

Proteomics based screening tool to detect molecular responses following aromatase inhibition

S.U. Ayobahan¹, E. Eilebrecht¹, M. Teigeler¹, M. Kotthoff¹, S. Kalkhof², C. Schaefers¹
and H. Hollert³

¹Fraunhofer Institute for Molecular Biology and Applied Ecology IME, Auf dem Aberg 1,
57392 Schmallenberg, Germany

²University of Applied Sciences Coburg, Germany

³RWTH Aachen University, Germany

E-mail contact: steve.ayobahan@ime.fraunhofer.de

Chemical exposure to endocrine disruptors can have adverse outcomes on organism health and function; however, the current reliance on end-points such as egg number, plasma VTG content and morphological changes to determine effects of endocrine disrupting chemicals has given rise to series of questions related to chemicals exhibiting similar effects but different mode-of-action (MoA). Mechanistic identification of biological responses preceding to apical endpoints has become crucial for analyzing, accessing and determining chemical effects. Proteomics, therefore, show appreciable promise as a molecular screening tool for identifying specific alterations between exposures and controls, which is therefore imperative in discriminating endocrine disruptors from substances with a non-endocrine MoA. Such tool waives the need for elongated high-tier testing.

The main aim of this study is to identify alteration in molecular-toxicity pathways that are specific to chemical-induced apical responses in zebrafish. The study focused on fadrozole, a known inhibitor of cytochrome P450 aromatase. Thus an excellent model substance to evaluate and validate proteomic methods with the integration of organ-specific effects. Spawning adult zebrafish groups (5 males, 5 females) maintained at 25-26°C on a 16:8 h light/dark cycle; were exposed for 21 days to fadrozole (0, 0.1, 1, 10 µg/L) and analysed for plasma vitellogenin content, egg numbers and organ histopathology. Livers and gonads were isolated for shotgun proteomics and qPCR to characterize substance induced specific molecular toxicity pathways. Proteins involved in steroid hormone secretion and estrogen stimulus such as vtg1, vtg3, vtg6 and lman1, were significantly deregulated. Several of the prominently affected pathways involved regulation of xenobiotic stimulus, lipid metabolism, metabolic processes, TCA metabolism and calcium signalling.

Our study demonstrated that the downstream induced-estrogen receptor suppression by aromatase inhibition triggered the downregulation of estrogen synthesis, which was assumed to induce the observed decrease in egg numbers and oocyte atresia with membrane folding in the ovary. We anticipate that this improvement leads to the identification of reliable biomarkers to determine chemical-induced adverse outcomes of ecological relevance in order to avoid unnecessary extensive testing.

PROTEOMICS BASED SCREENING TOOL TO DETECT MOLECULAR RESPONSES FOLLOWING AROMATASE INHIBITION



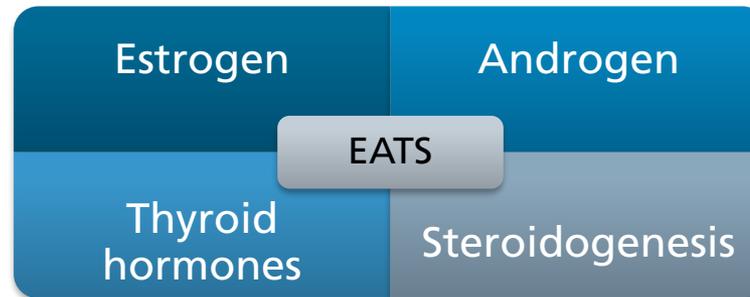
**Steve Ayobahan, Lisa Baumann, Matthias Kotthoff, Matthias Teigeler,
Henner Hollert, Christoph Schäfers, Stefan Kalkhof, Elke Eilebrecht**

BACKGROUND

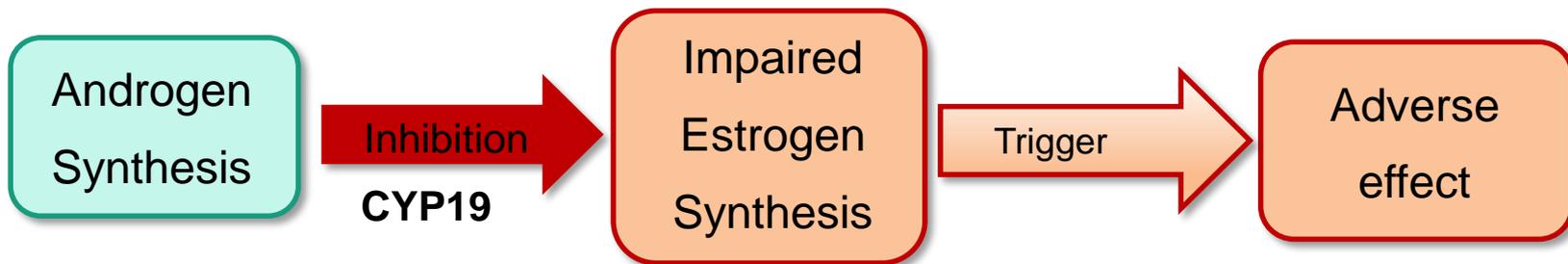
BACKGROUND

Endocrine Disruptors - are chemicals that interfere with the endocrine system and trigger an adverse developmental, reproductive and immune effects to exposed organism or its descendant population¹.

