

Discovery of Key Functional SNP Markers Associated with Feed Efficiency in Beef Cattle

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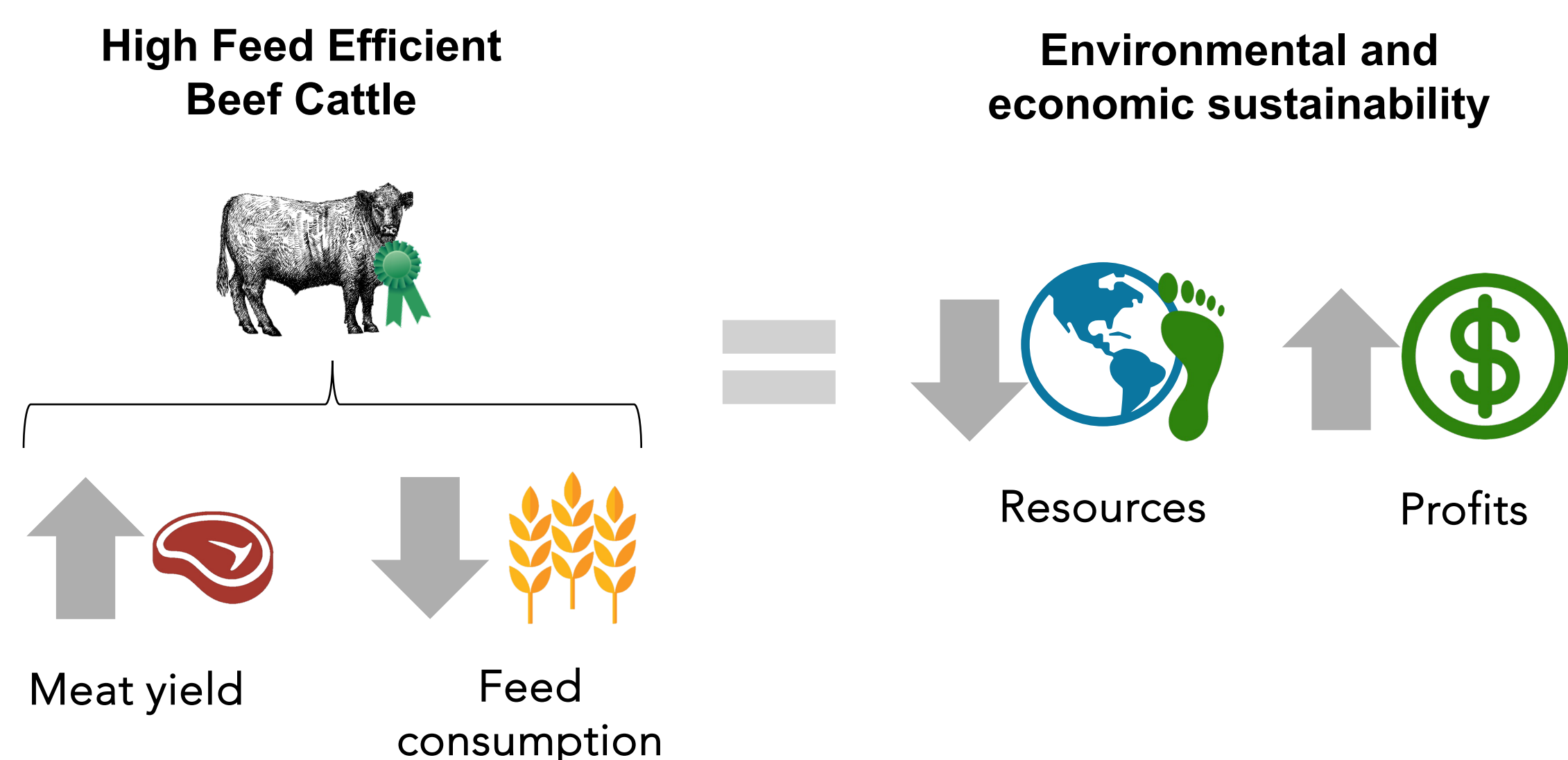
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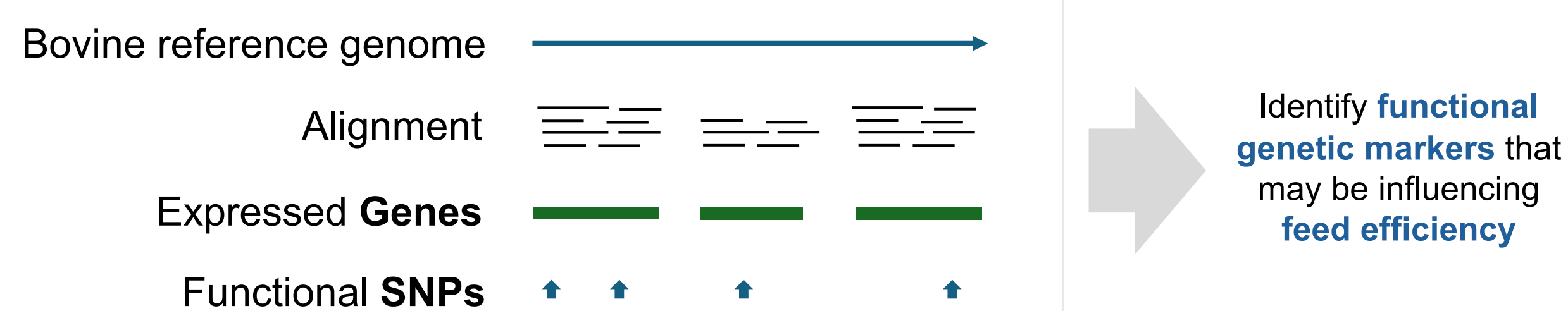
OBJECTIVES

