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Contribution of plasma proteins to the phenotypic signature of feed efficiency in Charolais bulls

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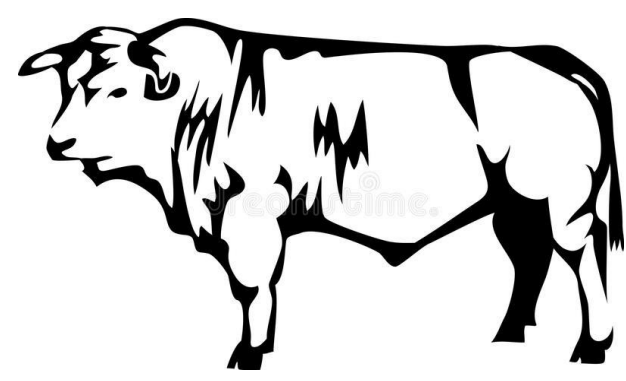
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Improving efficiency of feed utilization by reducing the amount of feed intake for the same level of production has economic and environmental importance for the beef cattle production. A major challenge is to have biomarkers for feed efficiency (RFI, FCE) that would allow for phenotyping on this multifactorial trait as well as better predictions for management and selection purposes.

2 objectives:

- To identify carcass traits, proteins, targeted metabolites or hormones that discriminates efficient and inefficient Charolais young bulls
- To propose proteins as potential biomarkers of feed efficiency

Experimental design



RFI, FCE

Efficient Charolais bulls
n=8

Inefficient Charolais bulls
n=9

11 targeted parameters
(hormones + metabolites)

22 carcass parameters
weights

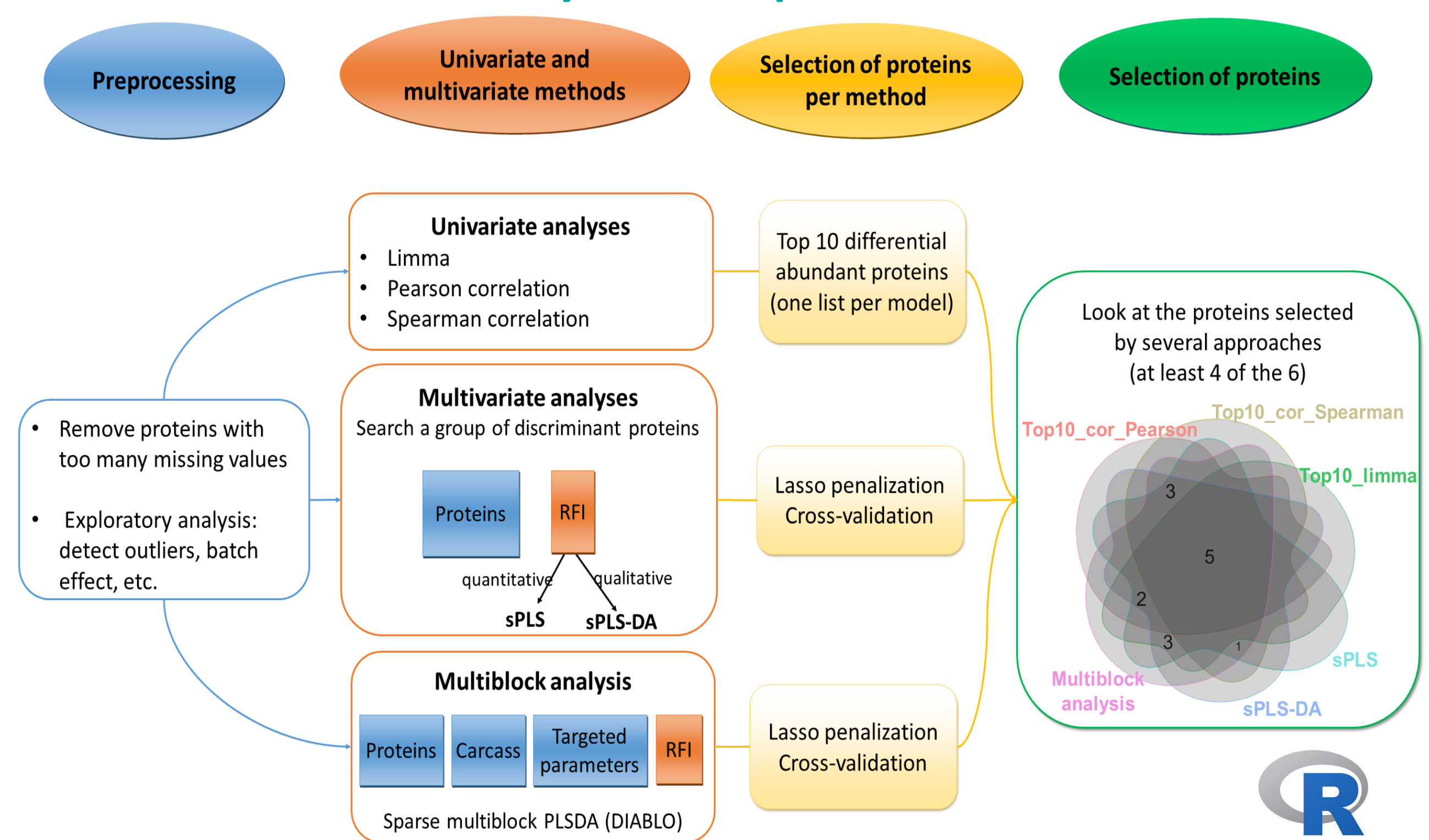
229 untargeted plasma protein
abundances

