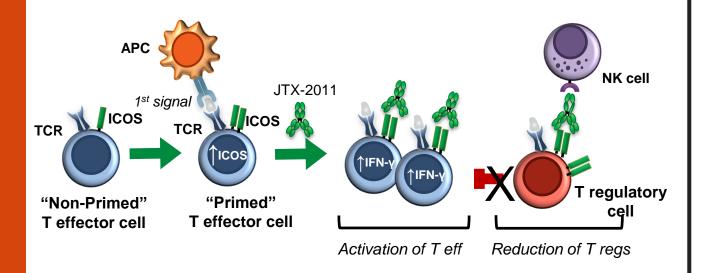
Biomarker Driven Indication Selection in JTX-2011 ICONIC Clinical Trial

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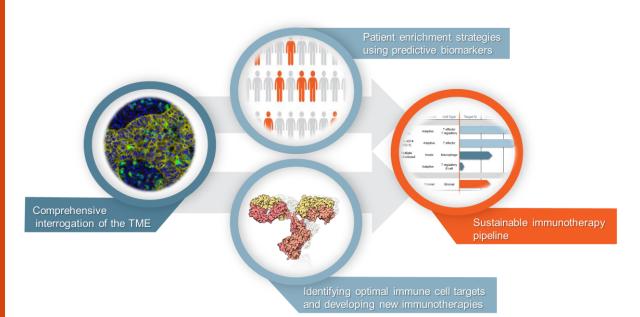
BACKGROUND

ICOS (Inducible T cell CO-Stimulator) is a co-stimulatory molecule expressed primarily on T lymphocytes. Clinical and preclinical data suggest that ICOS mediates anti-CTLA-4 driven anti-tumor responses¹⁻⁴. JTX-2011 is an ICOS agonist antibody in clinical development in advanced solid tumors (ICONIC trial). JTX-2011 is designed to generate an anti-tumor immune response via stimulation of T effector cells and preferential reduction of intra-tumoral T regulatory cells (Tregs). Single agent preclinical efficacy correlates with the percentage of ICOS-expressing T cells within the tumor. We report indication selection and patient enrichment strategy for ICONIC using in silico and IHC analysis and assessment of potential predictive biomarkers for JTX-2011 using ex vivo tumor histoculture system.



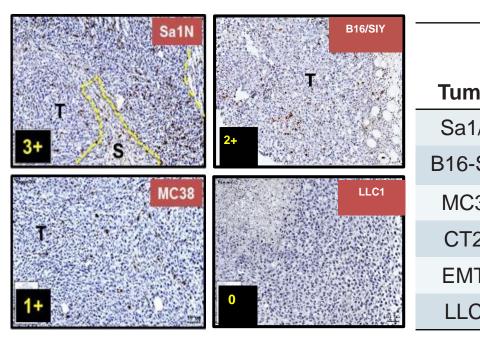
METHODS

Integrated analysis of RNA, DNA and clinical data was performed from the Cancer Genome Atlas for ICOS expression in histologic and molecularly defined tumors and immune cell signatures. ICOS expression was analyzed by IHC in a subset of indications based on ranking from in silico analysis. ICOS expression on intratumoral Tregs and PD-L1 were analyzed in a cohort of 126 head and neck squamous cell carcinomas (HNSCC) *Ex vivo* histoculture assays of human HNSCC was treated with JTX-2011 and assessed for IFN γ gene signature induction.



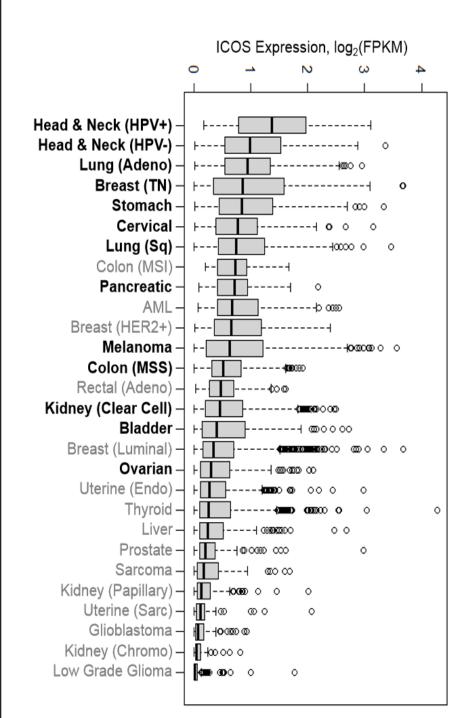
Translational Science Platform: Comprehensive interrogation of the TME to develop a sustainable innovative pipeline

