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Extruded linseed alone or in combination with fish oil modifies mammary gene expression profiles

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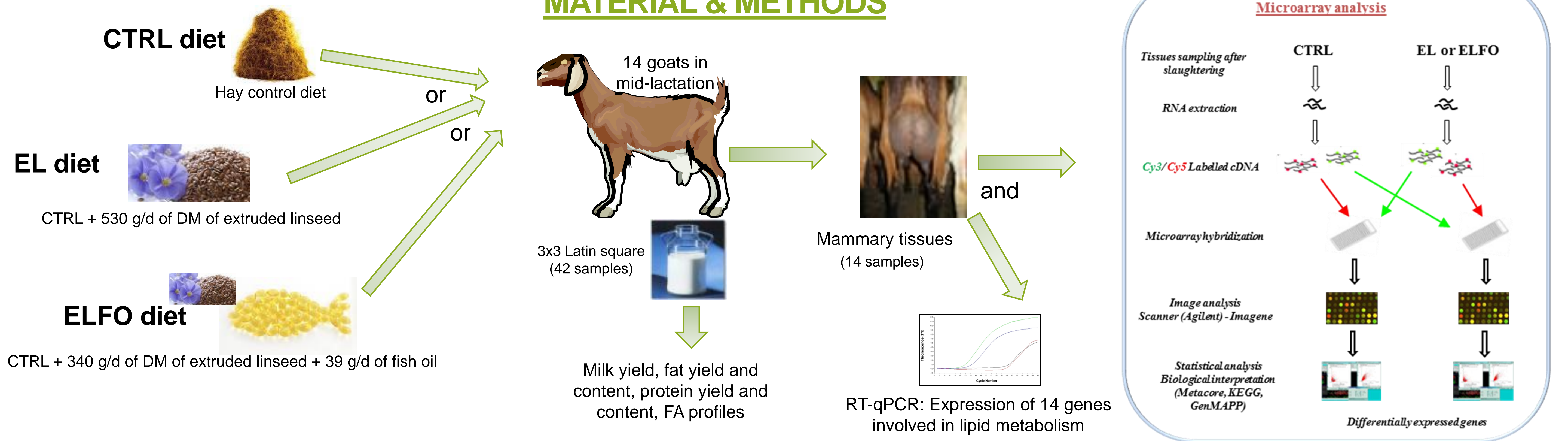


