



IMPACT OF FETAL EXPOSURE TO TESTOSTERONE ON FETAL INSULIN SENSITIVITY TISSUES: A MORPHOLOGICAL AND MOLECULAR APPROACH

GP 145



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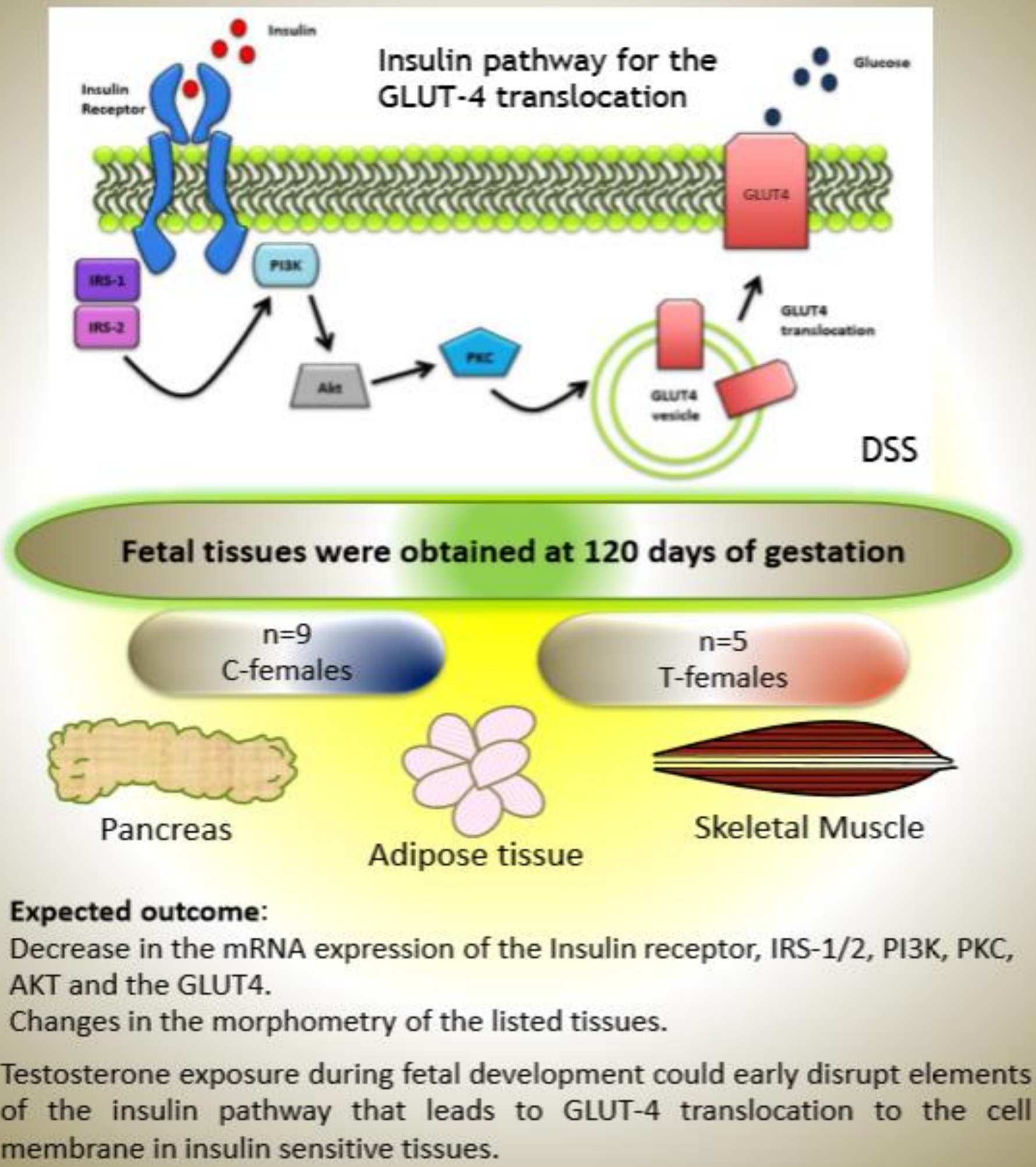
INTRODUCTION

The hyperandrogenemic environment during fetal life has been postulated to be a reprogramming factor to develop PCOS in postnatal life. Women with PCOS show not only reproductive impairments but also metabolic dysfunction that could be initiated during fetal life due to the hyperandrogenemic prenatal environment, or could be triggered postnatally. Hyperandrogenemia, hyperinsulinemia and insulin resistance are features of the PCOS, placing affected women at high risk in case of pregnancy, of perpetuating this syndrome to their daughters. One of the focus in the etiology of the metabolic traits of PCOS are the changes observed in insulin sensitive tissues. There is agreement in a possible defective signaling at the insulin receptor level, leading to the insulin resistance.

Is the Insulin resistance programmed prenatally in these women? Does the abnormally high levels of testosterone during fetal development have a role in modifying prenatally the insulin pathway in insulin sensitive tissues? This questions could be answered in animal models of PCOS. Our sheep model of prenatal testosterone exposure has been extensively used to study the programming of PCOS. It has the advantage that occurs without an impact on maternal insulin, glucose or lipids that could add another source of hormonal disarrangement to the fetus.