Figure 1: Response to ICOS antibody is associated with high ICOS levels on intra-tumoral T cells in mouse syngeneic tumor models



Tumors were harvested from untreated syngeneic mouse models at ~100 mm3, fixed and paraffin embedded, and subjected to ICOS IHC. Tumor models were evaluated for ICOS expression were scored as 0, 1+, 2+, or 3+. Representative images are shown in the top panel. The table in the bottom illustrates the correlation between monotherapy efficacy of ICOS antibody and expression of ICOS in each tumor model

Figure 2: Analysis of ICOS mRNA expression in TCGA by RNAseq and protein expression by indication within human tumors



(Left Panel) Ranking of tumor indications in TCGA based on ICOS FPKM (Right Panel) Ranking of indications based on protein expression analysis

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nor	ICOS IHC Score	Single Agent Efficacy	Combination Efficacy (+ anti-PD-1)
1/N	3+	++++	ND
-SIY	2+	+++	++++
38	1+	+	+++*
26	1+	+	++++
IT6	1+	+/++	+/-
C1	0	-	-

++++ indicates 61-100% tumor regression +++ indicates 41-60% tumor regression ++ indicates 21-40% tumor regression indicates 10-20% tumor regression ndicates no tumor regressio

Intra-tumoral levels of ICOS+ T cells increases post PD-1 treatment

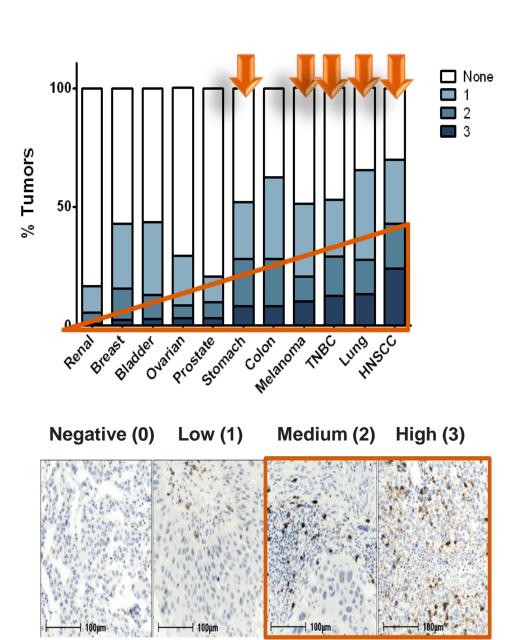


Figure 3: Setting thresholds based on IHC extrapolation to assess frequency of expression in each indication

