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Postmortem muscle proteomics reveals genetics and environmental enrichment effects: Implications for meat authentication



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Introduction and Background

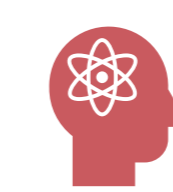
Extensification factors

Husbandry practices that reduce the intensity of farming systems to promote better **animal welfare** and potentially improve **meat quality**

- ✓ Slower-growing genetics
- ✓ Dietary supplementation
- ✓ Space allowance
- ✓ Environmental enrichment

Produce meat **higher in value**

- more vulnerable to **food fraud**
- ensuring **authenticity** is essential

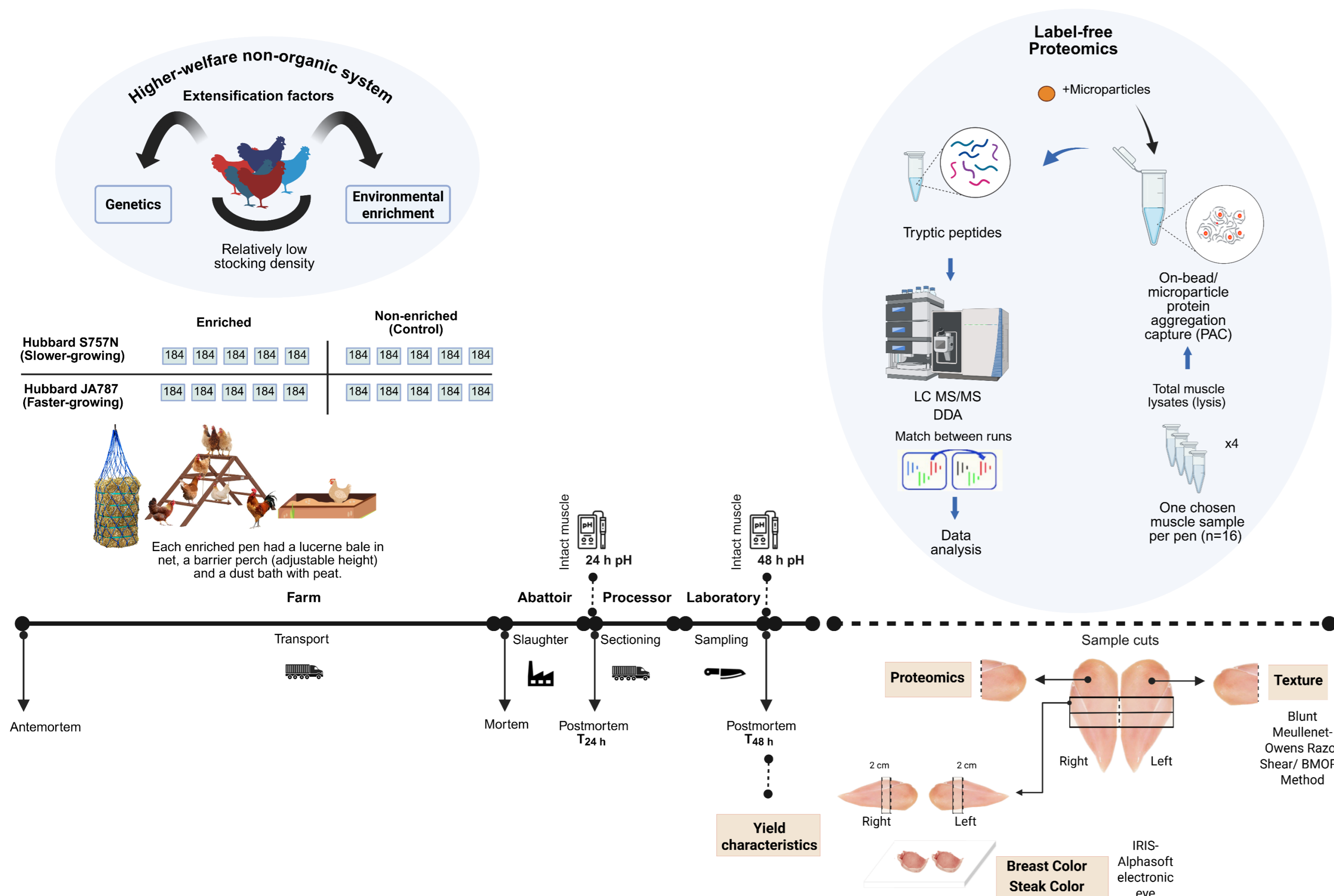


Requires an understanding of meat quality at **molecular level** and the influence of husbandry practices