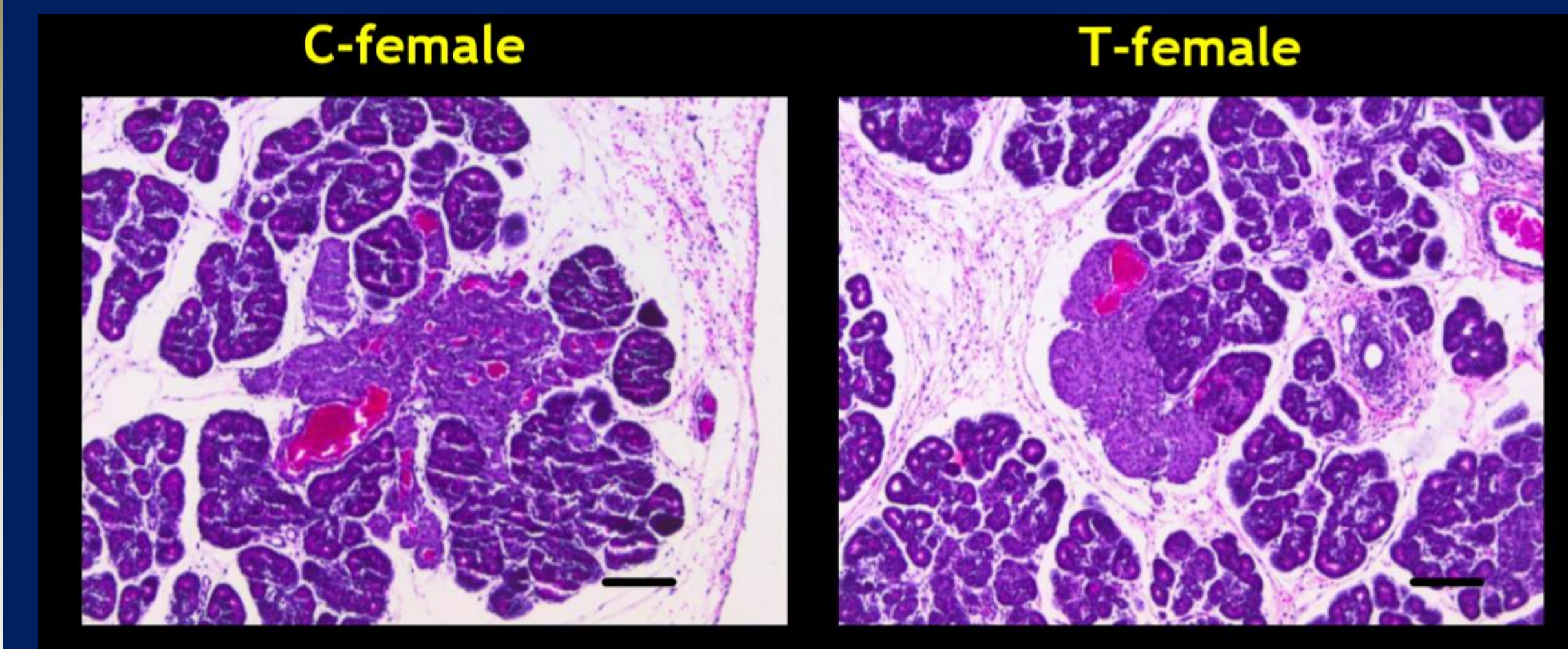
HYPOTHESIS

Exposure to testosterone during intrauterine development could affect the fetus, reprogramming the insulin sensitivity of the offspring's tissues.

