P2, P1cp and P2cp) are scaled to 1. Phenotypic covariance on upper diagonal, genetic covariance below and genetic variance on diagonal.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | P1 | P2 | P1cp | P2cp | Q1 | Q2 | Q1cp | Q2cp |
| P1 | h12 | ρP | ρx | ρPρX | h12q2r12 | h12h2q2r22ρG | h12q2r12ρX | h12h2q2r22ρGρX |
| P2 | h1h2ρG | h22 | ρPρX | ρX | h1h22q2r12ρG | h22q2r22 | h1h22q2r12ρGρX | h22q2r22ρX |
| P1cp | h12ρX | h1h2ρGρX | h12 | ρP | h12q2r12ρX | h12h2q2r22ρGρX | h12q2r12 | h12h2q2r22ρG |
| P2cp | h1h2ρGρX | h22ρX | h1h2ρGρX | h22 | h1h22q2r12ρGρX | h22q2r22ρX | h1h22q2r12ρG | h22q2r22 |
| Q1 | h12q2r12 | h1h2q2r12ρG | h12q2r12ρX | h1h2q2r12ρGρX | q2r12h12 | h1h2r12r22ρG | h12r12ρX | h1h2r12r22ρGρX |
| Q2 | h1h2q2r22ρG | h22q2r22 | h1h2q2r22ρGρX | h22q2r22ρX | h1h2r12r22ρG | q2r22h22 | h1h2r12r22ρGρX | h22r22ρX |
| Q1cp | h12q2r12ρX | h1h2q2r12ρGρX | h12q2r12 | h1h2q2r12ρG | h12r12ρX | h1h2r12r22ρGρX | h12q2r12h12 | h1h2r12r22ρG |
| Q2cp | h1h2q2r22ρGρX | h22q2r22ρX | h1h2q2r22ρG | h22q2r22 | h1h2r12r22ρGρX | h22r22ρX | h1h2r12r22ρG | q2r22h22 |

(P) Pure-bred phenotype based trait

(Pcp) Commercial cross-bred phenotype based trait

(Q) pure-bred marker-based trait

(Qcp) commercial cross-bred marker-based trait

Supplementary Table S1 exemplifies the methodology for the construction of the (co)variance matrices, using two traits measured on both pure-bred and commercial cross-breds, where the phenotypes have been standardised to have a phenotypic variance of 1. The genetic correlation in pure-bred sires between traits *i* and *j* measured in pure-breds is ρG and this is assumed to be the same when the breeding values are for *i* and *j* measured in cross-breds. However the correlation between a breeding value for pure-bred performance in *i* and cross-bred performance in the same trait *i* is assumed to be ρX, the same for all traits, due to lack of information. The correlation between breeding values for trait i as a pure-bred and trait j≠i as a crossbred is assumed to be ρGρX. This implicitly assumes the independence of the cross-bred breeding value for trait j and the pure-bred breeding value for trait i given the pure-bred breeding value for trait j, i.e. the best prediction of cross-bred breeding values from pure-bred breeding values is given by the pure-bred breeding value of the same trait. Further, it is assumed that: (i) the variance of breeding values for trait *i* is the same for pure-bred and cross-bred performance when phenotypes are scaled to have variance 1, i.e. in the table *h2* for trait *i* is the same in pure-breds and cross-breds. In the table ρP indicates a correlation between the phenotypes if *i* and *j*, which was also assumed to be the same in pure-breds and cross-breds. The accuracy of the marker estimated breeding value for trait i using the marker data for the component of the genetic value that is associated with markers ri for a given trait was predicted following the approach of Daetwyler *et al*. (2008). The marker genotyping panel is expected to capture a fraction q2 of the genetic variance in the traits (Daetwyler, 2009), and this was assumed to be the same for all traits, which means the maximum accuracy obtainable for a genomic predictor for the observed traits is q. In this study q was assumed to be 0.9.