- To understand the **functional genetics** underlying **feed efficiency** in beef cattle
- To identify **functional SNP markers** linked to **feed efficiency** in beef cattle

INTRODUCTION



- Selection for higher **feed efficient (FE)** [Residual Feed Intake; RFI (kg/d)] beef cattle can result in **higher lean meat yield**, while consuming the **same amount of feed**.



- RNA-Sequencing technology** can uncover the underlying functional genetics of feed efficiency, through identifying **key regulatory genes**, **functional SNP markers**, and linked **QTLs**.

METHODS

Roy Berg Kinsella Ranch
n = 738

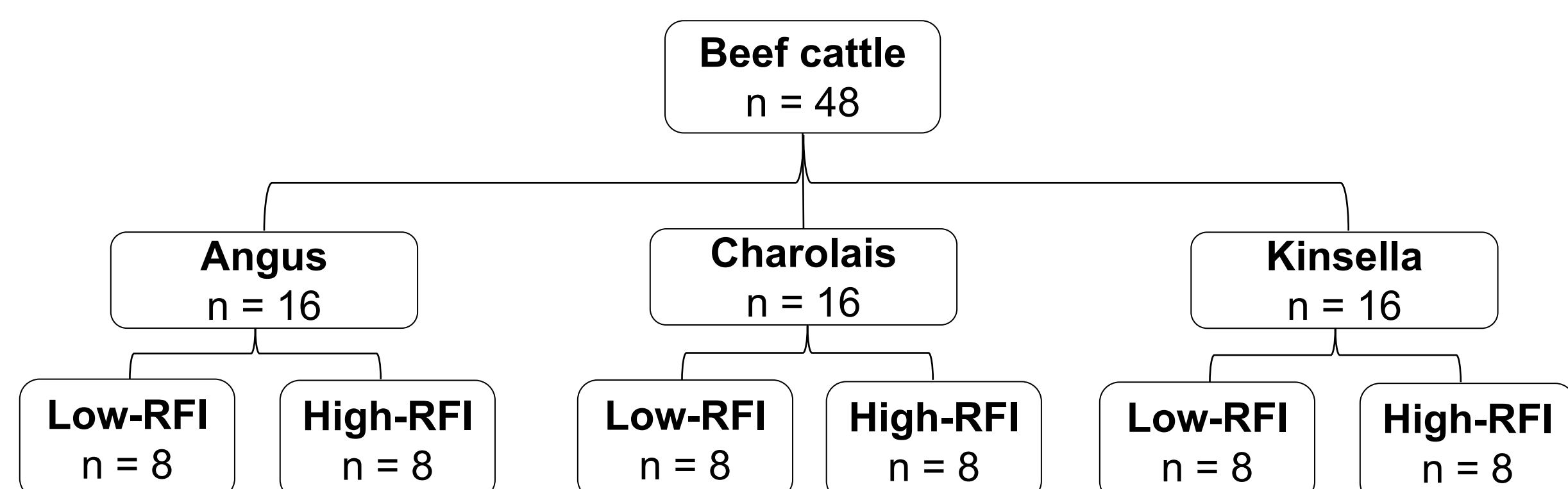
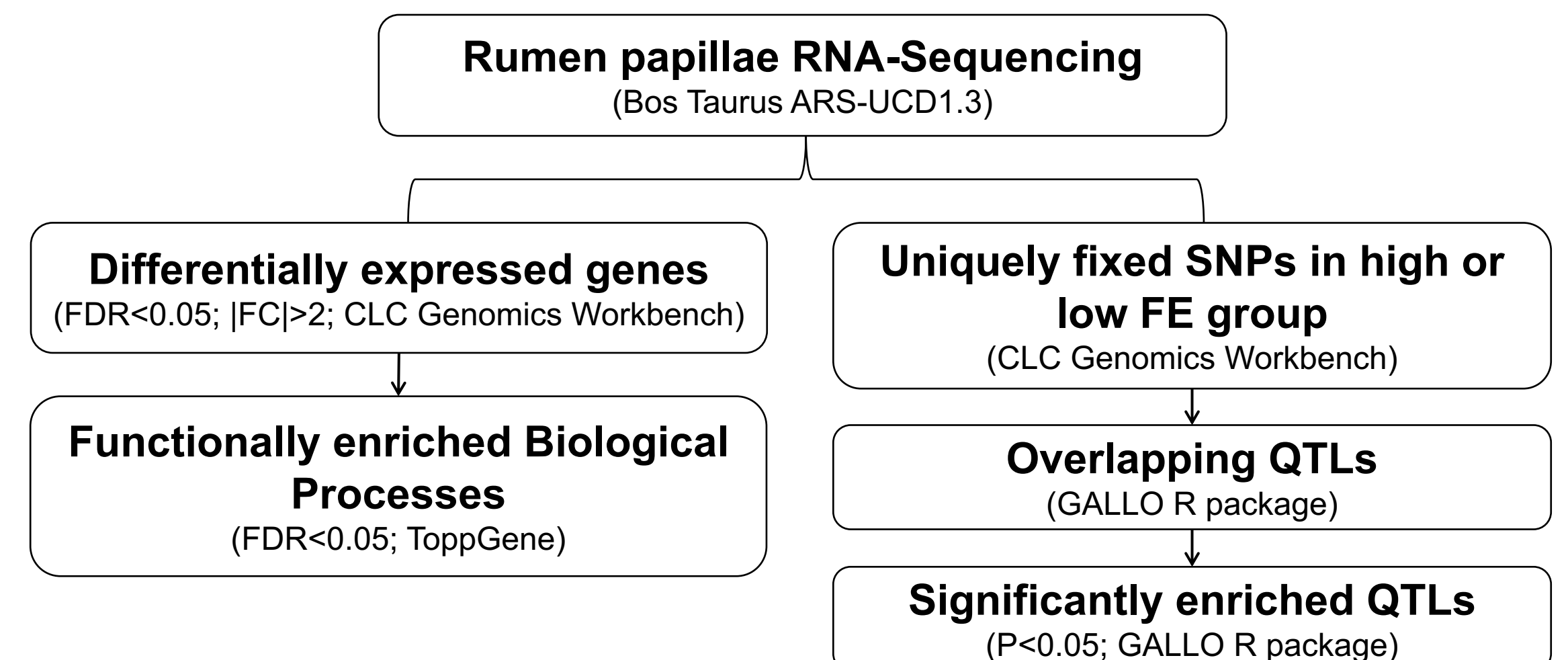


Figure 1. Diagram illustrating cattle population and RFI classification.



Figure 2. Diagram illustrating sample collection for RNA-sequencing.

WORKFLOW



RESULTS

Table 1. (A) 11 key regulatory genes differentially expressed between FE across all breeds (FDR<0.05; |FC|>2); **(B)** associated Biological Processes with all 11 key regulatory genes (P<0.05).