OECD Testing and Assessment framework for Endocrine Disruptors²



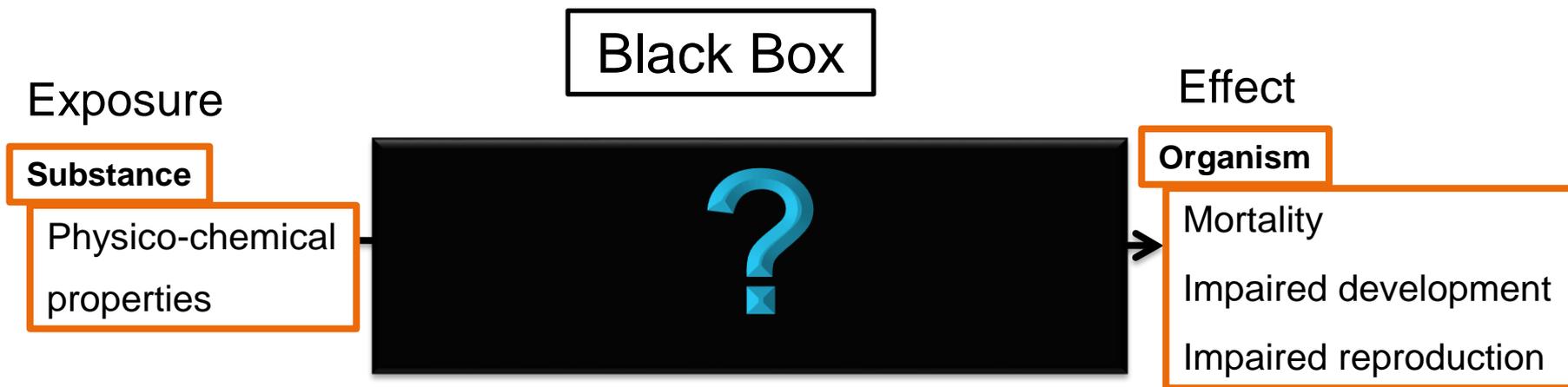
Aromatase inhibition



¹WHO-IPCS, International Program on Chemical Safety, 2002.

²OECD, Conceptual Framework for Testing and Assessment of Endocrine Disruptors, 2012a

THE BLACK BOX BETWEEN EXPOSURE AND EFFECT



For some substances, similar apical endpoints in standard tests but different MoAs result in **false interpretation and inconsistency in chemical labelling**.

Criteria for endocrine disruptors in a regulatory context:

- Adversity, mode-of-action, causality, relevance, **specificity**, potency

Is the effect really mediated by an **endocrine mode-of-action or non endocrine MoA**

TEST STRATEGY

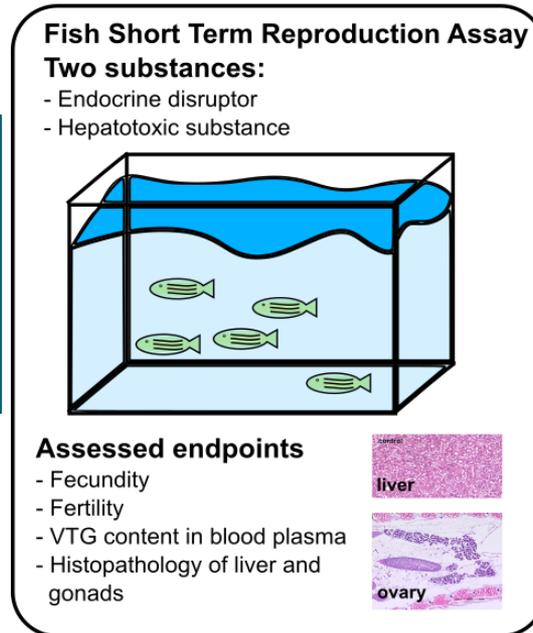
TEST STRATEGY

Reproduction Study: Fish short term reproduction assay (FSTRA)³

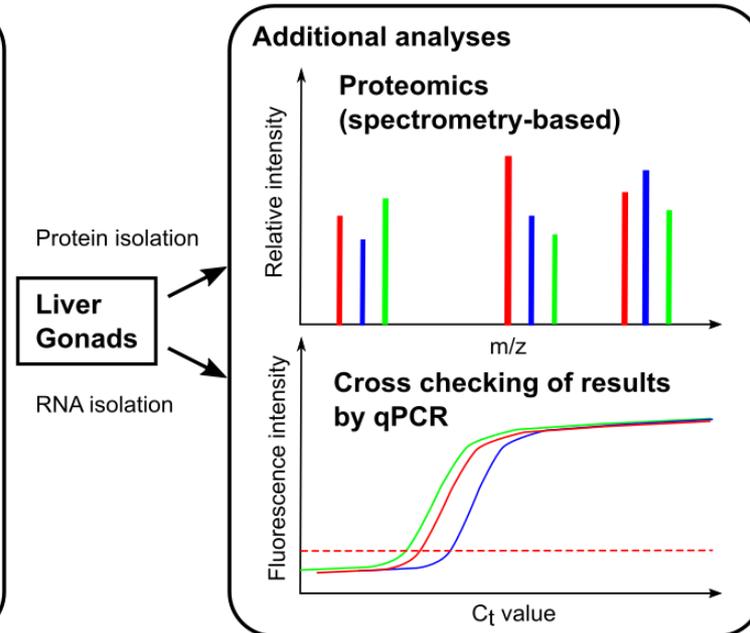
Objective: To identify alterations in molecular-toxicity pathways that are specific to chemical-induced apical responses.

- 21 days of exposure
- 5 males and females
- 3 treatment conditions and control
- Daily eggs count