Animal performance

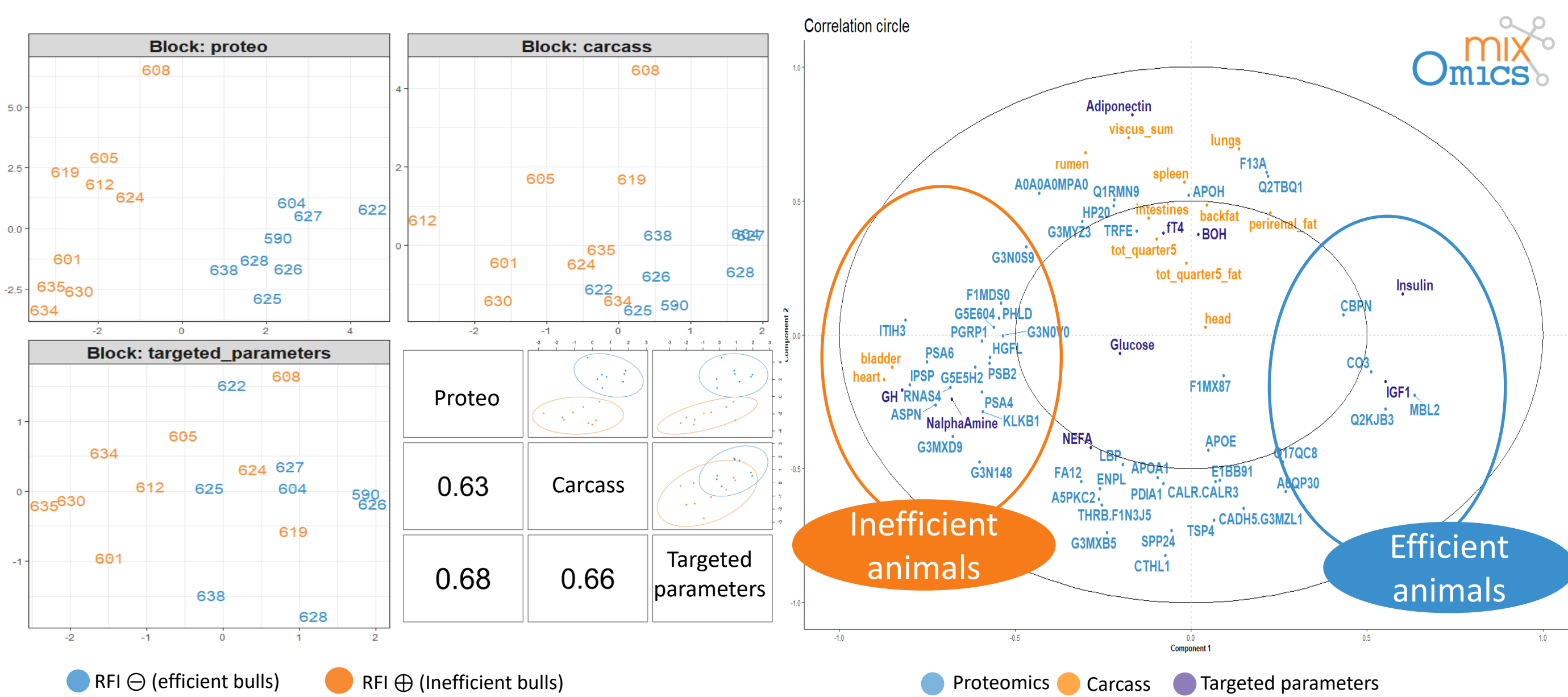
Parameter	RFI NEGATIVE	RFI POSITIVE
DMI, kg/d	7.69 (0.74)	8.96 (0.72)
RFI, kg DM	-0.75 (0.24)	0.69 (0.14)
ADG, kg/d	1.82 (0.22)	1.50 (0.20)
FCE, kg/kg	0.215 (0.014)	0.181 (0.014)
RESIDUAL.BW.GAIN, kg	0.07 (0.16)	-0.13 (0.14)