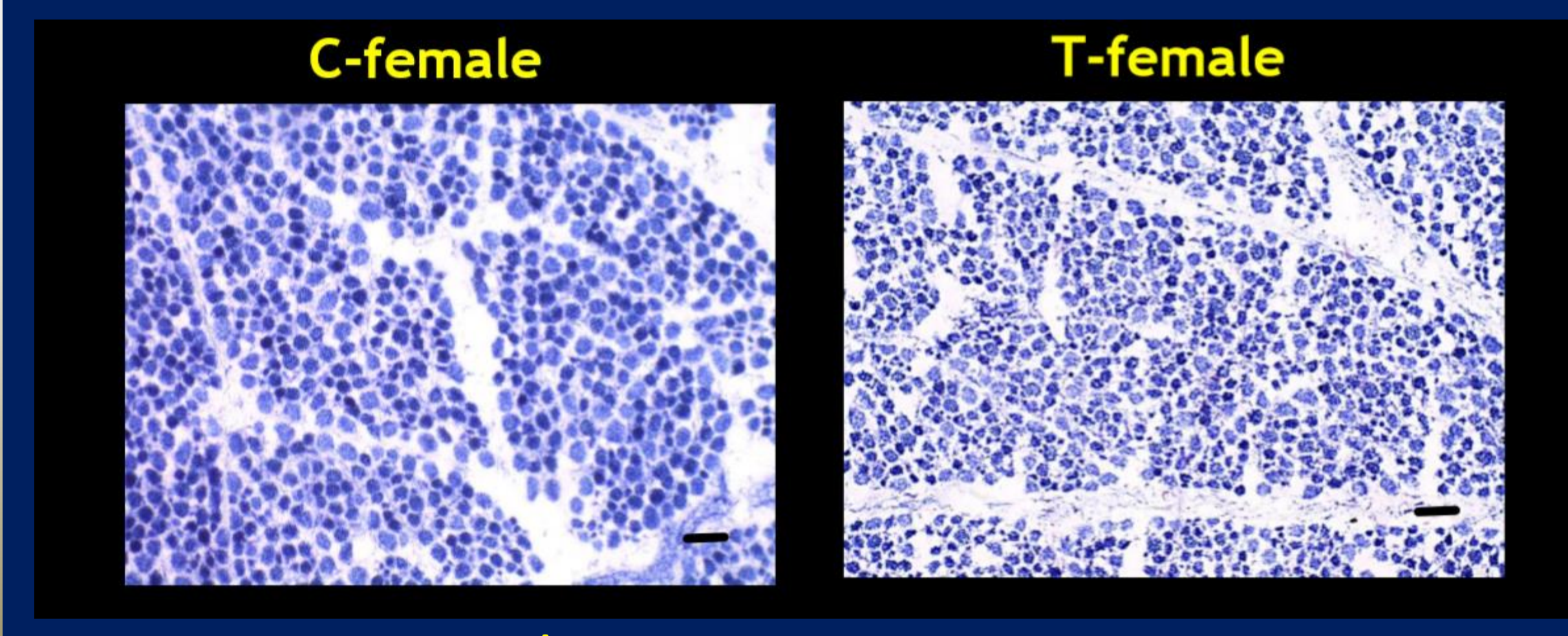


RESULTS

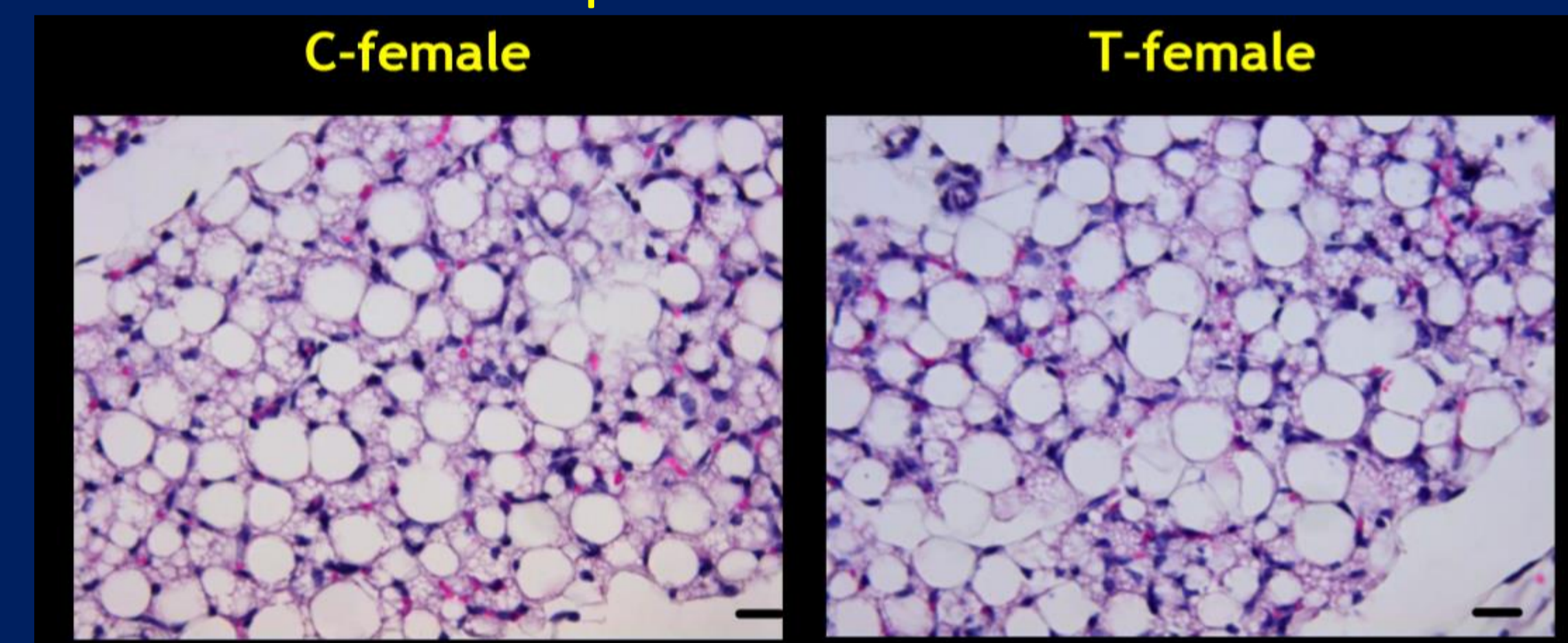