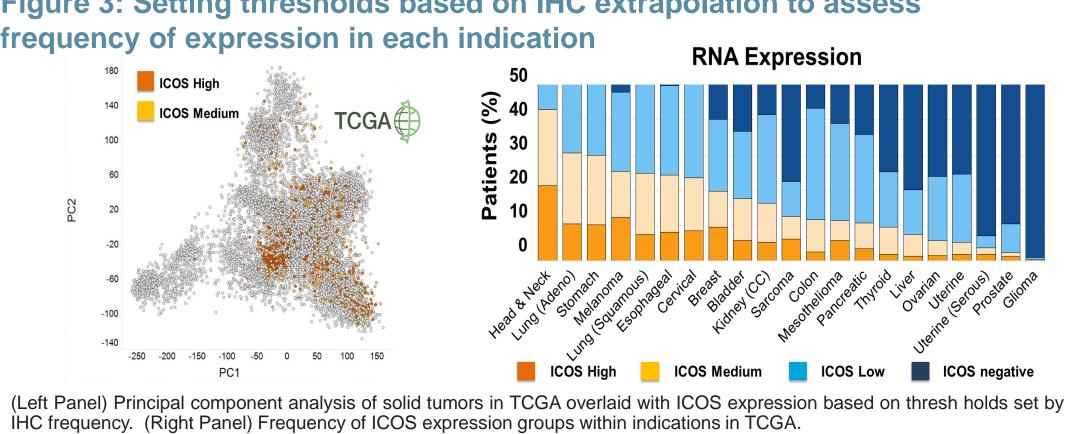
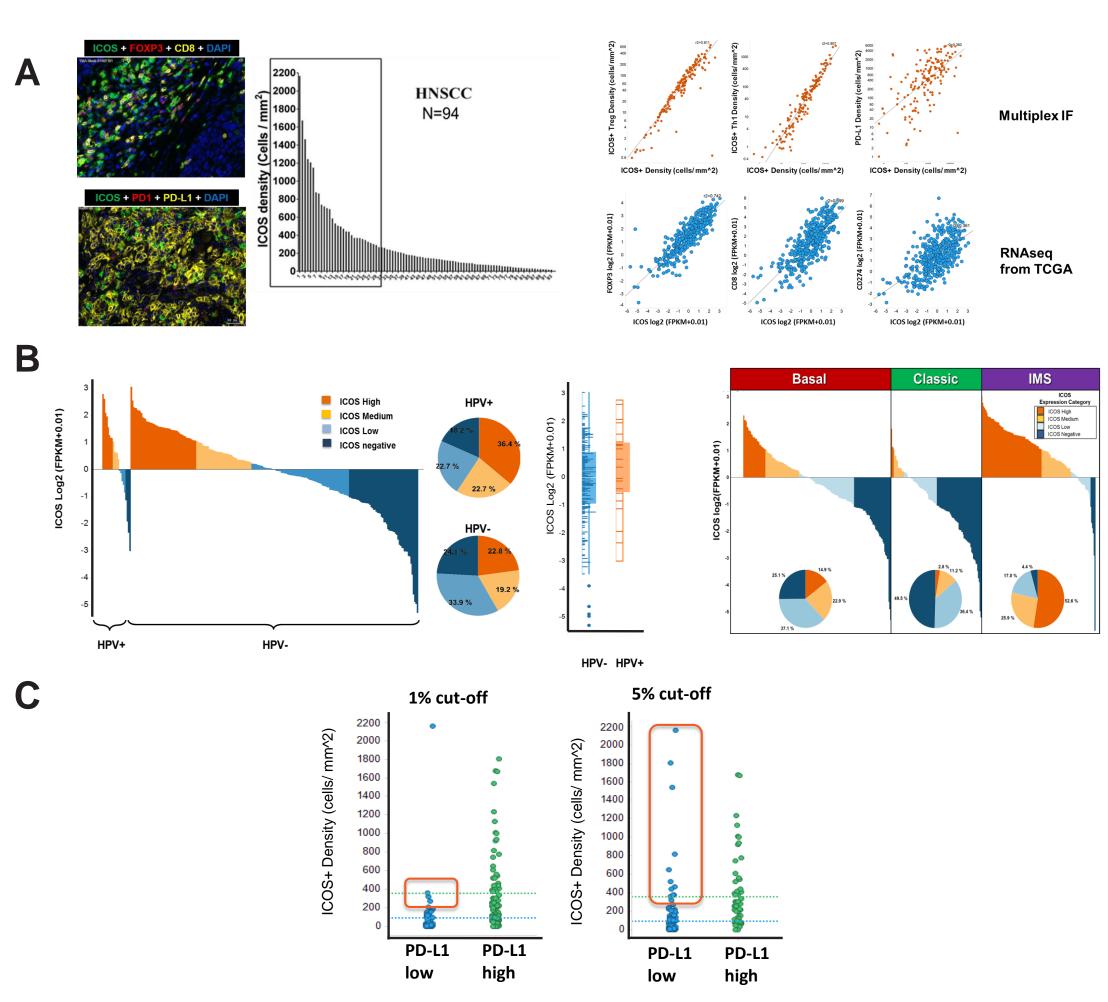