Determination of the Adverse Outcome

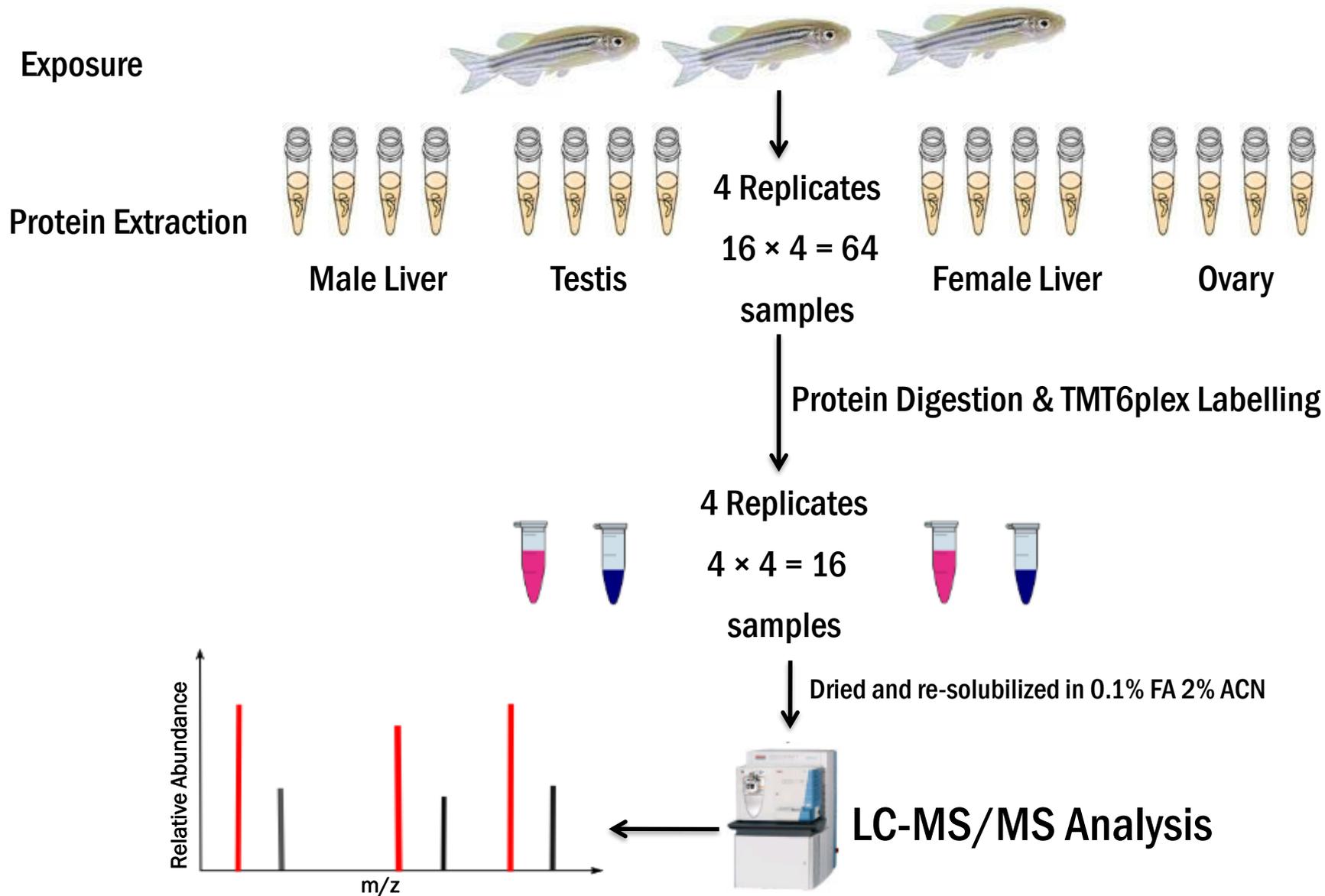


Identification of the Key Events



³OECD, Test No. 229: Fish short term reproduction assay. 2009.

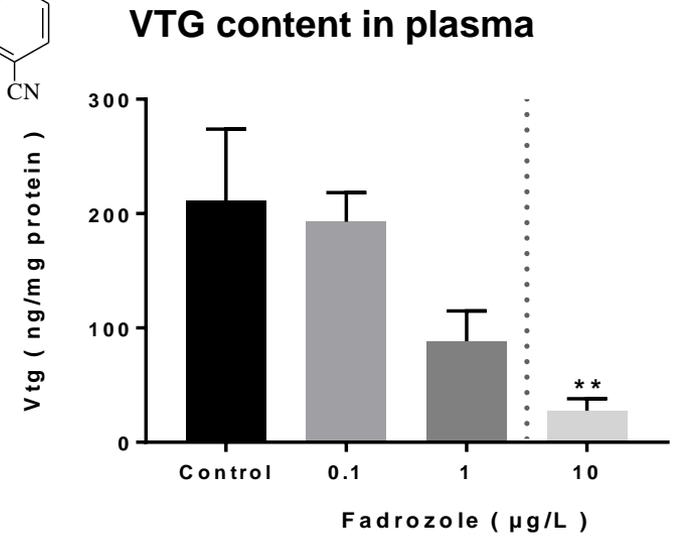
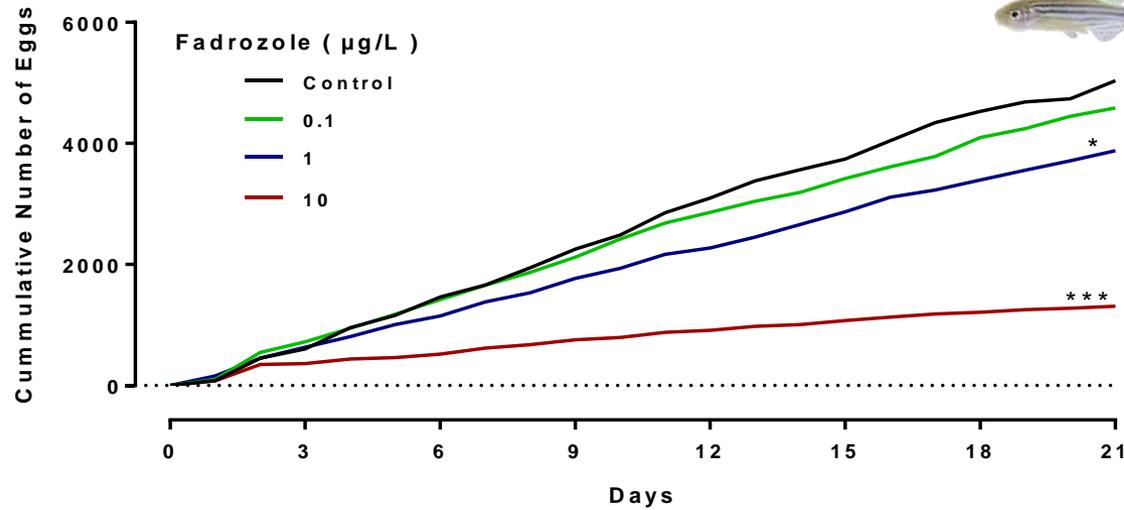
PROTEOMICS TECHNIQUE