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INTRODUCTION

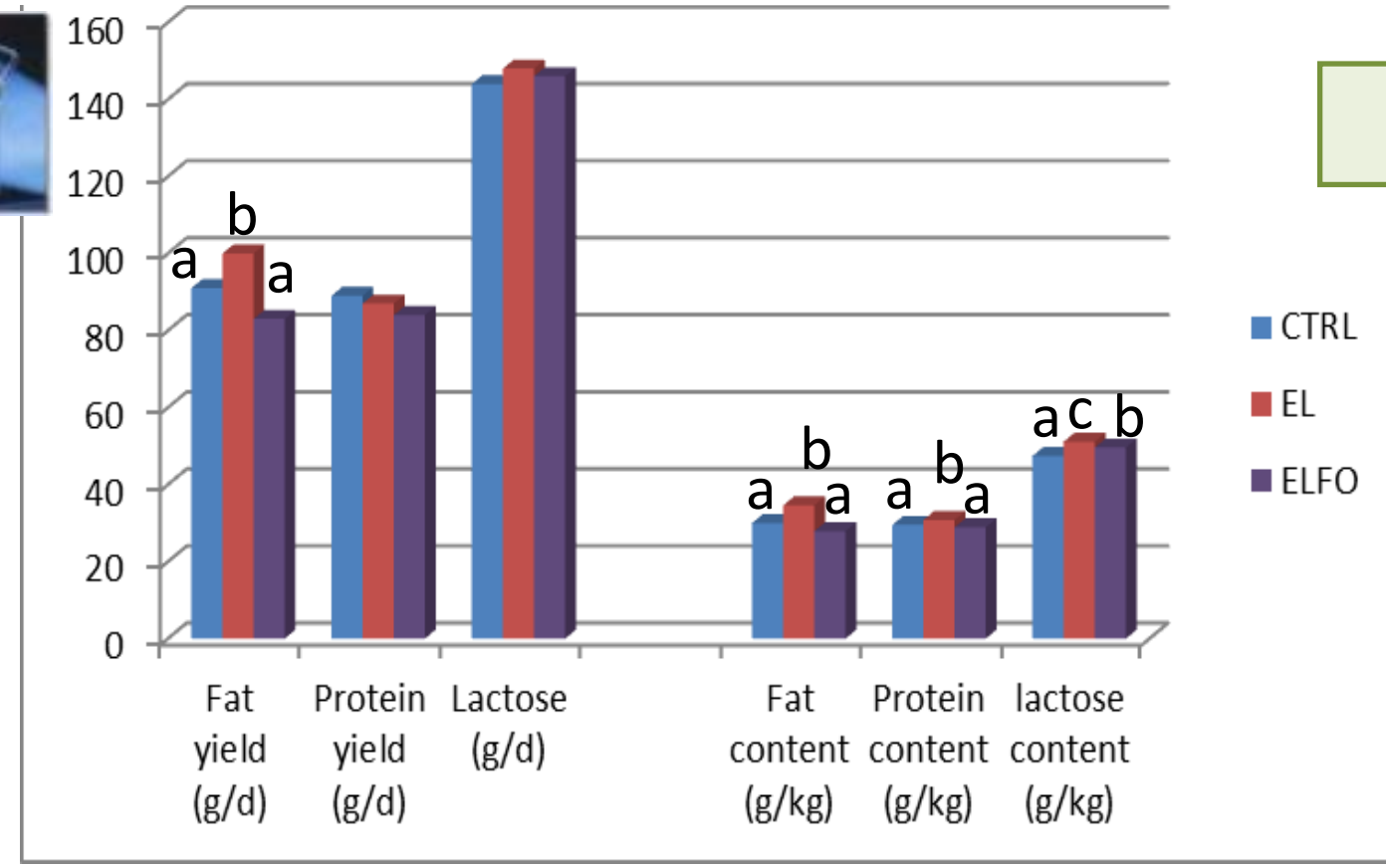
Nutrition is a major factor that regulates ruminant milk components synthesis particularly fatty acid (FA) composition which is an important determinant of milk nutritional quality for human consumers. Thus, in ruminants, nutritional strategies were developed with dietary supplementations such as plant oils or seeds rich in n-3 polyunsaturated FA to increase the milk nutritional value. In mammary gland, the milk components biosynthesis involves a large number of genes which nutritional regulation is not totally known in ruminants. In particular, in goats, although there are recent advances in functional genomic studies based on targeted approach using quantitative RT-PCR (reviewed in Bernard et al. 2008) or on global analyses using microarrays (Ollier et al., 2007; 2009), the effects of n-3 rich diets on mammary gene expression profiles are still poorly documented.