Pancreas



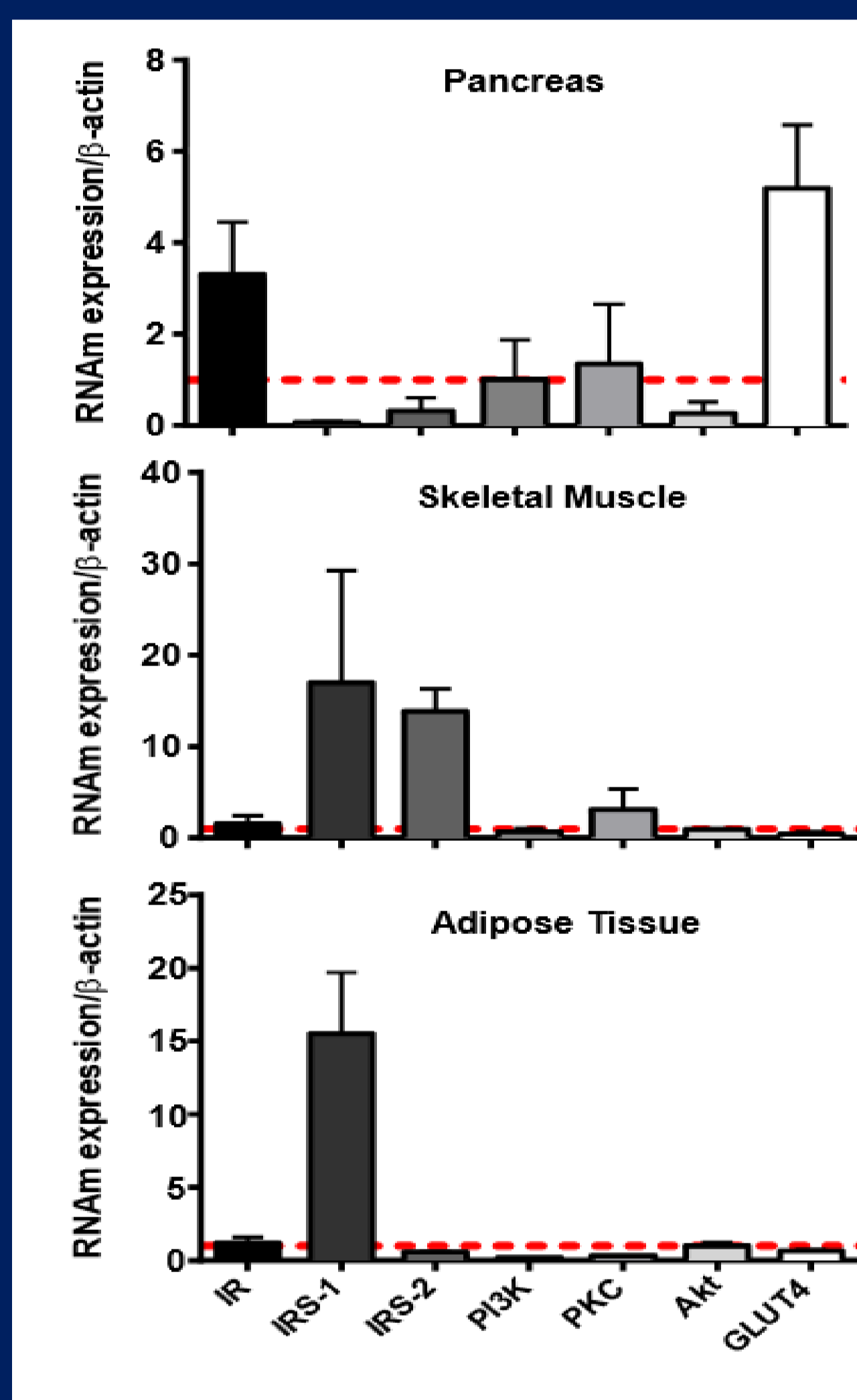
Skeletal Muscle