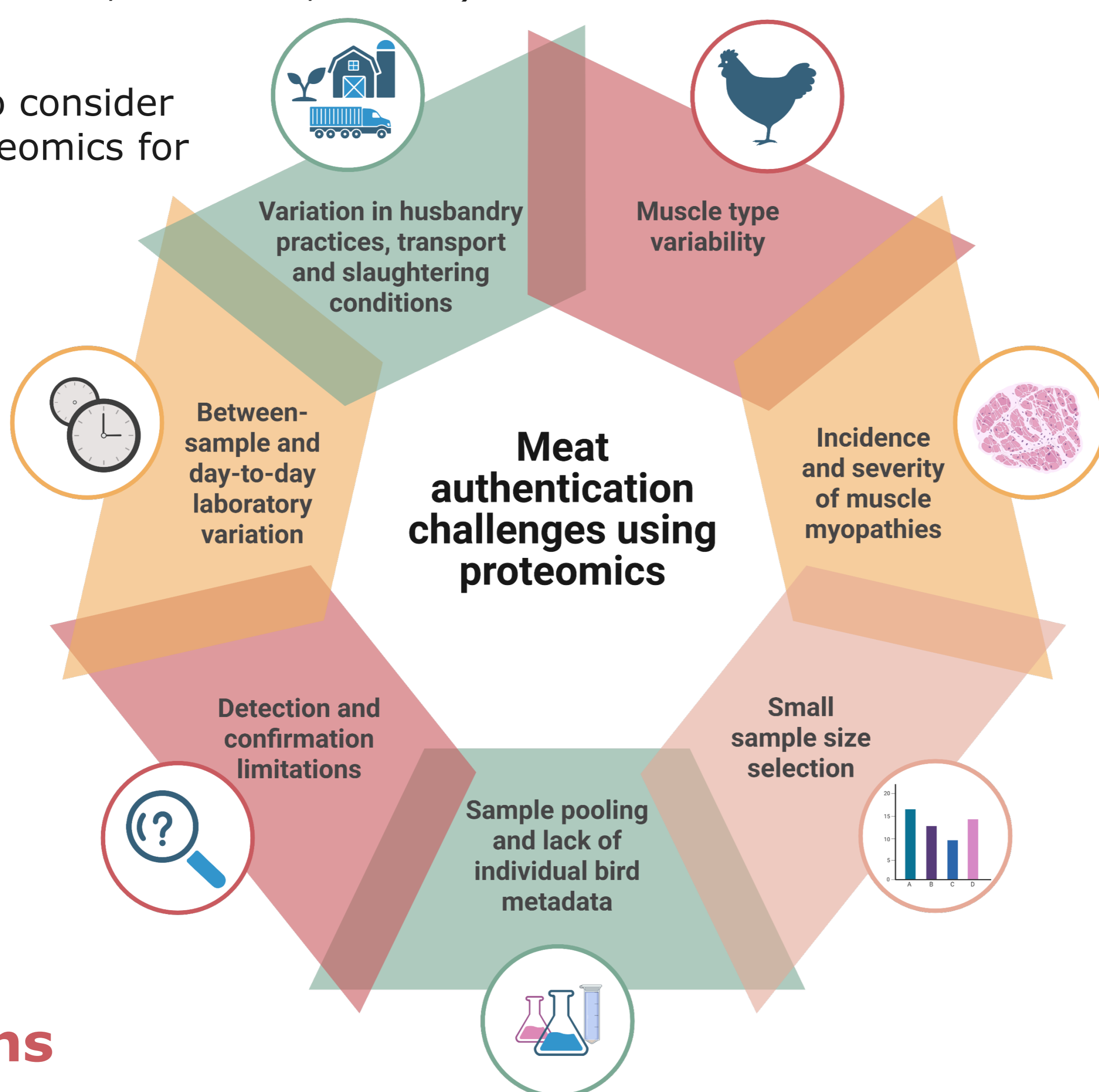
Insights enable identification of molecular markers and development of fit-for-purpose **authentication tools**

