Gene groups modulated upon bile acid exposure show altered expression in tissue from Barrett’s oesophagus. Kirca M., Duggan S.P., Behan F., Hamid M., Zaheer A., and Kelleher D. Department of Clinical Medicine, Institute for Molecular Medicine, Trinity College Dublin and St. James’s Hospital, Dublin, Ireland

Introduction: Bile acids are an important toxic component of the GORD refluxate. The current study aimed to validate and examine the expression of bile acid regulated genes, as suggested by genomic studies, in esophageal tissue derived from a cohort of BE patients. Methods: A cohort of genes significant altered in BE and EAC tissue and additionally modulated by bile acids exposure in esophageal cells were identified by an integrative genomic approach. RNA was extracted (BO (n=16), normal esophagus (n=14) and gene expression analyzed by real time qRT-PCR. Results: A number of ERK-MAPK modulating dual specificity protein phosphatases (DUSP) family members were differentially expressed in BE samples, specifically, DUSP5 and DUSP1. Up regulation of numerous secreted cytokines and growth factors such as LIF, GDF15 and IGFBP7 were confirmed in BO samples. Lipid homeostatic regulators such as the transcription factor retinoic orphan receptor (ROR)-alpha and fatty acid binding protein (FABP1) were also altered in BO samples. Conclusion: This study for the first time has validated the altered expression of bile acid regulated genes in BO comprised of poly-functional cytokines, phosphatases, growth factors and regulators of lipid homeostasis.