MATERIAL & METHODS



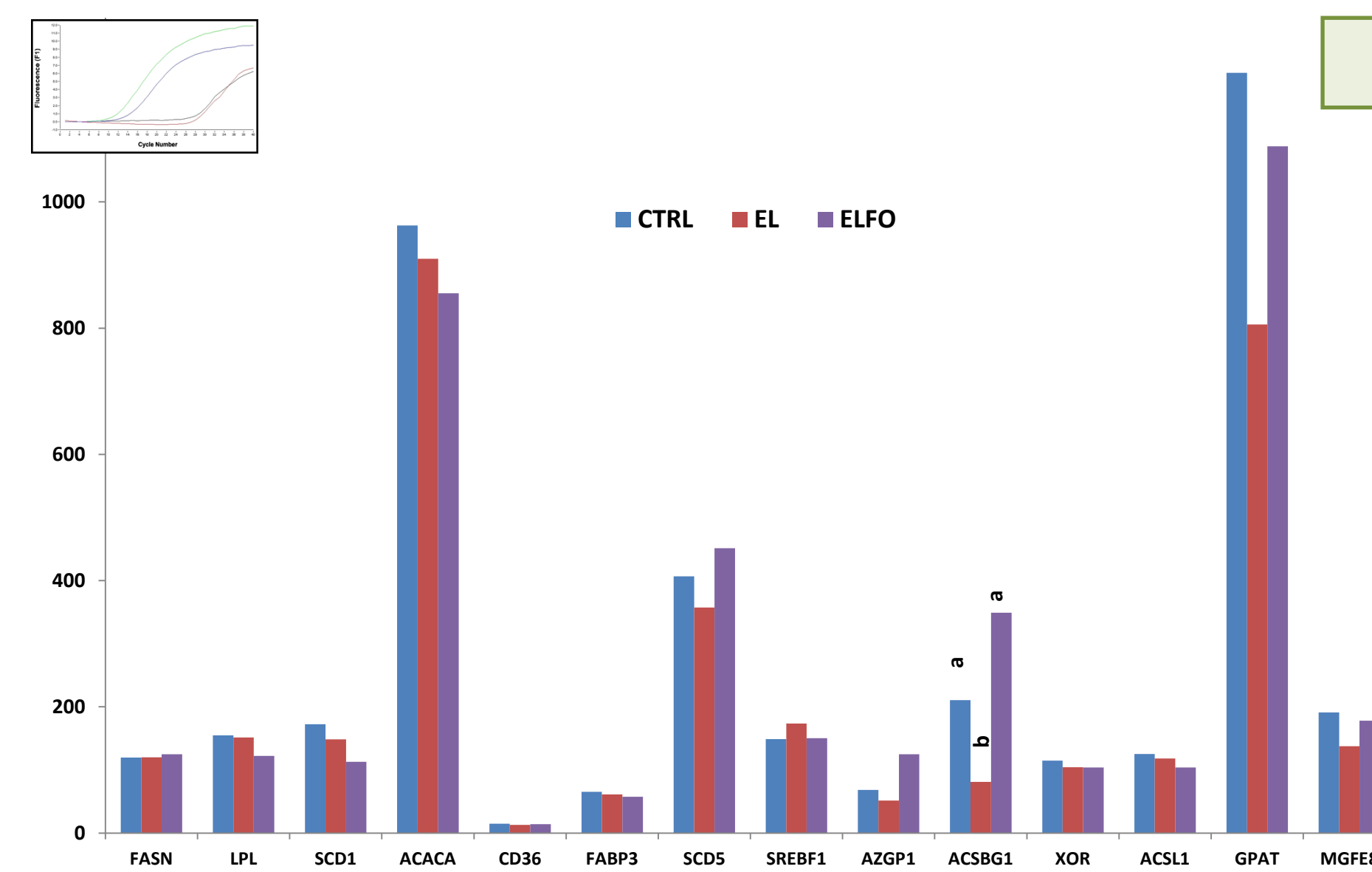
RESULTS

MILK PRODUCTION & COMPOSITION



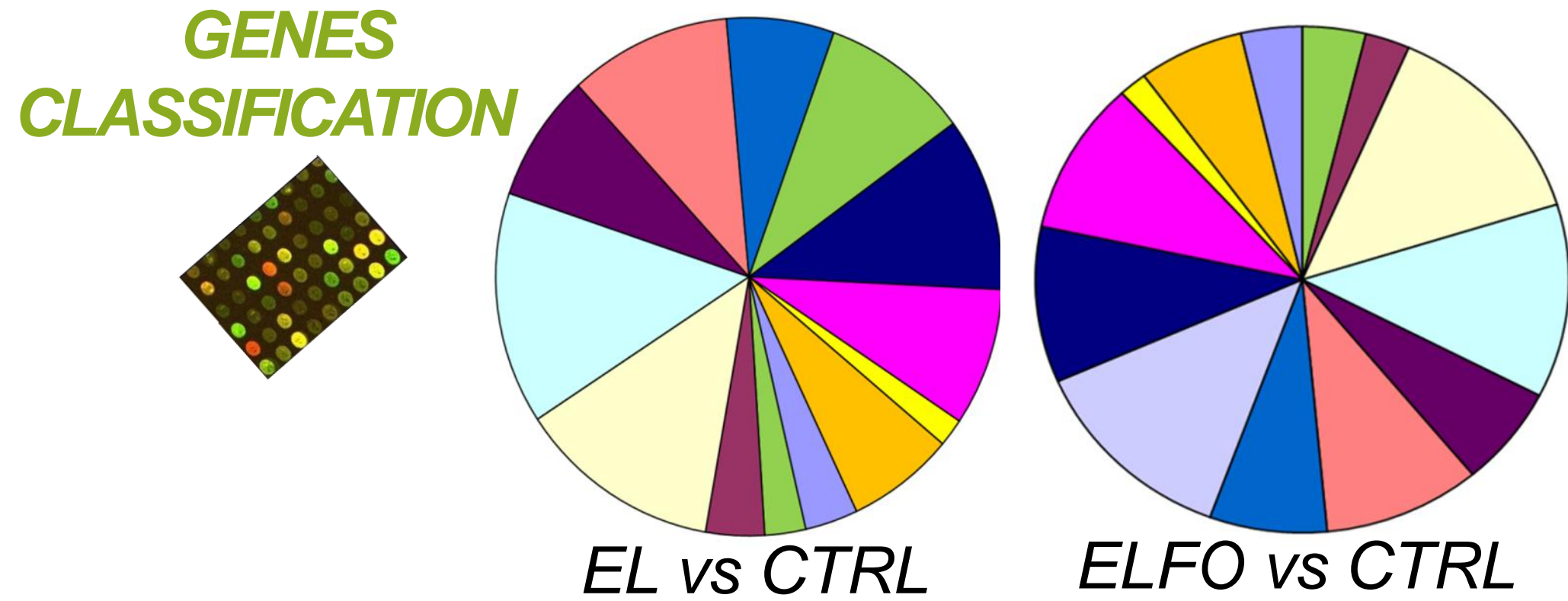
EL diet increased fat yield and fat and protein contents in milk compared with CTRL diet whereas the addition of fish oil (ELFO) counteracted the effects of EL. Both EL and ELFO enhanced lactose content relative to CTRL.

CANDIDATE GENES EXPRESSION



The expression of *SCD1* ($p < 0.1$) was down-regulated with ELFO compared with CTRL. The expression of *AZGP1* ($p < 0.1$) and *ACSBG1* ($p < 0.05$) genes were up-regulated with ELFO compared with EL whereas only *ACSBG1* ($p < 0.05$) was down-regulated with EL compared to CTRL diet.