(A)

11 Key Regulatory Genes

<i>EIF4B</i>	<i>USP43</i>
<i>RHOD</i>	<i>MYH1</i>
<i>SERPINB2</i>	<i>MYL2</i>
<i>TCEANC</i>	<i>MYLPF</i>
<i>CKM</i>	<i>TNNC2</i>
<i>ENSBTAG00000040518</i>	

(B)

Biological Processes

Muscle contraction
Muscle system process
Muscle filament sliding
Actin-myosin filament sliding
Muscle cell fate specification

Figure 3. Total uniquely fixed SNPs (100% frequency) identified within FE group across breeds.

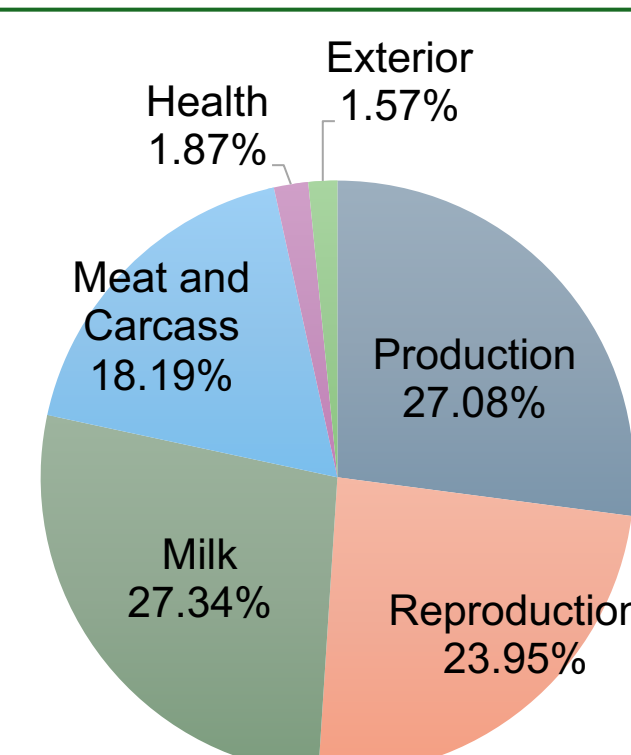
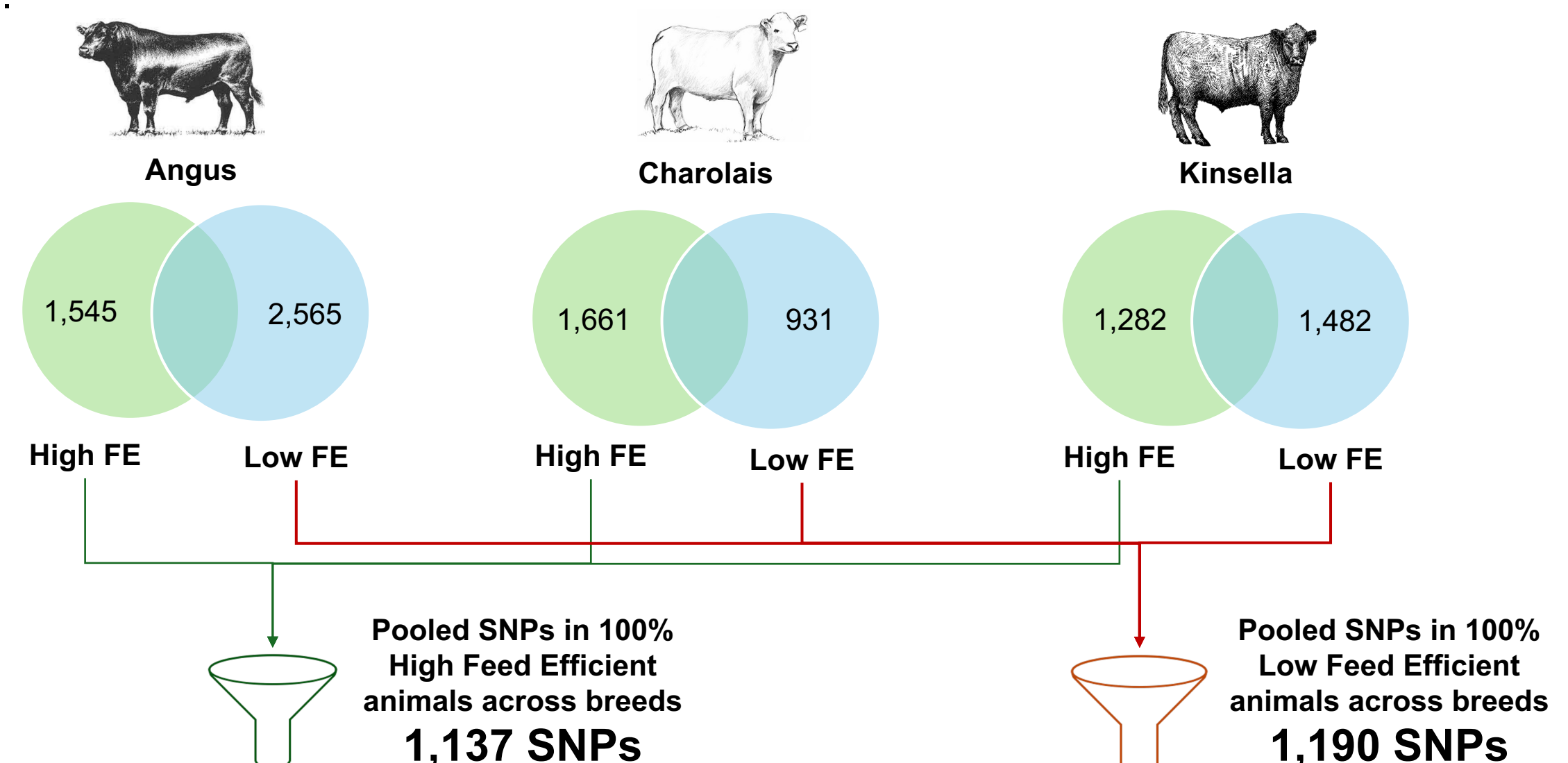


