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Construction and Analysis of a Uterine Corpus Endometrial Carcinoma Prognostic Model Based on Disulfidoptosis-Related lncRNAs

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KEYWORDS Disulfidoptosis. Immune Infiltration. Long Non-coding RNA. Prognostic Markers. Uterine Corpus Endometrial Carcinoma

ABSTRACT Disulfidoptosis, an emerging programmed cell death modality form, is linked to long non-coding RNAs (lncRNAs). This study aimed to develop a disulfidoptosis-related lncRNA (drlncRNA) predictive algorithm for endometrial carcinoma of uterine corpus (UCEC) and explore its association regarding overall survival (OS) and the tumour immune microenvironment (TME). Molecular profiling and patient-derived clinical information of UCEC individuals diagnosed in The Cancer Genome Atlas (TCGA) were analysed. Linear correlation coefficient identified drlncRNAs, and Cox and LASSO regression established a 4-drlncRNA prognostic model. Patients were grouped by risk score, with high-risk groups showing shorter OS. The model independently predicted OS, and high-risk patients had higher tumour mutation burden (TMB) and altered immune infiltration within tumour tissues. This drlncRNA model effectively predicts UCEC prognosis, aiding personalised treatment.