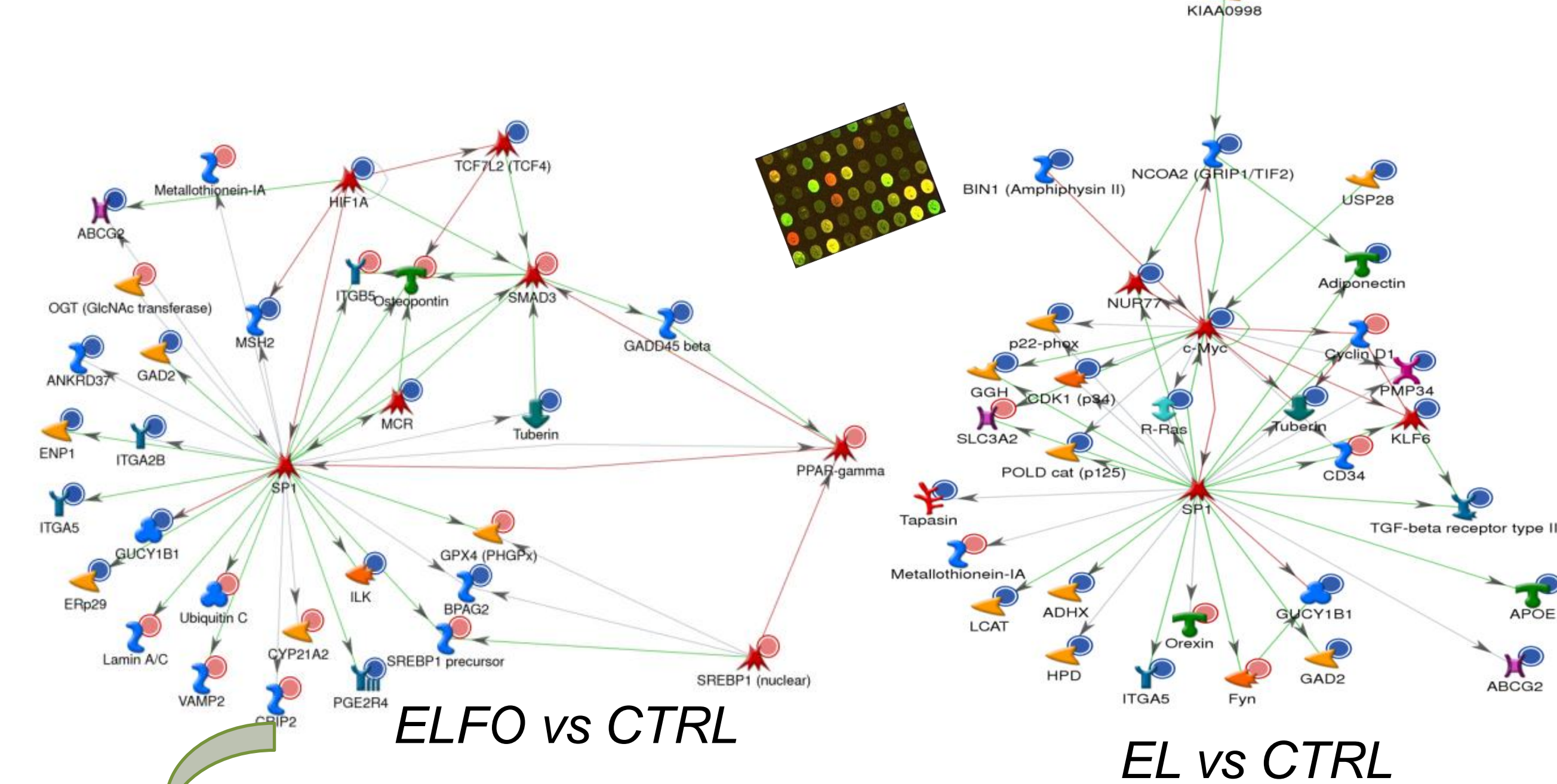
DIFFERENTIALLY EXPRESSED GENES CLASSIFICATION



LIPID METABOLISM & TRANSPORT CLASSES

e.g.	↓	↑
EL vs CTRL	ADIPOQ, APOE	ABC4
ELFO vs CTRL	FABP1	PPARG, SREBF1

REGULATOR NETWORKS



The bioinformatics analyses of the DEG list revealed two networks centered on an estrogen receptor (ESR1) and a transcriptional factor (SP1, represented here) with EL and ELFO diets compared to CTRL diet.

Statistical analyses revealed 346 and 316 differentially expressed genes (DEG) with the EL and ELFO compared to the CTRL diet, respectively. The classification of these DEG according to their gene ontology pointed out the cell cycle, proliferation, differentiation and death (ca. 13% of the DEG) together with the protein metabolism and transport classes (ca. 13% of the DEG) as the two main categories altered by EL or ELFO diets.

CONCLUSIONS & PERSPECTIVES

The increment of such holistic transcriptomics approach will provide new integrative view of molecular mechanisms involved in the nutritional regulation of goat mammary function during lactation. However, the expression of all these genes still needs to be evaluated in relation with milk fat composition and needs to be looked deeper into data mining analysis.