**Supplementary Table S2** *Existing and new recorded traits in the terminal index.* *based on pedigree Limousin data from BASCO (2012).*

|  |  |  |
| --- | --- | --- |
| **Recorded trait name1** | **Heritability** | **Phenotypic Variance** |
| BWT-direct1, kg | 0.23 | 9.0 |
| WT2001,kg | 0.33 | 807 |
| WT4001, kg | 0.40 | 1589 |
| MSC1, score (1-15, higher = higher muscularity) | 0.27 | 1.3 |
| FD1, mm | 0.29 | 6395 |
| MD1, mm | 0.26 | 2518 |
| GL-direct1, days | 0.29 | 23.8 |
| CD-direct1, score (1-5, higher = increased assistance required) | 0.12 | 1.0 |
| CCW2 ,kg | 0.44 | 859 |
| CCCS2, score | 0.11 | 9.8 |
| CCFS2, score | 0.13 | 4.1 |

1Definition of trait name abbreviations of existing TI traits : BWT, birth weight; WT200, weight at 200 days; WT400, weight at 400 days; MSC, muscle score; FD, fat depth; MD, muscle depth; GL, gestation length; CD, calving difficulty;

2New recorded traits included in the index: CCW, cross-bred carcass weight; CCCS, cross-bred carcass conformation score; CCFS, cross-bred carcass fat score.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **BWT-direct** | **WT200** | **WT400** | **MSC** | **FD** | **MD** | **GL-direct** | **CD-direct** | **CW** | **CCS** | **CFS** |
| **BWT-direct** | 1.00 | 0.50 | 0.41 | 0.38 | 0.09 | 0.47 | 0.55 | 0.58 | 0.15 | 0.15 | 0.00 |
| **WT200** | 0.27 | 1.00 | 0.85 | 0.42 | 0.22 | 0.60 | 0.10 | 0.29 | 0.50 | 0.18 | 0.08 |
| **WT400** | 0.19 | 0.85 | 1.00 | 0.53 | 0.12 | 0.55 | 0.05 | 0.10 | 0.60 | 0.20 | 0.10 |
| **MSC** | 0.10 | 0.48 | 0.43 | 1.00 | 0.00 | 0.63 | 0.19 | 0.07 | 0.30 | 0.60 | 0.00 |
| **FD** | 0.05 | 0.17 | 0.22 | 0.16 | 1.00 | 0.18 | 0.00 | 0.05 | 0.10 | 0.10 | 0.40 |
| **MD** | 0.10 | 0.32 | 0.43 | 0.49 | 0.16 | 1.00 | 0.20 | 0.10 | 0.30 | 0.60 | 0.10 |
| **GL-direct** | 0.20 | 0.07 | 0.00 | 0.12 | 0.00 | -0.01 | 1.00 | 0.21 | 0.10 | 0.10 | 0.00 |
| **CD-direct** | 0.31 | 0.02 | 0.03 | 0.01 | 0.00 | 0.00 | 0.11 | 1.00 | 0.10 | 0.10 | 0.00 |
| **CW** | 0.15 | 0.50 | 0.60 | 0.30 | 0.10 | 0.30 | 0.10 | 0.10 | 1.00 | 0.00 | 0.00 |
| **CCS** | 0.15 | 0.18 | 0.20 | 0.60 | 0.10 | 0.60 | 0.10 | 0.10 | 0.00 | 1.00 | 0.10 |
| **CFS** | 0.00 | 0.08 | 0.10 | 0.00 | 0.40 | 0.10 | 0.00 | 0.00 | 0.00 | 0.10 | 1.00 |

**Supplementary Table S3** *Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlations between existing and new recorded traits in the terminal index. (*ρX1 *=1.0),**based on pedigree Limousin data from BASCO (2012).*

Definition of trait name abbreviations: BWT, birth weight; WT200, weight at 200 days; WT400, weight at 400 days; MSC, muscle score; FD, fat depth; MD, muscle depth; GL, gestation length; CD, calving difficulty ; CW, carcass weight; CCS, carcass conformation score; CFS, carcass fat score.

1ρx is the genetic correlation between pure-bred and cross-bred performance.

**Supplementary Table S4** *Heritability, phenotypic variance and economic weights for profit traits in the terminal index, based on pedigree Limousin data from BASCO (2012).*

|  |  |  |  |
| --- | --- | --- | --- |
| **Profit trait name1** | **Heritability** | **Phenotypic variance** | **Economic weight (£)** |
| CW, kg | 0.44 | 860 | 1.2 |
| CFS, score (1-15) | 0.13 | 4.10 | -6 |
| CCS, score (1-15) | 0.11 | 9.83 | 7 |
| GL-direct, days | 0.29 | 23.81 | -1 |
| CD-direct, (score 1-5) | 0.12 | 1.02 | -2.88 |

1Definition of trait name abbreviations: CW, carcass weight; CFS, carcass fat score; CCS, carcass conformation score; GL, gestation length; CD, calving difficulty.