Materials and Methods



- Proteomics revealed slower-growing (SG) exhibited higher abundance of proteins than faster-growing (FG) related to **detoxification and oxidative stress management** (GPX3, LOC100859645, GSTA3, AKR1A1), **actin filament binding** and **actin filament-based processes** (FLNA, MYLK2, MYH11, TPM1, TAGLN, SH3BP1, ANXA6)

- Implications to consider when using proteomics for authentication:



Conclusions

- Authentication requires **exclusion of muscle myopathies** to avoid confounding pathological effects
- Higher **inter-session variability** (i.e., FG) underscores importance of careful **sample selection** and **adequate sample size**
- In a well-controlled intervention experiment, quality traits (texture, colour) were reflected at proteomic level, supporting their use as **intrinsic markers** for verifying meat origin and welfare-related production practices

Results and Discussion

Myopathy-related outlier* identified, distinct from main factors

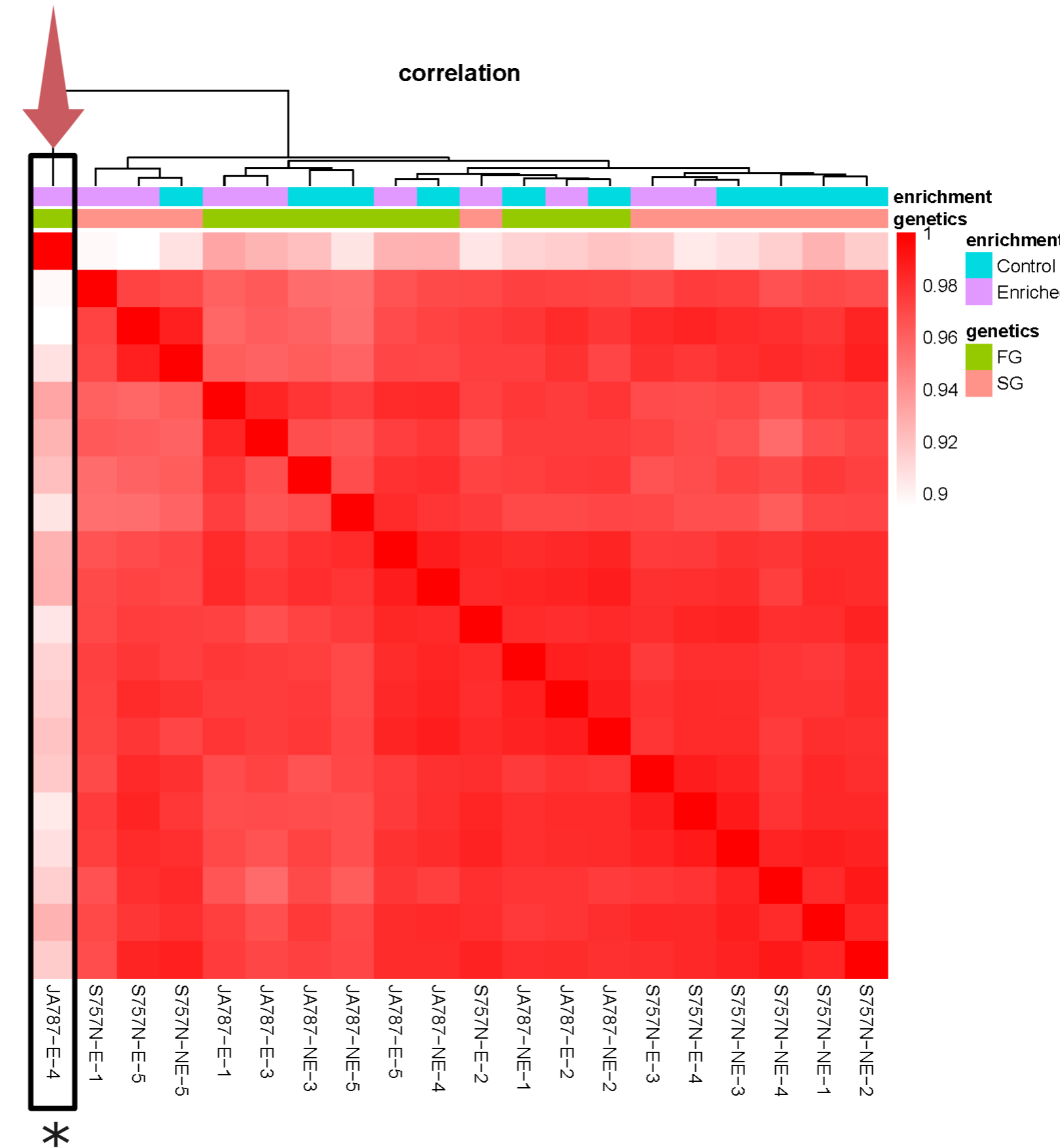


Fig. 1 Heatmap correlations matrix based on identified proteins without imputation (n=20)

- Enrichment: SG showed elevated expression of **stress-response** and **cellular repair proteins** incl. AIMP1, B2M, SOD1