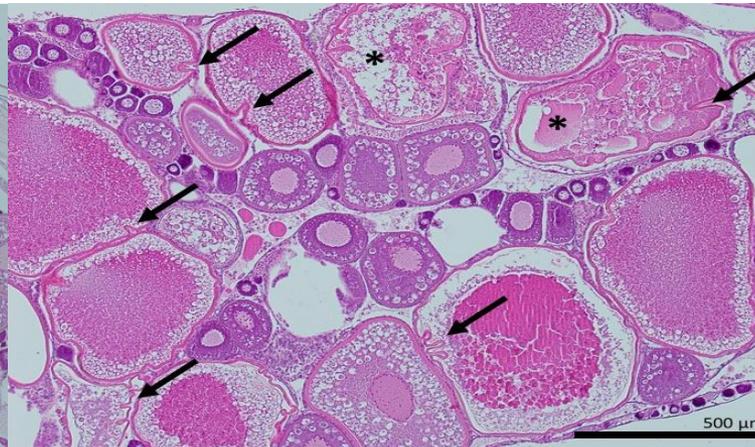
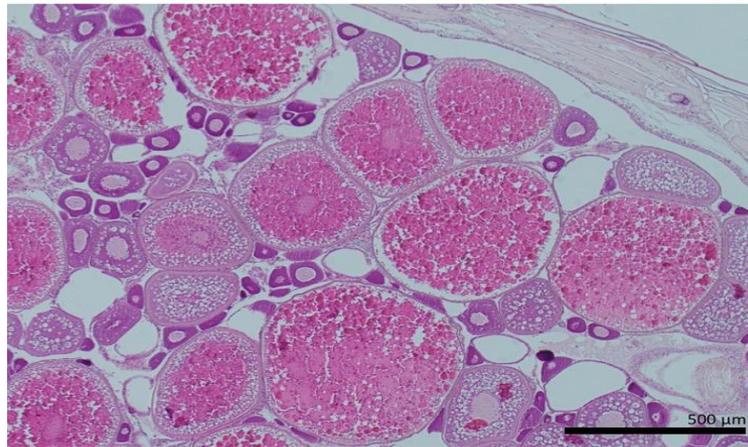
RESULTS FROM FSTRA STANDARD ENDPOINTS

RESULTS – FSTRA ENDPOINTS

Reproduction



Histopathology - Ovary



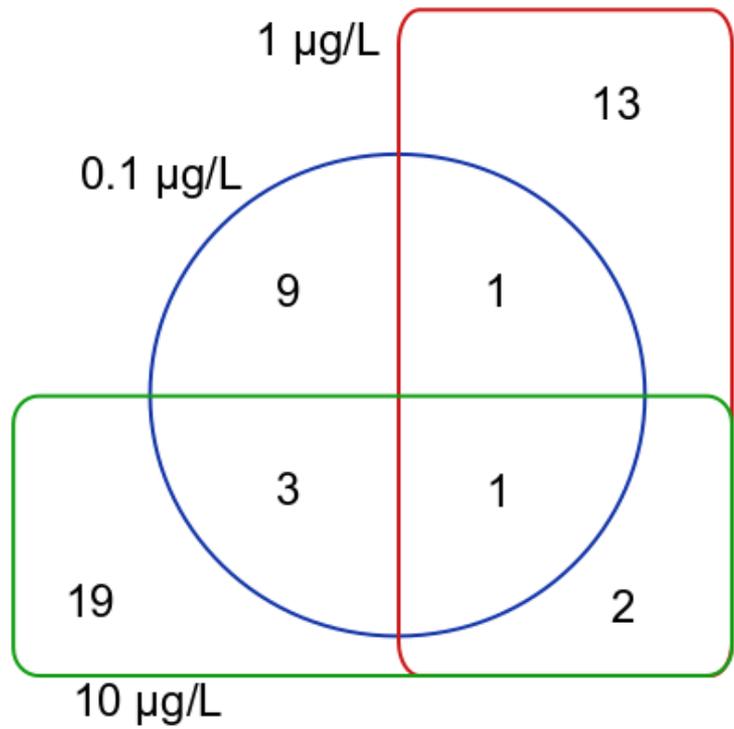
Fadrozole (10µg/L)