Figure 4. Percent (%) SNP markers uniquely fixed in high (green) or low (red) feed efficient animals across breeds, overlapping cattle QTL classes.

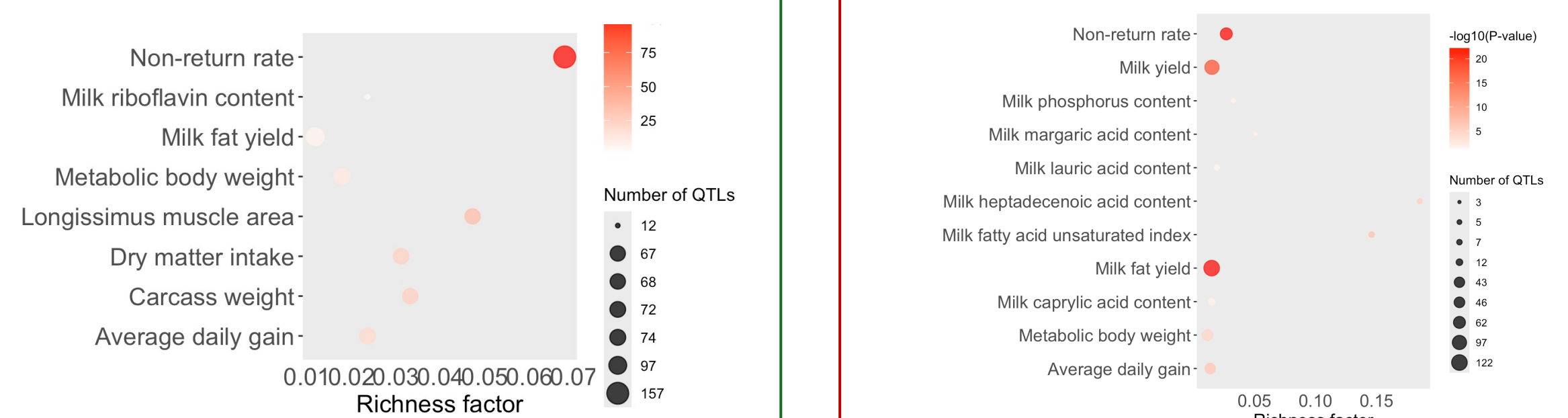


Figure 5. Significantly enriched QTL types with SNP markers uniquely fixed in high (green) or low (red) feed efficient animals across breeds (P<0.05).

CONCLUSIONS

11 key regulatory genes linked to feed efficiency were identified across breeds. 1,137 and 1,190 uniquely fixed SNPs within high or low feed efficient cattle, respectively. Further studies will define and validate potential functional SNPs to be included in genomic evaluations.