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CIP2A expression is upregulated in triple-negative breast cancer

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Introduction: Expression of cancerous inhibitor of protein phosphatase 2A (CIP2A) has been correlated with the clinical aggression and progression of breast cancer. CIP2A inhibits protein phosphatase 2A promoting proliferation and survival. This study aims to compare the transcript and protein expression in triple negative breast cancer (TNBC) and determine the significance of CIP2A localisation using formalin fixed paraffin embedded (FFPE) breast cancer tissue. Breast cancers with increased CIP2A are potential candidates for novel PP2A activation therapy.

Methods: CIP2A transcript expression was assessed using a dataset of 477 breast cancer cases from The Cancer GenomeAtlas (TCGA). 44 FFPE breastcancer tissues were laser microdissected and lysed to quantify the transcript expression using a Luminex® beadbased assay. Immunohistochemistry was used to quantify CIP2A protein and localisation on FFPE tissue sections.

Results: CIP2A is overexpressed (>2-zscore) in 8% of breast cancer and 18% in TNBC when analysing TCGA RNASeq datasets. Protein expression of CIP2A was expressed above threshold (>3 Allred score) in 33% of TNBC cases (*N*=15) as compared to 21% of ER positive cases (*N*=19). CIP2A protein was generally localised in the cytoplasm 90% of positive cases, with localisation in the cell membrane in 31%

of CIP2A positive tumours.

Conclusion: Our study provides preliminary evidence of a novel therapeutic group within the TNBC potentially eligible for CIP2A targeted therapy or reactivation of PP2A. Our results merit further investigation and currently a study was initiated using a cohort of breast tumours (*N*=572).

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