- Arrows: membrane folding
- Asterisks: Atretic oocytes

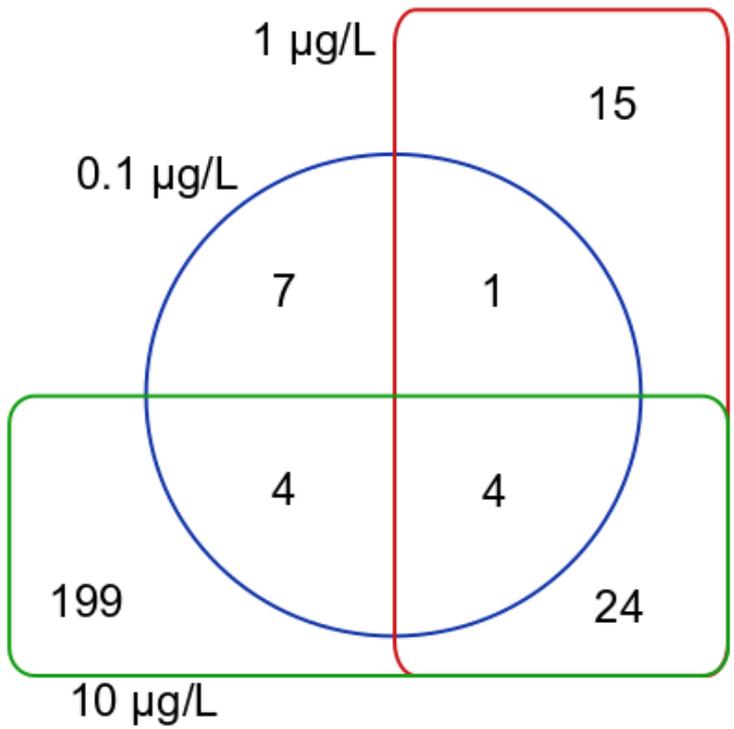
PROTEOMICS RESULTS

PROTEOMIC ANALYSIS OF FEMALE LIVER & OVARY

Venn diagram – Female Liver

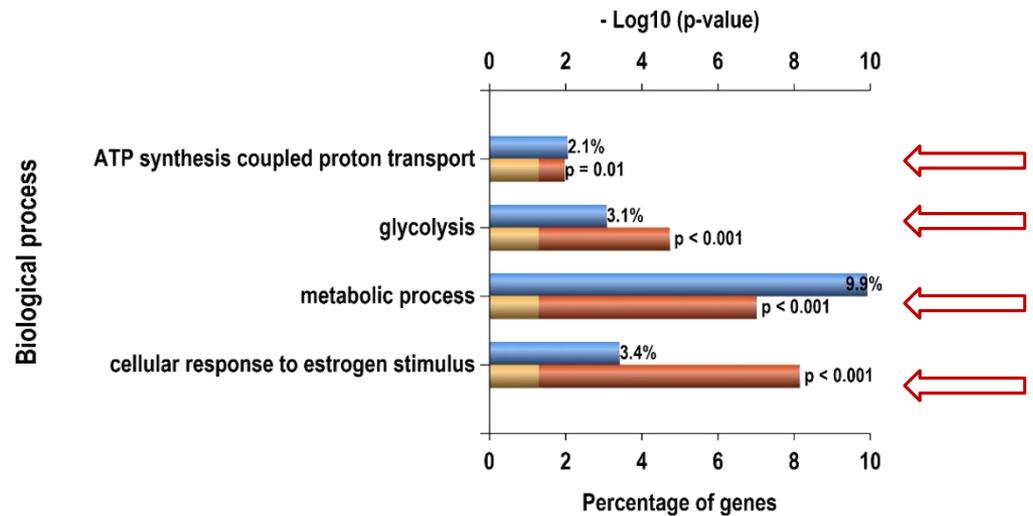


Venn diagram – Female Ovary



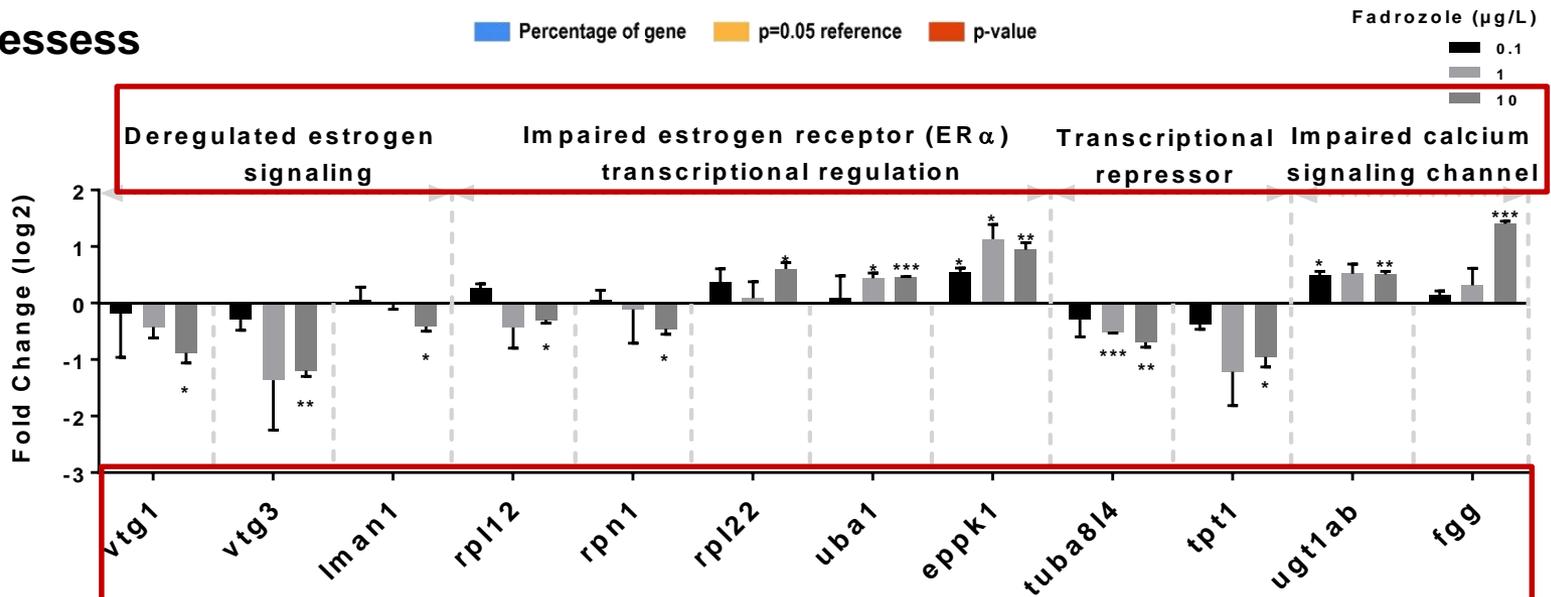
PROTEOMIC ANALYSIS OF FEMALE LIVER

Biological Process Liver Female



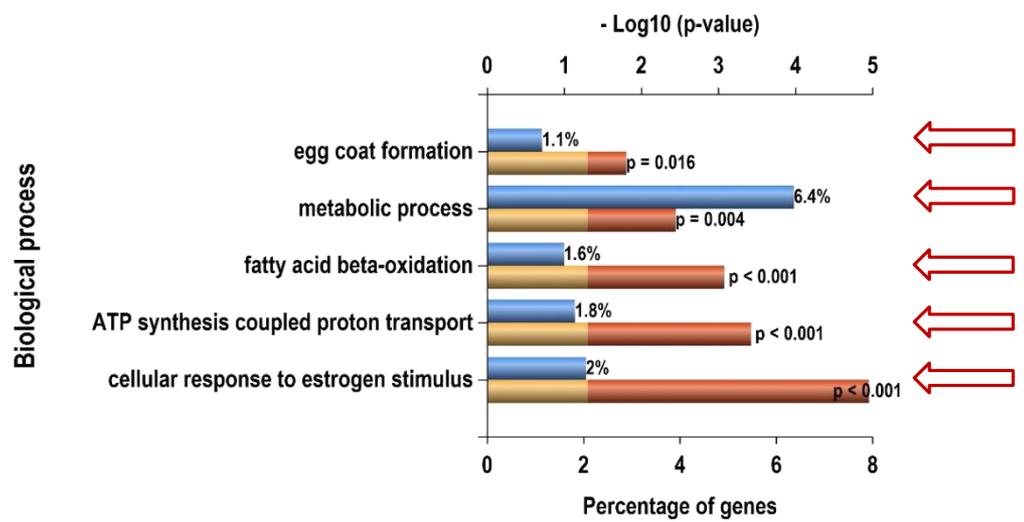
Potential molecular biomaker

Regulated Processes



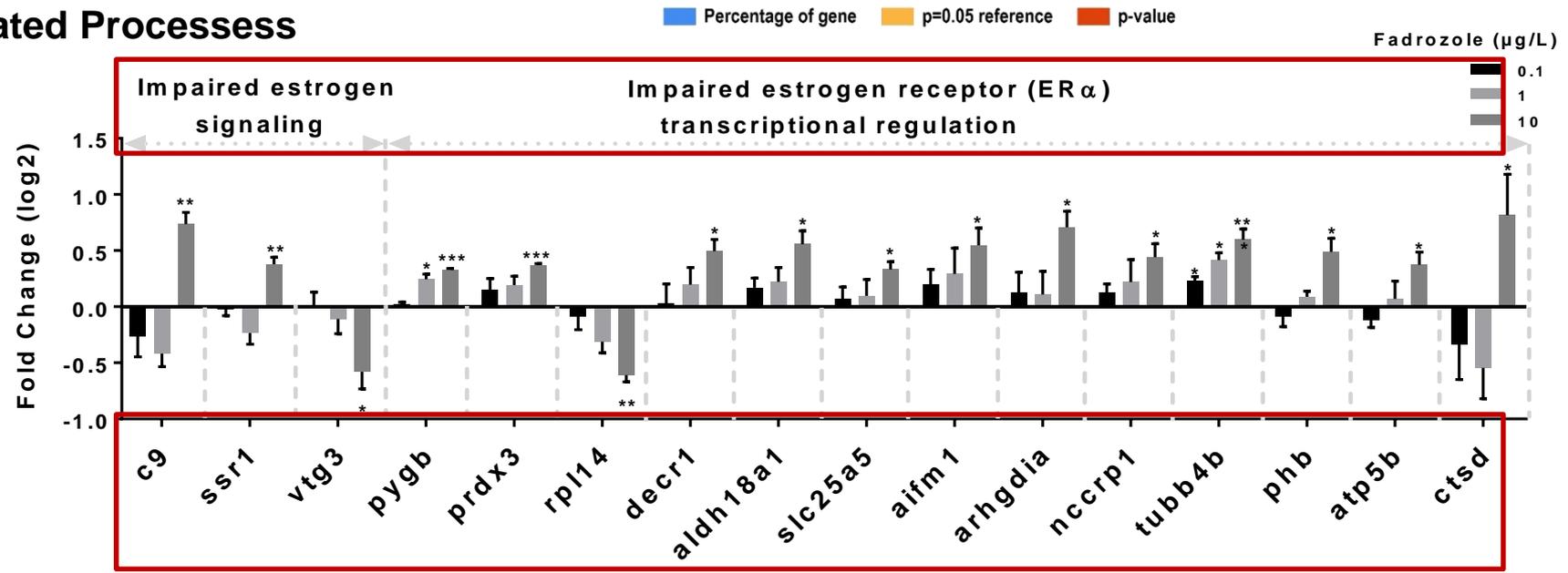
PROTEOMIC ANALYSIS OF OVARY

Biological Process Ovary



Potential molecular biomaker

Regulated Processes



TAKE HOME MESSAGE

- ❖ Proteomics results fit to FSTRA apical endpoints and can provide important data for adverse outcome pathway.
- ❖ Proteomics-based analysis of sex-specific responses revealed primary impairment in estrogen synthesis following aromatase inhibition.
- ❖ Comparing treatment to normal conditions would help to determine candidate molecular toxicity biomarkers for early prediction of apical endpoints.
- ❖ The obtained result further support the need for the integration of – omics approach into new test strategies to provide a link between apical effects and specific chemical-induced MoAs.

Thank you very much for your attention!

ACKNOWLEDGEMENT



Supervisors

- Prof. Dr. Christoph Schäfers
- Prof. Dr. Henner Hollert

Co-supervisors

- Eilebrecht Elke
- Stefan Kalkhof
- Matthias Teigeler
- Matthias Kotthoff

Technical Staffs

- Stephanie Denzer
- Uwe Boshof
- Marlene Mönig
- Patrick Zurek
- Franziska-Frederike Wege
- Jens Nowak
- Heinrich Jürling
- Angela Bauer
- Kevin Severin

