

Additional files

File name: Additional file 1

File format: .docx

Title of data: Residual feed intake (RFI) and feed conversion ratio (FCR) values for all the animals included in the current study are used to classify the animals into high (H) and low (L) feed efficiency groups.

Description of data: A Word document containing a table containing the classification of the animals used in the current study into residual feed intake (RFI) and feed conversion ratio (FCR) groups.

File name: Additional file 2

File format: .docx

Title of data: Descriptive statistic for the Kinship coefficient obtained overall in all samples and within each feed efficiency group.

Description of data: A Word document containing a table with the descriptive statistic for the Kinship coefficient obtained overall in all samples and within each feed efficiency group.

File name: Additional file 3

File format: .docx

Title of data: Mapping statistics for whole-genome bisulfite sequencing data from the milk of Assaf ewes used to identify differentially methylated loci (DMLs) and regions (DMRs).

Description of data: A Word document containing the mapping statistics obtained from the whole-genome bisulfite sequencing data of the milk from Assaf ewes, used to identify differentially methylated loci.

File name: Additional file 4

File format: .xlsx

Title of data: Differentially methylated regions (DMRs) identified in the comparison between high- and low-feed-efficiency groups for residual feed intake (RFI), feed conversion ratio (FCR), and consensus (Cons).

Description of data: An Excel file containing the differentially methylated regions (DMRs) identified in the comparison between the high- and low-feed-efficiency groups for residual feed intake (RFI), feed conversion ratio (FCR), and consensus (Cons)

File name: Additional file 5

File format:.xlsx

Title of data: Enriched KEGG pathways identified for genes harboring differentially methylated regions obtained from high- and low-feed-efficiency groups for residual feed intake (RFI), feed conversion ratio (FCR), and consensus (Cons).

Description of data: An Excel file containing the enriched KEGG pathways identified for the genes harboring differentially methylated regions.

File name: Additional file 6

File format: .docx

Title of data: Boxplots showing the distributions of the squared Spearman correlation (ρ^2) and root mean squared error (RMSE) for the 100 steps of random sampling of animals in the training and test sets.

Description of data: A Word document with a figure of boxplots showing the distribution of squared Spearman correlation (ρ^2) and root mean squared error (RMSE) values.