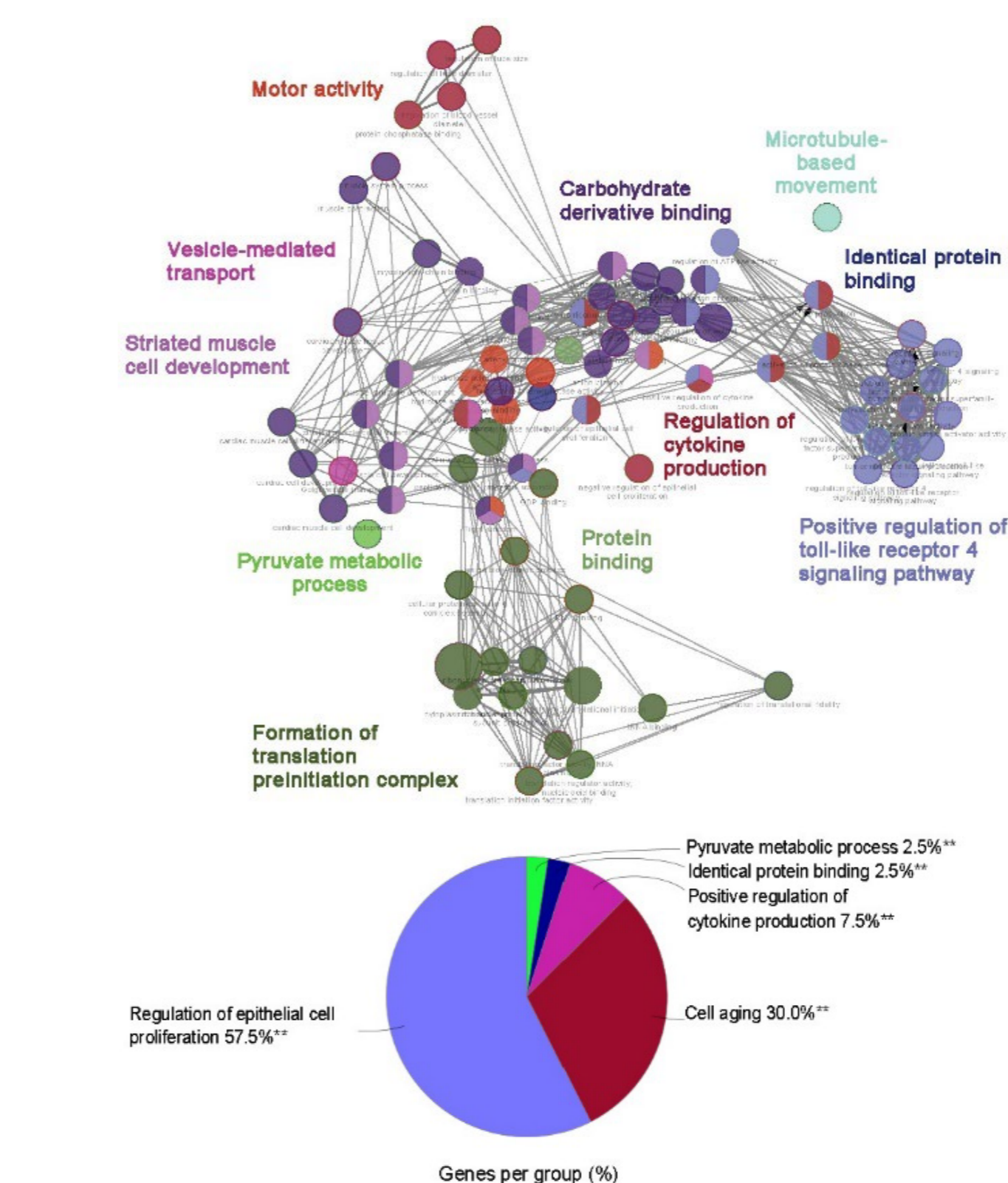


Fig. 3. Proteomics responses of slower-growing (SG) broilers to on-farm environmental enrichment. ClueGO functional group annotation network of enrichment-regulated proteins in SG broilers, based on similarity of their associated