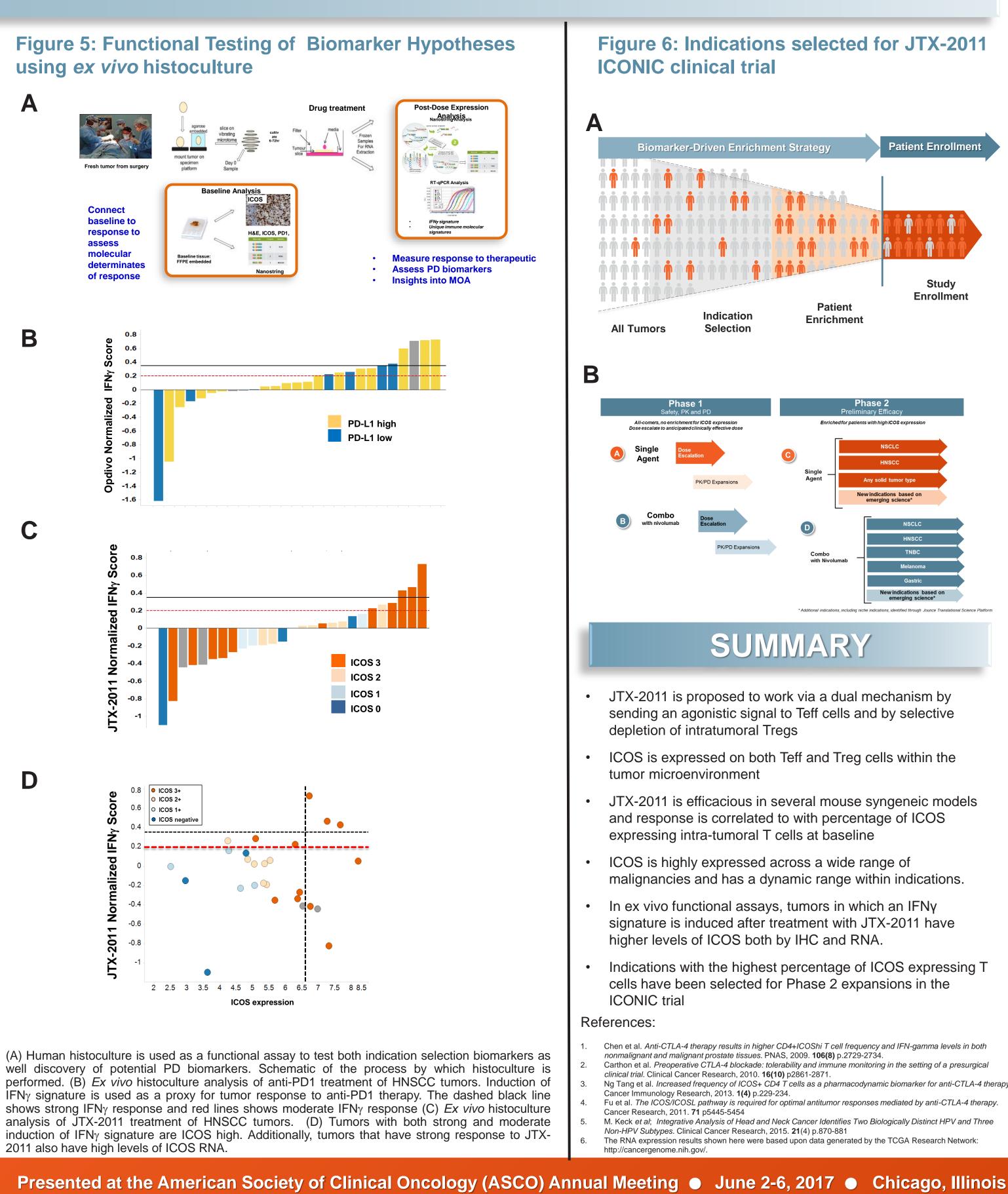
Figure 4: Head and Neck Squamous Cell Carcinoma



(A) ICOS is expressed over a dynamic range within HNSCC and is tightly associated with Tregs as demonstrated by IF and RNAseq from the TCGA database. (B) Distribution of ICOS Expression Across HPV subtypes molecularly defined HNSCC Subgroups. Samples from the HNSC TCGA RNAseq dataset were subgrouped based on the maximum spearman correlation with the published centroids from each subgroup (Keck et al, 2015). RNAseq samples were binned into high, medium, low, and absent ICOS using thresholds based on proportions observed in across multiple indications using IHC (Figure 3). Distributions of ICOS expression are shown based on RNA-Seq expression. (C) High ICOS density is observed in PD-L1 positive patients. Co-staining of ICOS and PDL1 was performed by multiplex IF on HNSCC tumor samples. There is a subset (7-17%) of patients that are PD-L1 low with high ICOS (>200 cell/mm2) infiltration.

RESULTS

using ex vivo histoculture



2011 also have high levels of ICOS RNA.

ABSTRACT#

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