Collaboration

Lisa Baumann

CONTACT FOR FURTHER QUESTIONS

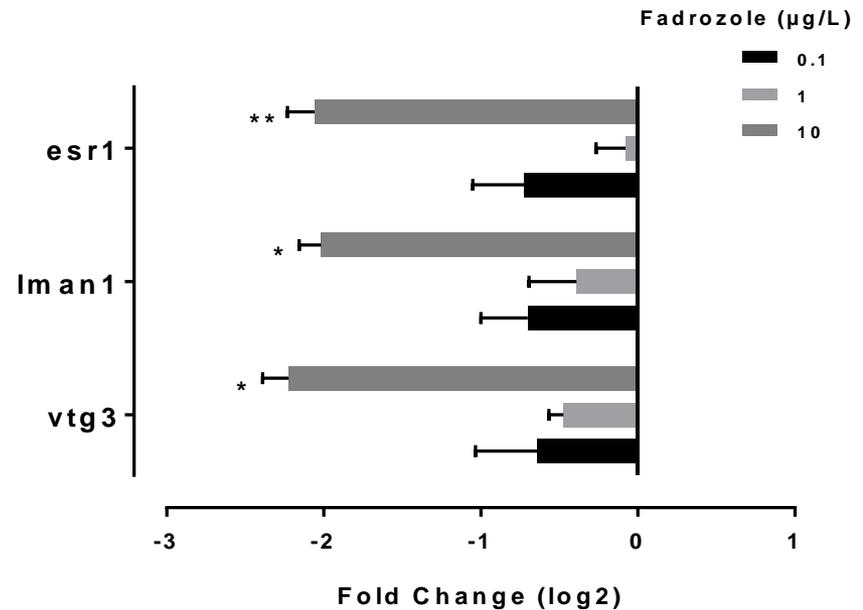
- **MSc Steve Ayobahan**

- steve.ayobahan@ime.fraunhofer.de

- **Dr. Elke Eilebrecht**

- elke.eilebrecht@ime.fraunhofer.de

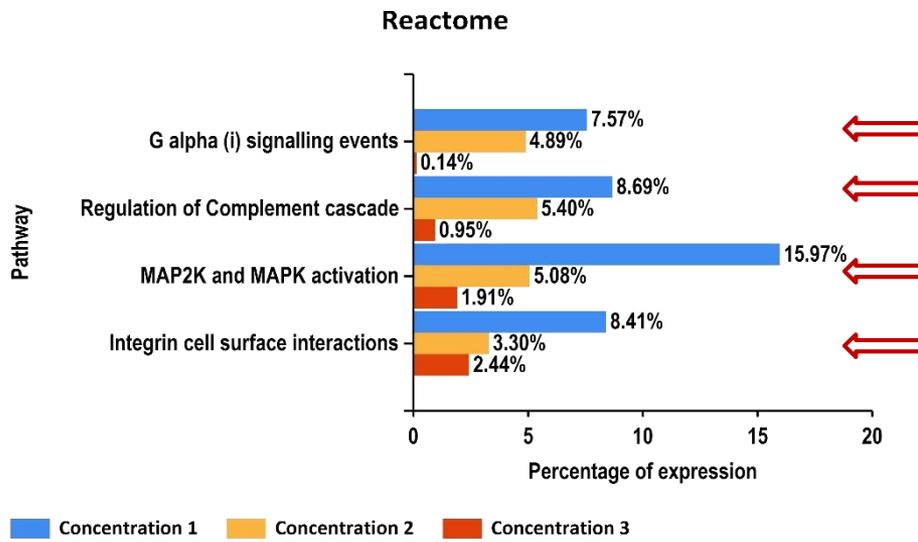
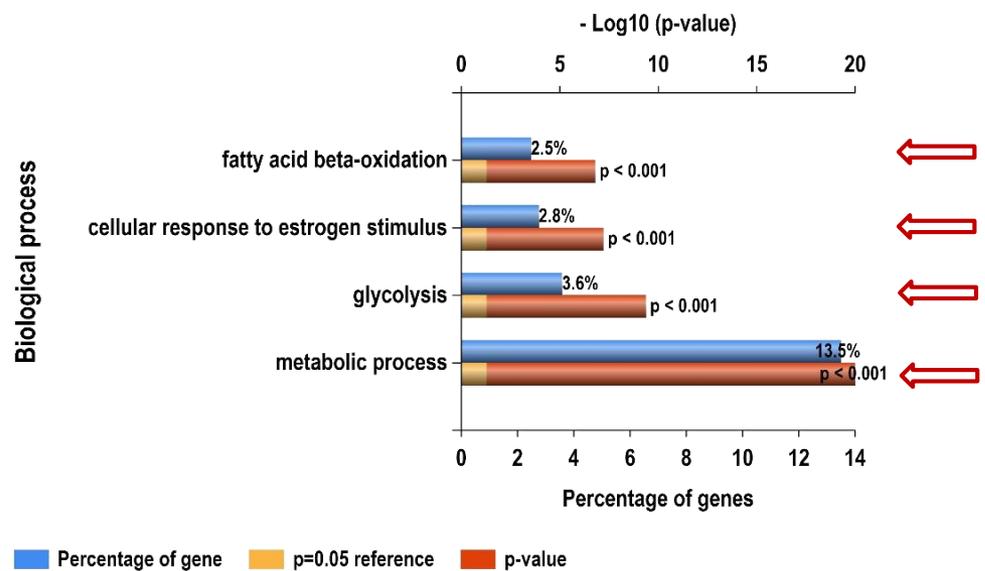
Female Liver – Validation of expression changes of proteins involved in steroid biosynthesis



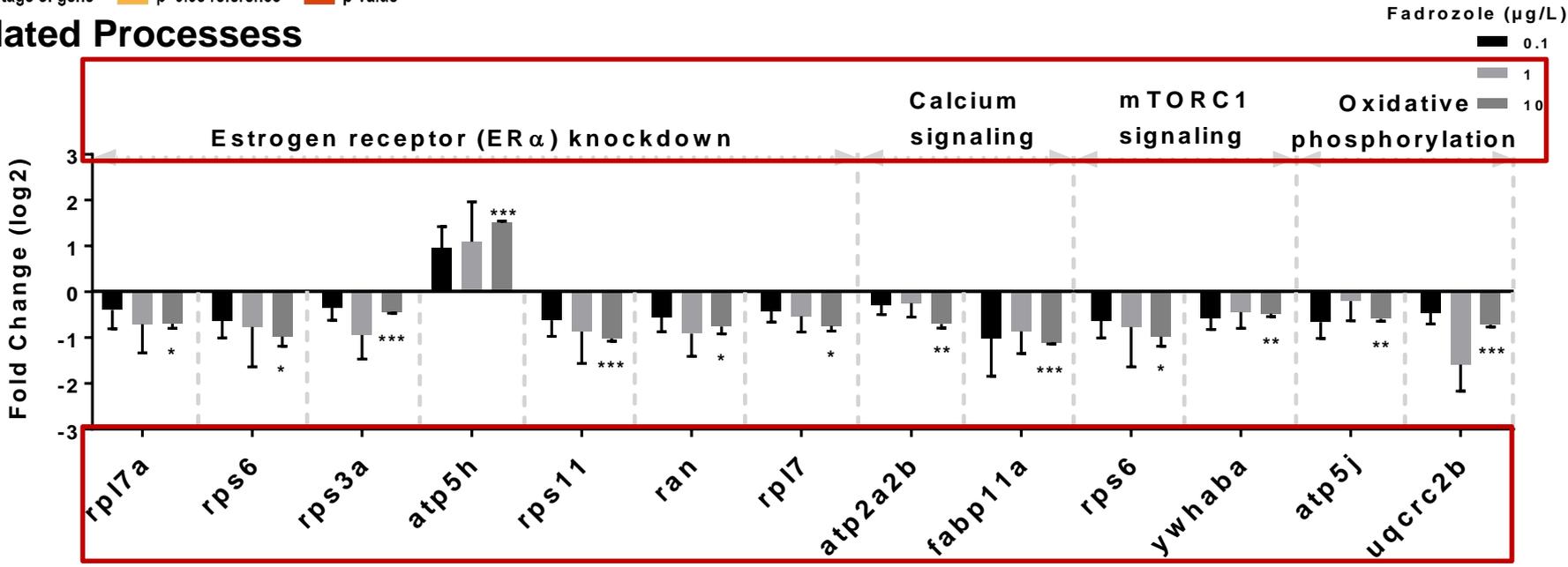
The direction of expression changes of validated genes were consistent with proteomic analysis.

