Conclusion This case posed diagnostic and management dilemmas whether it is purely a cancer of the cervix or still representing an intestinal primary. The cancer is not HPV related so it can slip through the net of cervical screening and the main distinguished clinical feature was profuse mucus vaginal discharge which greatly reduced after radiotherapy. The combination of neoadjuvant chemotherapy followed by surgery was successful in this case. These enteric type cervical cancer represent a rare heterogeneous group of cancers with variable presentations and prognosis.

Introduction/Background Cervical cancer (CC) remains the fourth most common and lethal cancer type in women; therefore, a comprehensive understanding of the underlying mechanisms and development of novel diagnostic, prognostic and therapeutic approaches are critical steps for improving CC management. We have previously performed a detailed comparative proteomic analysis between HeLa, SiHa and CD33A CC cell lines and the normal cervical keratinocytes HCK1T cells (Pappa et al, Oncol Rep. 42:1441, 2019) aiming to elucidate novel and potential therapeutic targets. Among hundreds of deregulated proteins between cancer and normal cell lines, LIMA1 or EPLIN, a protein decreased or lost in neoplasia, was statistically downregulated in all CC cell lines. Since LIMA1 role in CC is not fully elucidated yet, we aimed to downregulate its expression in HCK1T cells and assess the putative induction of cancer characteristics, such as increased proliferation, migration and invasion. Additionally, we studied the global m6A RNA methylation pattern in the presence and absence of LIMA1, aiming to highlight a potential role of epitranscriptomics in cancer onset and progression.

Methodology We downregulated LIMA1 expression in the HCK1T cell line using a lentiviral vector (LV) carrying a shRNA for either LIMA1 (shLIMA1) or no target (shNT) at a multiplicity of infection (MOI) 25. Following LIMA1 quantification both at protein and mRNA level, we assessed proliferation, invasion, migration and colony formation efficiency in shNT or shLIMA1 LV-transduced HCK1T cells. Proliferation was assessed using CCK8, while invasion and migration using Transwell®, with or without matrigel-coated inserts, respectively. Qualitative and quantitative assessment of m6A RNA methylation was done by qPCR and colorimetric EpiQuick® kit respectively.

Result(s) Transduction with shLIMA1 LV led to a 98% mean decrease of LIMA1 expression (n=3), leading to a 126% (p=0.021, n=3) and 103% (p=0.0091, n=3) increase in migration and invasion respectively, while we did not observe any difference in cell proliferation and colony formation efficiency. Preliminary data regarding m6A RNA methylation point towards a slight increase following LIMA1 knockdown.

Conclusion LIMA1 may play an important role in cancer progression and metastasis and can set the grounds for novel and personalised therapy treatments for CC patients.