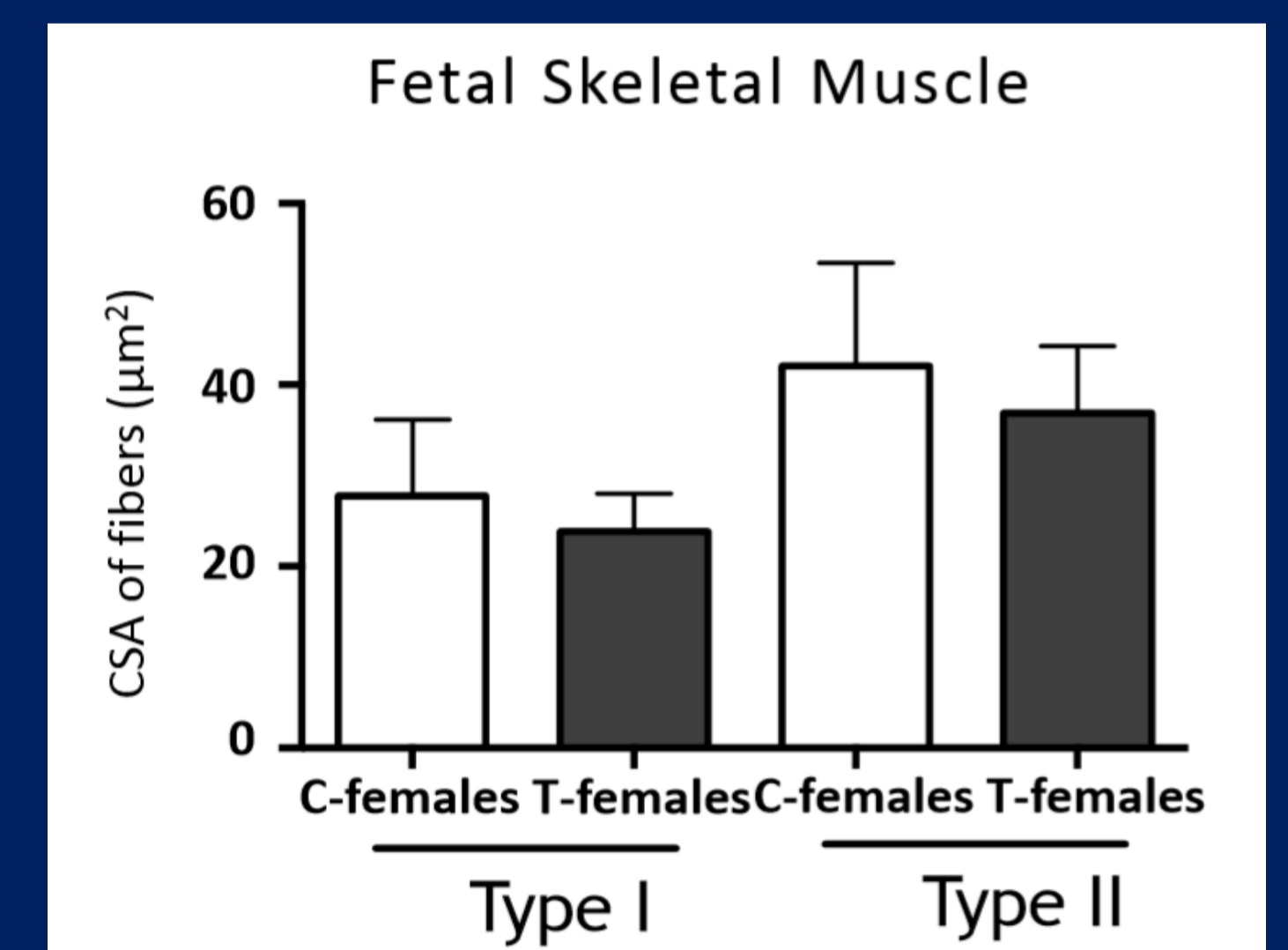
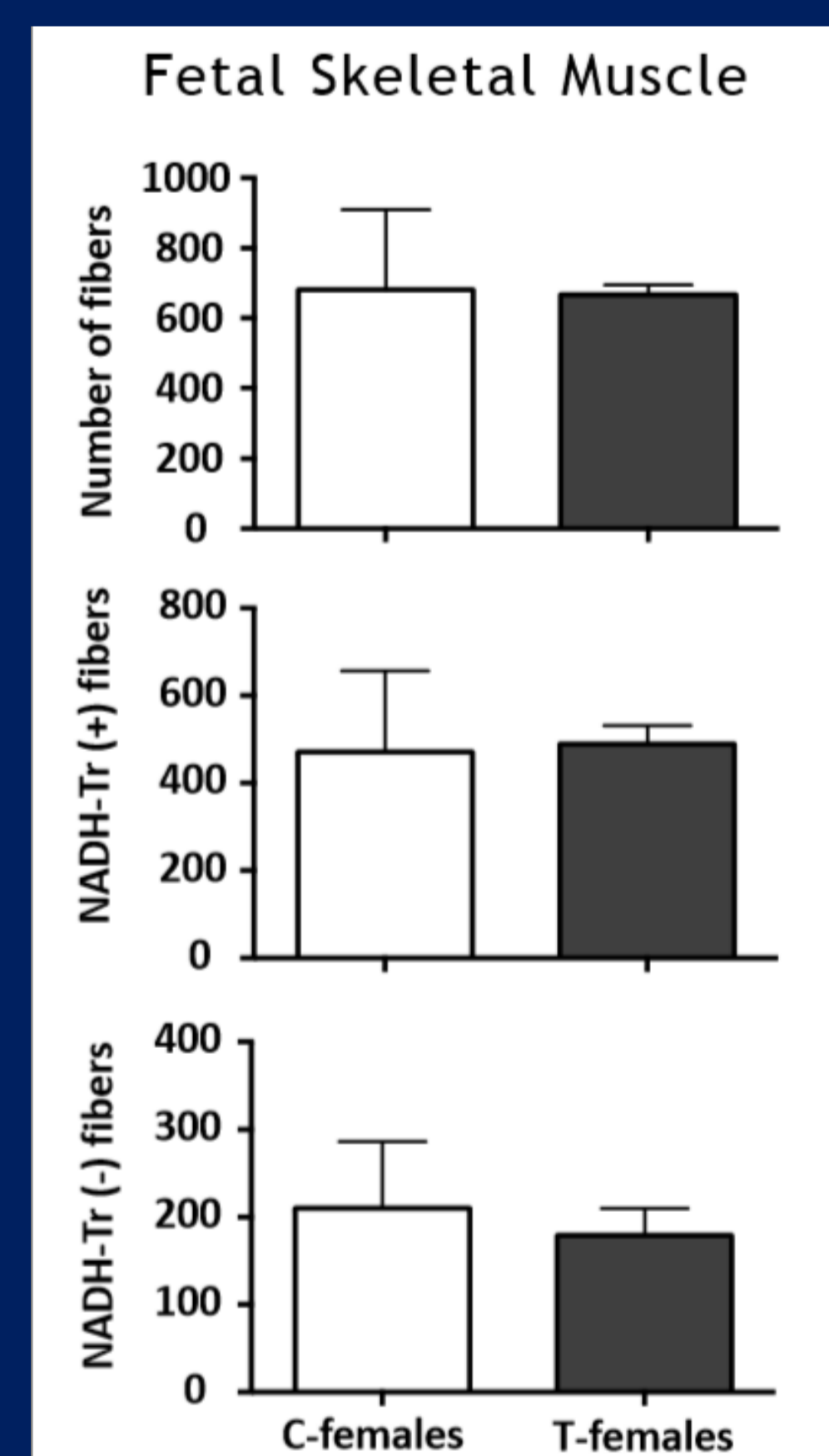
Adipose Tissue