PROTEOMIC ANALYSIS OF MALE LIVER

Biological Process Liver Male



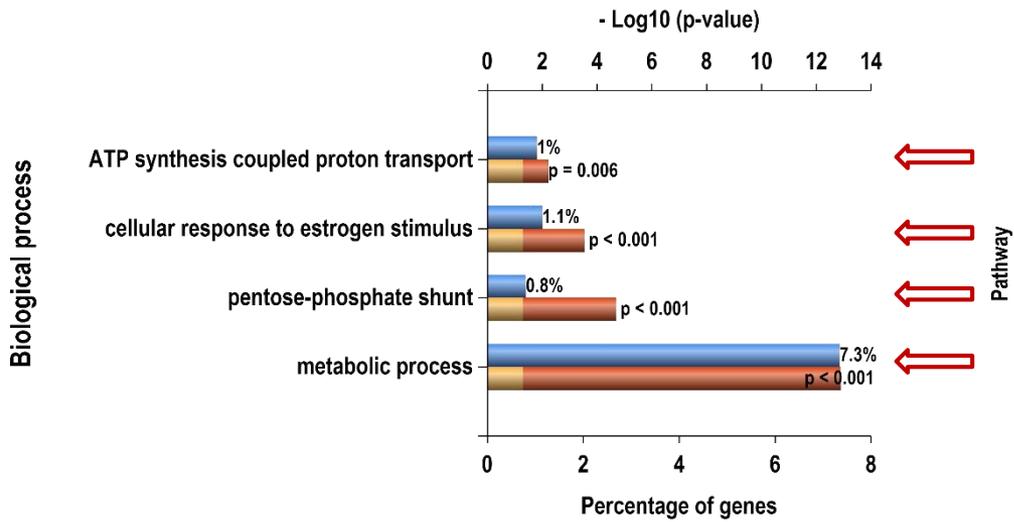
Regulated Processes



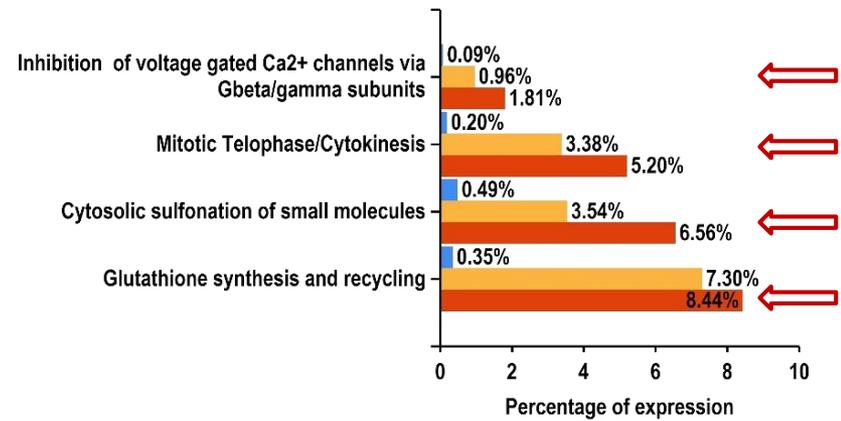
Potential molecular biomarker

PROTEOMIC ANALYSIS OF TESTIS

Biological Process Testis



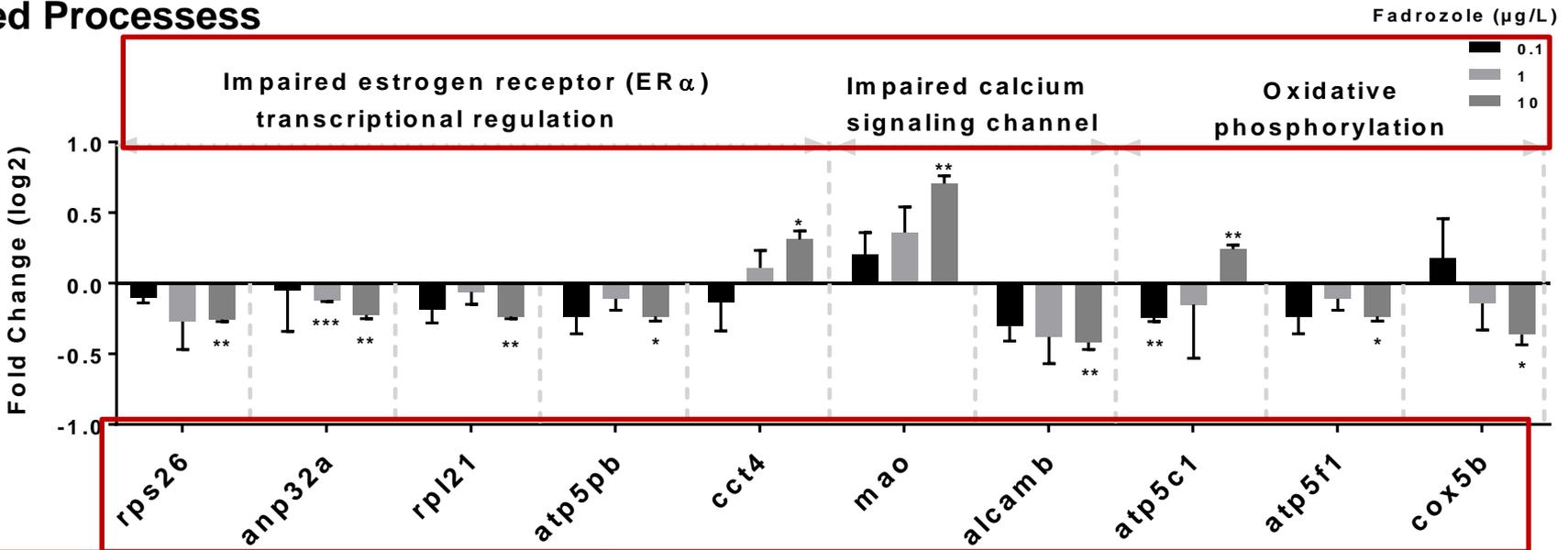
Reactome



Percentage of gene p=0.05 reference p-value

Concentration 1 Concentration 2 Concentration 3

Regulated Processes



Potential molecular biomarker