**Supplementary Table S5** *Estimates of genetic correlations between existing and new recorded traits and profit traits in the terminal index, based on pedigree Limousin data from BASCO (2012).*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **CW** | **CFS** | **CCS** | **GL-direct** | **CD-direct** |
| **BWT-direct** | 0.15 | 0.00 | 0.15 | 0.55 | 0.58 |
| **WT200** | 0.50 | 0.80 | 0.18 | 0.10 | 0.29 |
| **WT400** | 0.60 | 0.10 | 0.20 | 0.05 | 0.10 |
| **MSC** | 0.30 | 0.00 | 0.60 | 0.19 | 0.07 |
| **FD** | 0.10 | 0.40 | 0.10 | 0.00 | 0.05 |
| **MD** | 0.30 | 0.10 | 0.60 | 0.20 | 0.10 |
| **GL-direct** | 0.10 | 0.00 | 0.10 | 1.00 | 0.21 |
| **CD-direct** | 0.10 | 0.00 | 0.10 | 0.21 | 1.00 |
| **CW** | 1.00 | 0.00 | 0.00 | 0.10 | 0.10 |
| **CCS** | 0.00 | 1.00 | 0.00 | 0.10 | 0.10 |
| **CFS** | 0.00 | 0.00 | 1.00 | 0.00 | 0.00 |

Definition of trait name abbreviations: CW, carcass weight; CFS, carcass fat score; CCS, carcass conformation score; GL, gestation length; CD, calving difficulty; BWT, birth weight; WT200, weight at 200 days; WT400, weight at 400 days; MSC, muscle score; FD, fat depth; MD, muscle depth; CW, carcass weight; CCS, carcass conformation score; CFS, carcass fat score.

**Supplementary Table S6** *Estimates of genetic correlations between profit traits in the terminal index.* *based on pedigree Limousin data from BASCO (2012).*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **CW** | **CFS** | **CCS** | **GL-direct** | **CD-direct** |
| **CW** | 1.00 | 0.00 | 0.00 | 0.10 | 0.10 |
| **CFS** | 0.00 | 1.00 | 0.00 | 0.00 | 0.00 |
| **CCS** | 0.00 | 0.00 | 1.00 | 0.10 | 0.10 |
| **GL-direct** | 0.10 | 0.00 | 0.10 | 1.00 | 0.21 |
| **CD-direct** | 0.10 | 0.00 | 0.10 | 0.21 | 1.00 |

Definition of trait name abbreviations: CW, carcass weight; CFS, carcass fat score; CCS, carcass conformation score; GL, gestation length; CD, calving difficulty.

**Supplementary Table S7** *Information sources used in the model, based on pedigree Limousin data from BASCO (2012).*

|  |  |  |
| --- | --- | --- |
| Information source name1 | Number of animal records (Male) | Number of animal records (Female) |
| BWT-direct (on candidate) | 1 | 1 |
| BWT-direct (on paternal half-sibs) | 3 | 3 |
| WT200-direct (on candidate) | 1 | 1 |
| WT200-direct (on paternal half-sibs) | 4 | 4 |
| WT400 (on candidate) | 1 | 1 |
| WT400 (on paternal half sibs) | 3 | 3 |
| MSC (on candidate) | 0 | 0 |
| MSC (on paternal half sibs) | 1 | 1 |
| FD (On candidate) | 0 | 0 |
| FD (On paternal half sibs) | 1 | 1 |
| MD (on candidate) | 1 | 1 |
| MD (on paternal half sibs) | 1 | 1 |
| GL-direct (on candidate) | 1 | 1 |
| GL-direct (on paternal half sibs) | 5 | 5 |
| CD-direct (on candidate) | 1 | 1 |
| CD-direct (on paternal half sibs) | 16 | 16 |
| BWT (on progeny) | 8 | 1 |
| WT200 (on progeny) | 8 | 1 |
| WT400 (on progeny) | 6 | 1 |
| MD (on progeny) | 2 | 1 |
| FD (on progeny) | 2 | 1 |
| MSC (on progeny) | 0 | 1 |
| GL (on progeny) | 10 | 1 |
| CD (on progeny) | 33 | 1 |
| CCWT (on progeny) 2 | 20 | 0 |
| CCCS (on progeny) 2 | 20 | 0 |
| CCFS (on progeny) 2 | 20 | 0 |

1Definition of trait name abbreviations: BWT, birth weight; WT200, weight at 200 days; WT400, weight at 400 days; MSC, muscle score; FD, fat depth; MD, muscle depth; GL, gestation length; CD, calving difficulty.

2Traits used only in the conventional progeny test simulation: CCWT, commercial carcass weight, CCCS, commercial carcass conformation score and CCFS, commercial carcass fat score.