genes. Chart shows functional groups for the user genes that are higher in enriched environments. Significance levels **p < 0.001; *0.001 < p < 0.05

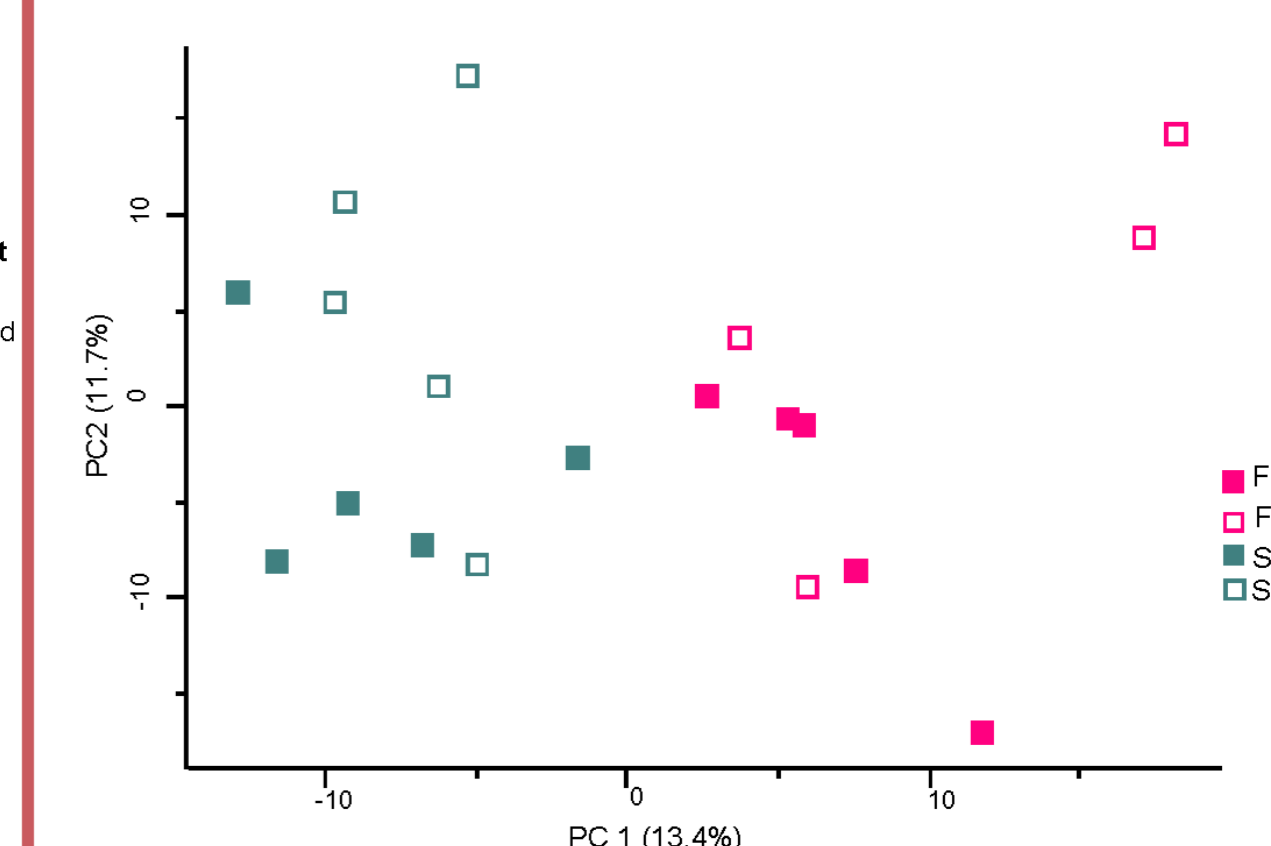


Fig. 2 Principal component analysis (PCA) plot performed across all treatments (n=19)