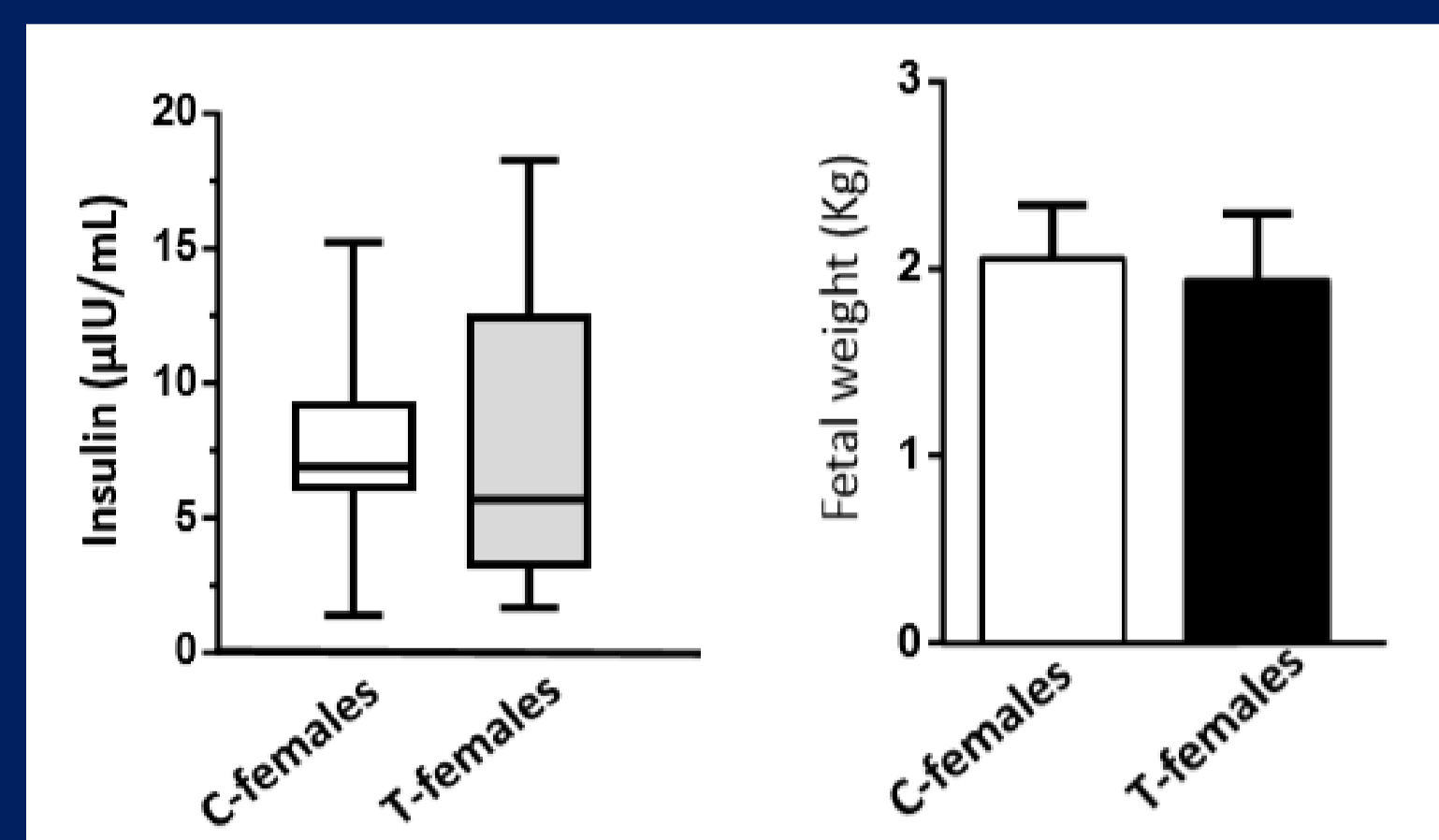
Representative photomicrographies showing no significant differences in the morphological characteristics of the insulin sensitive fetal tissue. Bar= 100 µm in pancreas and skeletal muscle and 25 µm adipose tissue.



