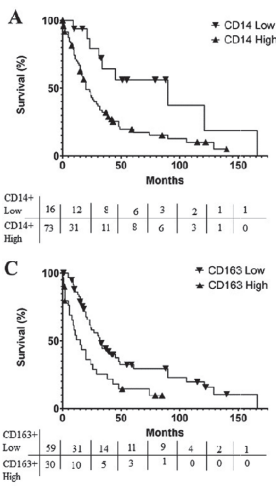


**Abstract 748 Figure 2** Immune infiltration based on primary tumor location  
Increase in immune infiltrate in primary tumors as distance from liver increases. P-values determined by Jonckheere-Terpstra Test with FDR corrections



**Abstract 748 Figure 3** CD14 and CD163 Correlate with OS  
A+C) Kaplan Meier Curve of OS for (A) CD14 (Median OS: 20 vs. 90 months, log-rank p-value <0.01) and (C) CD163 (Median OS: 15 vs. 32 months, log-rank p-value <0.01). B+D) Multivariate Cox Hazard Models. Assumptions of Cox Hazard Model were checked with Schoenfeld residual values, significance level <0.01

**Conclusions** The TIME of CC varies significantly by primary tumor location and between primary and metastatic lesions. D-ECC has a favorable immune profile compared to ICC and H-ECC, with a better milieu for antigen presentation including increased mesothelin and less suppressive macrophages, which may support better response to checkpoint blockade. The data supported the hypothesis that higher densities of intra-tumoral M2 macrophages and myeloid cells correlated with worse OS, even after controlling for clinical variables, suggesting that these cell populations may represent promising immunotherapeutic targets in CC.

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**749 SPATIAL PROFILING OF THE TUMOUR MICROENVIRONMENT IN HEAD AND NECK CANCER TO IDENTIFY BIOMARKERS OF RESPONSE TO THERAPY**

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**Background** Immune checkpoint inhibitors (ICI) have shown durable and long-term benefits in a subset of head and neck squamous cell carcinoma (HNSCC) patients. To identify patient-responders from non-responders, biomarkers are needed which are predictive of outcome to ICI therapy. Cues in the tumour microenvironment (TME) have been informative in understanding the tumour-immune contexture.

**Methods** In this study, the NanoString GemoMx™ Digital Spatial Profiling (DSP) technology was used to determine the immune marker and compartment specific measurements in a cohort of HNSCC tumours from patients receiving ICI therapy.

**Results** Our data revealed that markers involved with immune cell infiltration (CD8 T-cells) were not predictive of outcome to ICI therapy. Rather, a number of immune cell types (CD4, CD68, CD45, CD44, CD66b) were found to correlate with progressive disease.

**Conclusions** This study, to our knowledge, represents the first spatial analysis of HNSCC tumours.

**Ethics Approval** The study was approved by the Queensland University of Technology Ethics Board.

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**750 MALAT1 LNCRNA CONTROLS METASTATIC REACTIVATION OF DORMANT BREAST CANCER BY IMMUNE EVASION**

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**Background** Long non-coding RNAs (lncRNAs) are involved in various biological processes and diseases. Malat1 (metastasis-associated lung adenocarcinoma transcript 1), also known as Neat2, is one of the most abundant and highly conserved nuclear lncRNAs. Several studies have shown that the expression of lncRNA Malat1 is associated with metastasis and serving as a predictive marker for various tumor progression. Metastatic relapse often develops years after primary tumor removal as a result of disseminated tumor cells undergoing a period of latency in the target organ.<sup>1-4</sup> However, the correlation of tumor intrinsic lncRNA in regulation of tumor dormancy and immune evasion is largely unknown.

**Methods** Using an in vivo screening platform for the isolation of genetic entities involved in either dormancy or reactivation of breast cancer tumor cells, we have identified Malat1 as a positive mediator of metastatic reactivation. To functionally uncover the role of Malat1 in metastatic reactivation, we have developed a knock out (KO) model by using paired gRNA CRISPR-Cas9 deletion approach in metastatic breast and other cancer types, including lung, colon and melanoma. As proof of concept we also used inducible knockdown system under in vivo models. To delineate the immune microenvironment, we have used 10X genomics single cell RNA-seq, ChIRP-seq, multi-color flowcytometry, RNA-FISH and immunofluorescence.

**Results** Our results reveal that the deletion of Malat1 abrogates the tumorigenic and metastatic potential of these tumors