Mean (standard deviation)
in each group of efficiency

Workflow analysis of proteomic dataset



Parameters that discriminate RFI+ and RFI- bulls: multiblock integration

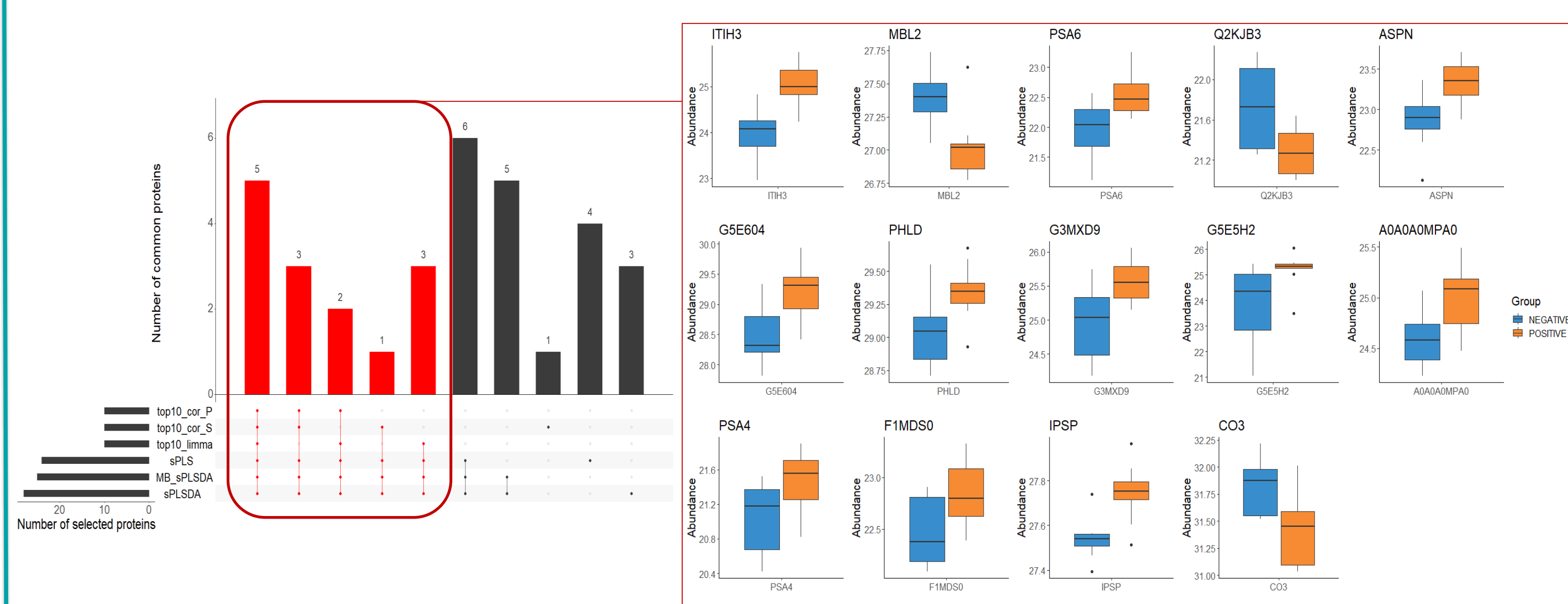


Cross-validation selection of 25 proteins, 3 carcass parameters and 8 hormones or metabolites

Efficient bulls when compared to inefficient:

- Smaller bladder and heart,
- Lower GH, adiponectin, FT4, α amino nitrogen and NEFA concentrations,
- Higher insulin and IGF1 concentrations,
- 20 plasma proteins (incl. ITIH3, IPSP, ASPN and PSA6) less abundant, and 5 plasma proteins (incl. MBL2, ANGPTL3, CO3) more abundant.

Candidate biomarker proteins: combination of methods



Among the 229 plasma proteins identified by proteomics, 14 proteins are proposed as potential biomarkers of RFI by multiple feature selection methods (see workflow).

These proteins were mainly related to proteolysis and its regulation, lipid storage, response to triglycerides, immune response, and angiogenesis.

The use of multi-block sPLSDA to integrate 3 datasets helped us finding a biosignature of feed efficiency (RFI) combining proteins, targeted parameters and carcass characteristics. Among these datasets, proteomic data best discriminated the two RFI groups. Lastly, by using multiple feature selection method, we identified 14 potential candidate proteins that may be potential low-invasive biomarkers for RFIs. Further exploration across a larger number of animals (contrasting diets, different breeds, etc.) is necessary to determine the robustness of these results and confirm these potential biomarkers.