

The Transcriptomic and Lipidomic Landscape of Human Squamous Cell Carcinoma In Situ

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Abstract

Squamous cell carcinoma in situ (SCCIS) is the most common precancerous lesion in humans impacting about 58 million Americans per year and is associated with cumulative lifetime UV exposure. SCCIS appears to be promoted by immunosuppression. SCCIS can progress into cutaneous squamous cell carcinoma which kills approximately 3000 Americans per year and costs billions of healthcare dollars to treat. Effective treatment of SCCIS would decrease the number of precursor lesions that could transform into cutaneous squamous cell carcinoma which kills thousands of patients per year and costs billions of healthcare dollars for treatment. A more comprehensive understanding of SCCIS biology will identify biomarkers of disease that could represent potential therapeutic targets. To identify these biomarkers we will define the spatial transcriptomic and lipidomic landscape of SCCIS from immunocompetent and immunosuppressed patients which will improve our biological understanding of the disease. The integration of high resolution spatial transcriptomic and lipidomic data will create a unique “omics” space providing new insights into SCCIS biology and support for multiple RO1 grant applications.