

Article title: Transcriptome analysis of adipose tissue from pigs divergent in feed efficiency reveals alteration in gene networks related to adipose growth, lipid metabolism, extracellular matrix and immune response

Journal name: Molecular Genetics and Genomics

Authors: Justyna Horodyska^{1,2}, Henry Reyer², Klaus Wimmers^{2,3}, Nares Trakooljul², Peadar G. Lawlor⁴, Ruth M. Hamill^{1*}

¹Teagasc, Food Research Centre, Ashtown, Dublin 15, Ireland

²Leibniz Institute for Farm Animal Biology (FBN), Institute for Genome Biology, Dummerstorf, Germany

³Faculty of Agricultural and Environmental Sciences, University Rostock, Germany

⁴Teagasc, Pig Development Department, AGRIC, Moorepark, Fermoy, Co. Cork, Ireland

*Corresponding author: Ruth.Hamill@teagasc.ie

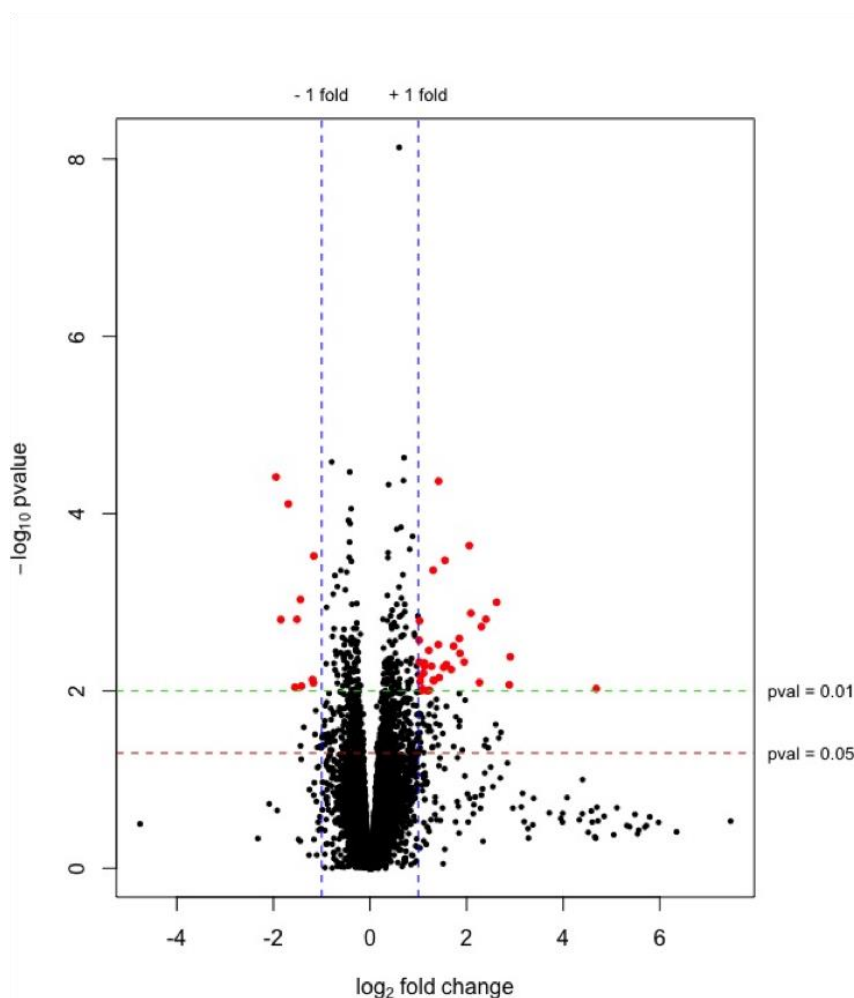


Fig S1 Volcano plot representing log₂ fold changes and -log₁₀(p-values) of genes expressed in adipose tissue from high-FE pigs. The lines indicate suggestive significance threshold at $P < 0.01$ (green line), at $P < 0.05$ (red line) and threshold of log₂ fold change $\geq |1|$ (fold change $\geq |2|$; blue lines). Red dots depict significantly differentially expressed genes at $P < 0.01$ and log₂ fold change $\geq |1|$ (fold change $\geq |2|$). Positive and negative fold changes refer to up- and down-regulated genes in high-FE pigs, respectively.