- Enrichment: FG responded by upregulating **proteasome pathway activity**, indicative of increased protein degradation

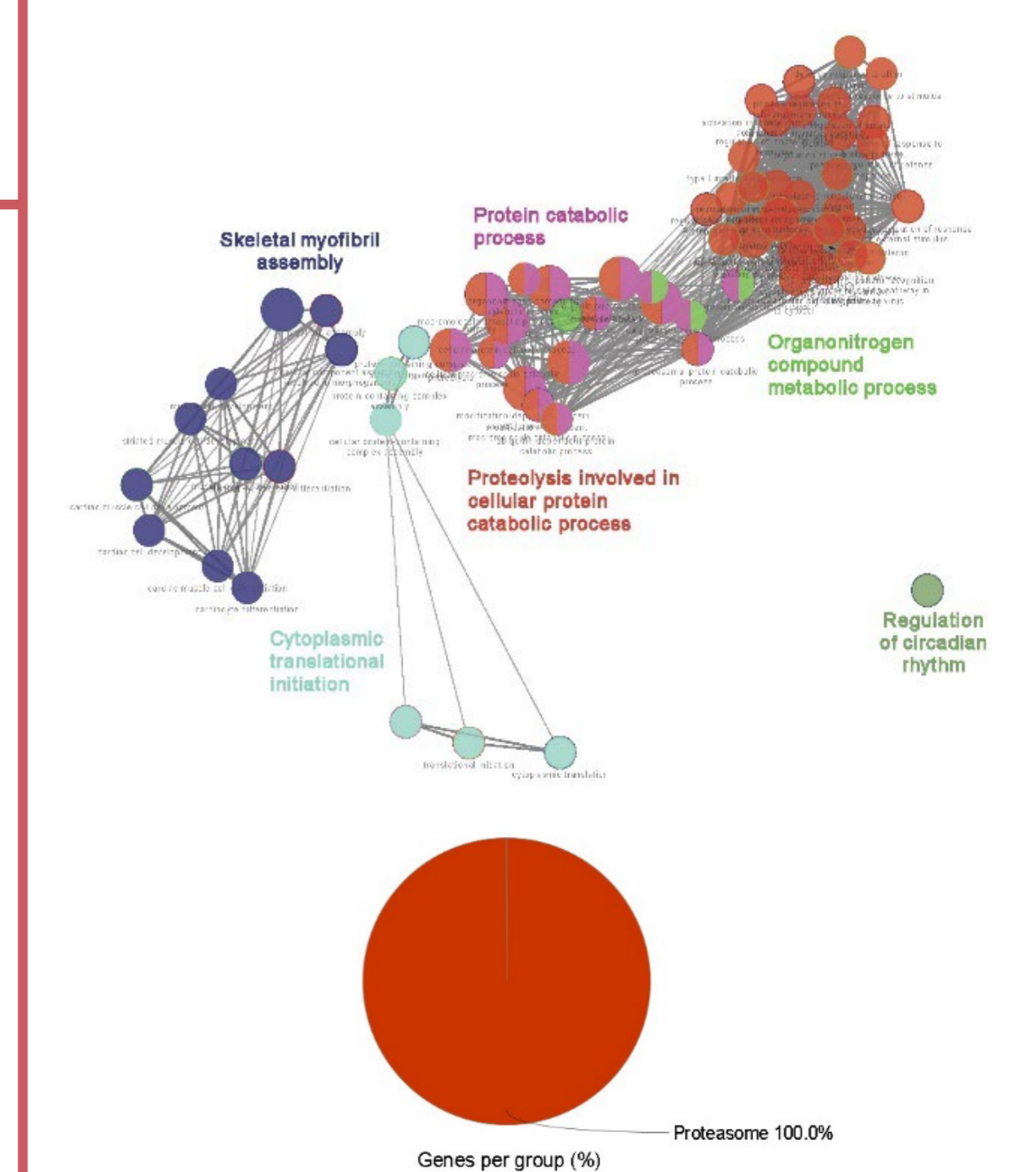


Fig. 4. Proteomics responses of faster-growing (FG) broilers to on-farm environmental enrichment. ClueGO functional group annotation network of enrichment-regulated proteins in FG broilers, with annotations as described for Fig. 3