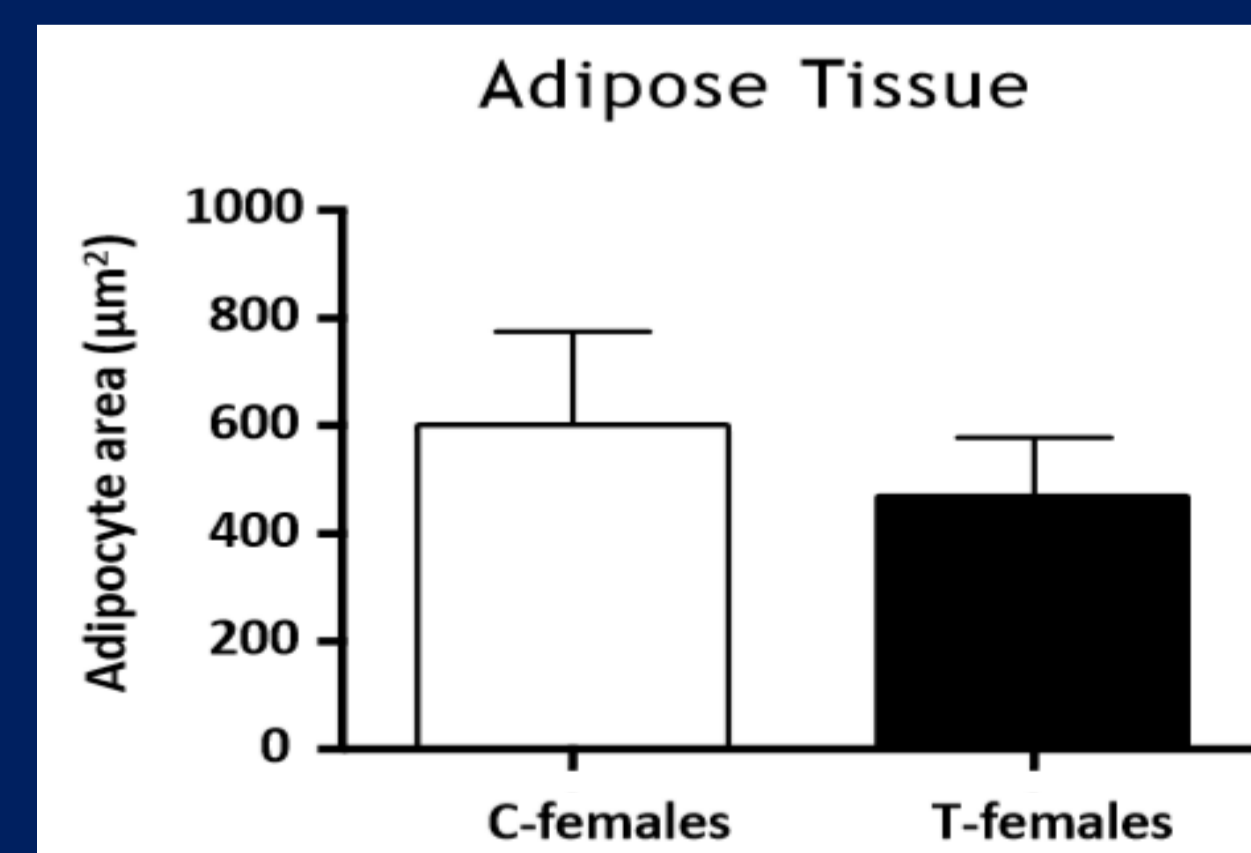
Transcriptional activation of the insulin signaling pathway in T-exposed fetuses compared to control fetuses. The red line indicates the level of expression of the signaling factors in the control female fetuses. Transcriptional activation is higher in T-females in some factors in a tissue-specific manner.



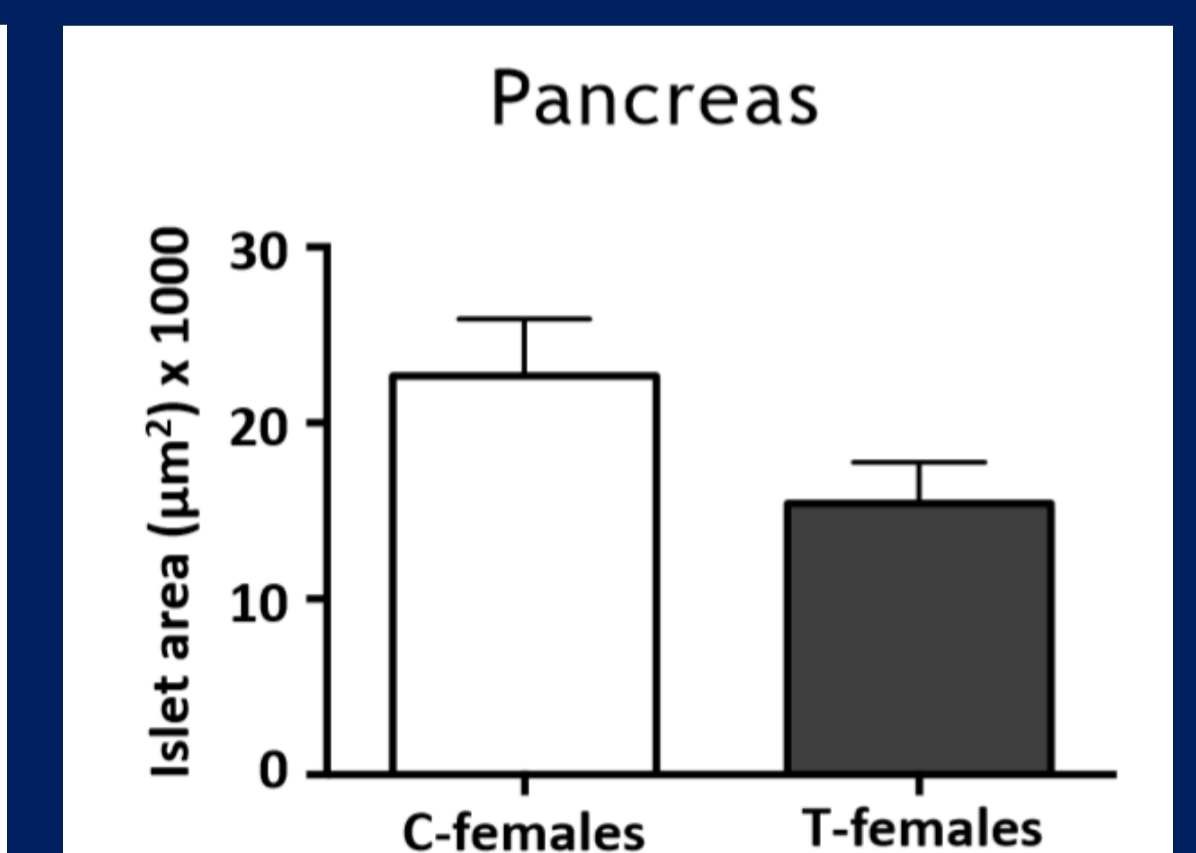
The composition of the skeletal muscle was similar between both groups of fetuses regarding the total amount of fibers and its phenotype.



