postoperative VI by univariate and multivariate logistic regression showed. The nomogram predicts the occurrence of VI had a robust predict performance, which was demonstrated by the AUC (AUCtraining=0.775 and AUCvalidating=0.769) and the calibration curves and DCA.

Conclusion Our study is the first to develop a multifactorial diagnostic model integrated preoperative parameters of MRI, serum SIRI, and PAR level to predict VI in CC patients with early stage. Our nomogram may assist surgeons in determining the length of vaginal resection when performing a procedure.

Disclosures The authors have no financial conflicts of interest.

Abstract #864 Figures 1–5

Methodology We conducted whole exome RNA sequencing on 14 histopathologically reviewed SCCC cases. Pathological review included expert assessment and immunohistochemical analysis notably using neuroendocrine and SWI/SNF complex markers, p16, RB1, TTF1 and POU2F3. Various bioinformatics tools were employed for fusion transcript detection, mutational analyses, gene expression profiling, and clustering analyses. Differential diagnoses, such as undifferentiated carcinoma and squamous cell carcinoma specimens, were also analysed.

Results The mutational profile of SCCC was heterogeneous, with notable findings including RB1 mutations in 2 cases, TP53 mutations in 2 cases, RAS/RAF mutations in 2 cases, PIK3CA mutations in 2 cases, and HRD-related gene alterations in 3 cases. Gene expression profiling identified 7 tumors overexpressing NEUROD1, 2 tumors overexpressing ASCL1, and 2 tumors overexpressing POU2F3. Additionally, 3 tumors lacked a specific transcriptional profile. Notably, the two POU2F3-expressing tumors did not exhibit neuroendocrine features, presenting a diagnostic challenge. Immunohistochemistry for POU2F3 proved valuable in this context.

Clustering analyses correlated each of the subtypes identified in these cervical tumours with their well-described lung counterparts.

Conclusion This study presents the first comprehensive transcriptomic analysis of a series of SCCC confirming the existence in the uterine cervix of small cell carcinoma subtypes described in other organs and highlighting the diagnostic challenge of the POU2F3-overexpressing subtype lacking neuroendocrine immunohistochemical features. These findings have potential implications for reclassifying a subset of undifferentiated carcinomas of the cervix and may inform therapeutic adaptations in the management of SCCC.

#901 UNRAVELING THE TRANSCRIPTOMIC LANDSCAPE OF SMALL CELL CARCINOMA OF THE UTERINE CERVIX: INSIGHTS INTO SUBTYPES AND DIAGNOSTIC CHALLENGES

Introduction/Background Small cell carcinoma of the uterine cervix (SCCC) is a rare neuroendocrine tumour associated with HPV infection. Transcriptomic subtypes have been described in small cell carcinomas of the lung, including NEUROD1 and ASCL1-driven tumours with a neuroendocrine phenotype, as well as a distinct POU2F3 subtype lacking neuroendocrine features. This study aimed to investigate the existence and characteristics of these subtypes in HPV-related SCCC using RNA sequencing.

Methodology We conducted whole exome RNA sequencing on 14 histopathologically reviewed SCCC cases. Pathological review included expert assessment and immunohistochemical analysis notably using neuroendocrine and SWI/SNF complex markers, p16, RB1, TTF1 and POU2F3. Various bioinformatics tools were employed for fusion transcript detection, mutational analyses, gene expression profiling, and clustering analyses. Differential diagnoses, such as undifferentiated carcinoma and squamous cell carcinoma specimens, were also analysed.

Results The mutational profile of SCCC was heterogeneous, with notable findings including RB1 mutations in 2 cases, TP53 mutations in 2 cases, RAS/RAF mutations in 2 cases, PIK3CA mutations in 2 cases, and HRD-related gene alterations in 3 cases. Gene expression profiling identified 7 tumors overexpressing NEUROD1, 2 tumors overexpressing ASCL1, and 2 tumors overexpressing POU2F3. Additionally, 3 tumors lacked a specific transcriptional profile. Notably, the two POU2F3-expressing tumors did not exhibit neuroendocrine features, presenting a diagnostic challenge. Immunohistochemistry for POU2F3 proved valuable in this context. Clustering analyses correlated each of the subtypes identified in these cervical tumours with their well-described lung counterparts.

Conclusion This study presents the first comprehensive transcriptomic analysis of a series of SCCC confirming the existence in the uterine cervix of small cell carcinoma subtypes described in other organs and highlighting the diagnostic challenge of the POU2F3-overexpressing subtype lacking neuroendocrine immunohistochemical features. These findings have potential implications for reclassifying a subset of undifferentiated carcinomas of the cervix and may inform therapeutic adaptations in the management of SCCC.