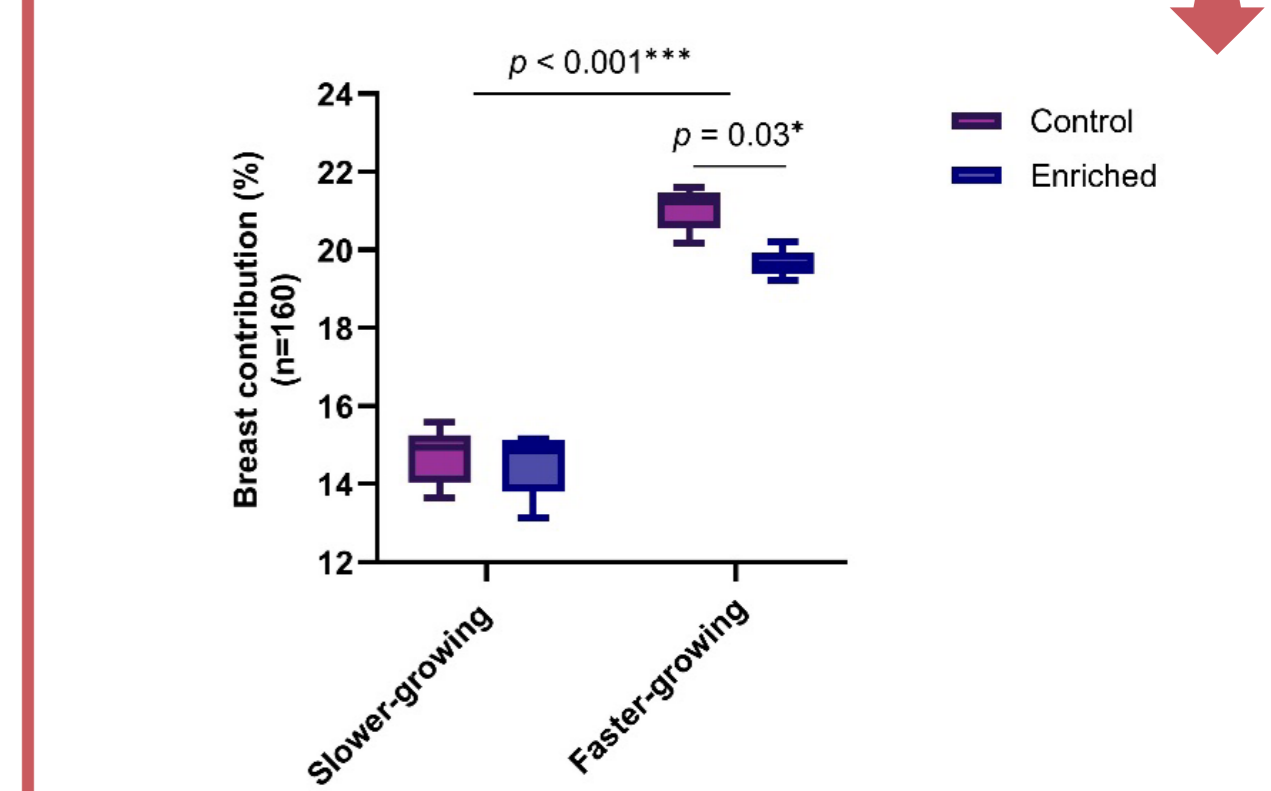
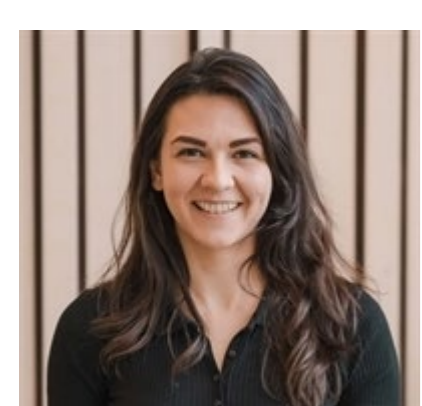


Fig. 5. Breast weight contribution (%) to the carcass



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