Fetal insulin plasma levels were similar between groups. No difference was observed in fetal weight at 120 days gestation between groups.



The area of the adipocytes and of the pancreatic islets were similar between groups.



CONCLUSIONS

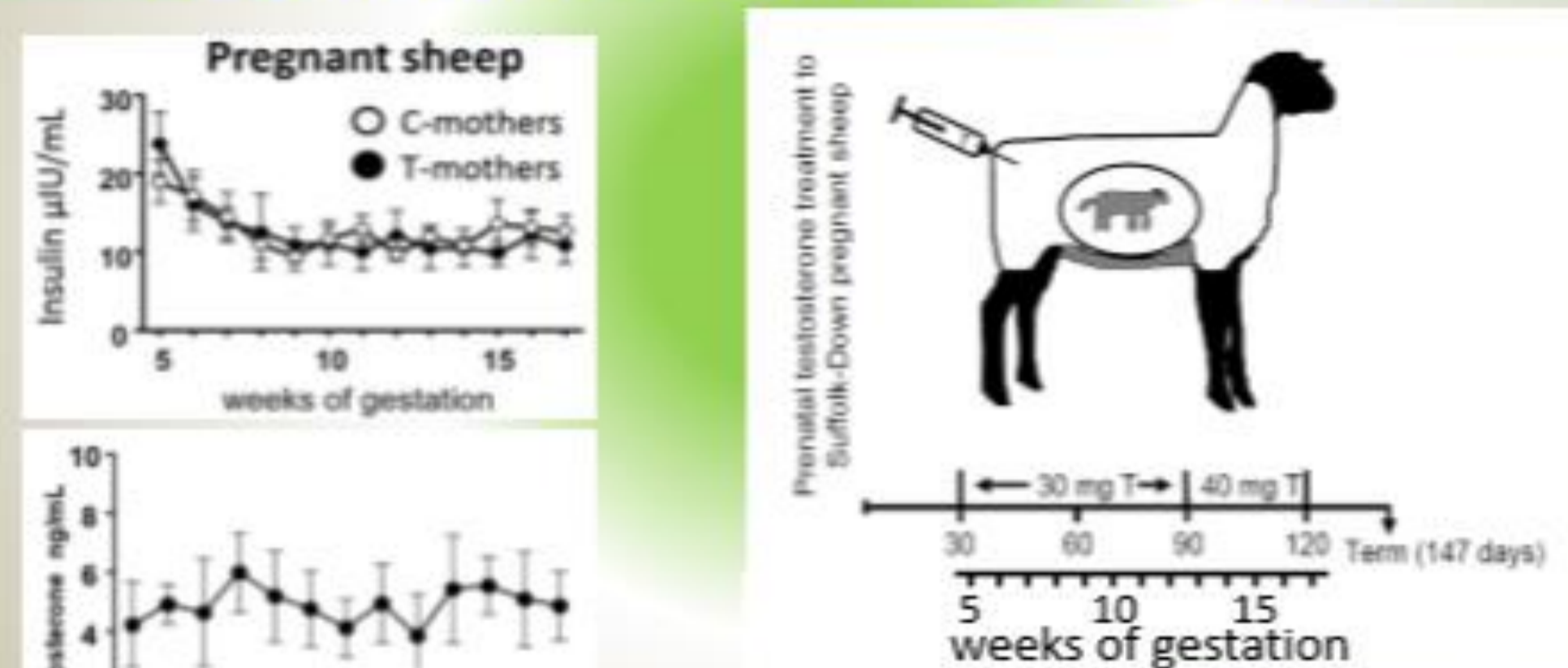
These results provide evidence that testosterone exposure during fetal sheep development induces differential transcriptional activation of the insulin signaling, without significant effects on morphological organogenesis.

Normal sheep pregnancy

- Systematic decline in insulin levels and in insulin sensitivity.
- Reduced pancreas response to insulinotropic agents.
- Minimum peripheral glucose utilization.
- Increased mobilization of adipose tissue to supply with NEFA to the mother and glucose to the fetus.
- Potential insulin resistance in peripheral maternal tissues.

Sheep model of prenatal androgenization

Pregnant sheep + Testosterone treatment



Hyperandrogenemic mothers insulin resistance (+)
Hyperinsulinemia (-)

Unbiased model of prenatal programming effects of testosterone

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