

Supplementary Materials
for
Immunogenomic determinants of tumor microenvironment correlate
with superior survival in high-risk neuroblastoma

Running title: Immunogenomic determinants correlate with superior survival in high-risk neuroblastoma

Feature: Immunotherapy Biomarkers

Authors: Riyue Bao^{1,2,3}, Stefani Spranger^{4,5}, Kyle Hernandez^{6,7}, Yuanyuan Zha⁷, Peter Pytel⁸, Jason J. Luke^{2,3}, Thomas F. Gajewski^{7,8}, Samuel L. Volchenboum¹, Susan L. Cohn¹, Ami V. Desai^{1,*}

¹Department of Pediatrics, The University of Chicago, Chicago, IL 60637

²Hillman Cancer Center, UPMC, Pittsburgh, PA 15232

³Department of Medicine, The University of Pittsburgh, Pittsburgh, PA 15232

⁴Koch Institute for Integrative Cancer Research at MIT, Massachusetts Institute of Technology, Cambridge, MA 02139

⁵Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139

⁶Center for Translational Data Science, Chicago, IL 60637

⁷Department of Medicine, The University of Chicago, Chicago, IL 60637

⁸Department of Pathology, The University of Chicago, Chicago, IL 60637

***Corresponding author:**

Ami V. Desai, MD, MSCE

Assistant Professor of Pediatrics

University of Chicago School of Medicine

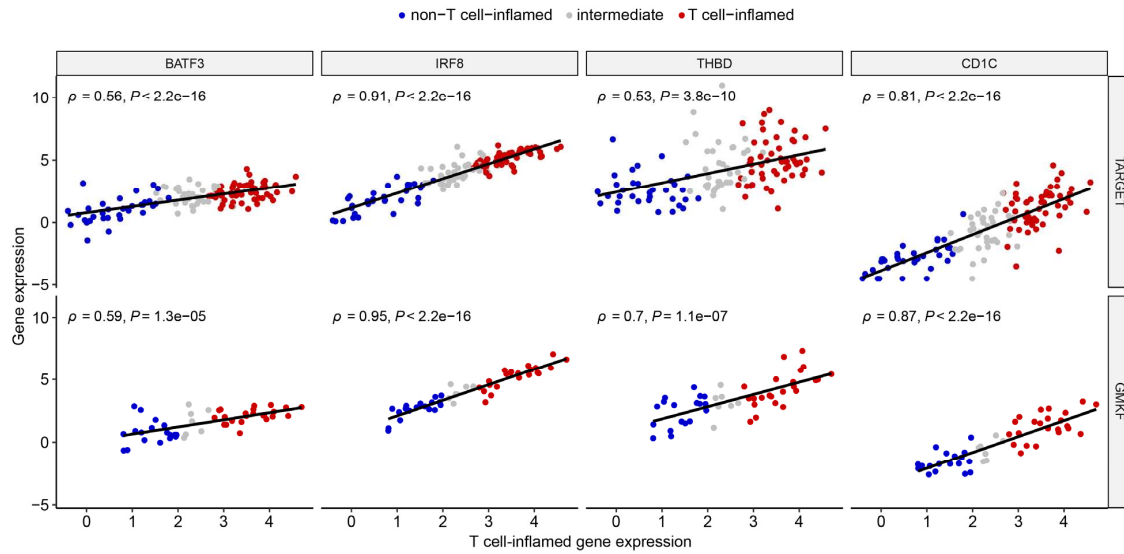
5841 South Maryland Ave MC4060

Chicago, IL 60637

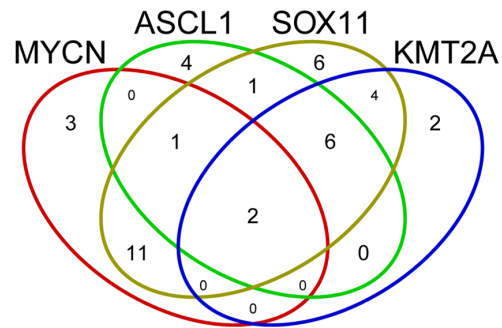
Phone: 773-702-6808

E-mail: adesai12@peds.bsd.uchicago.edu

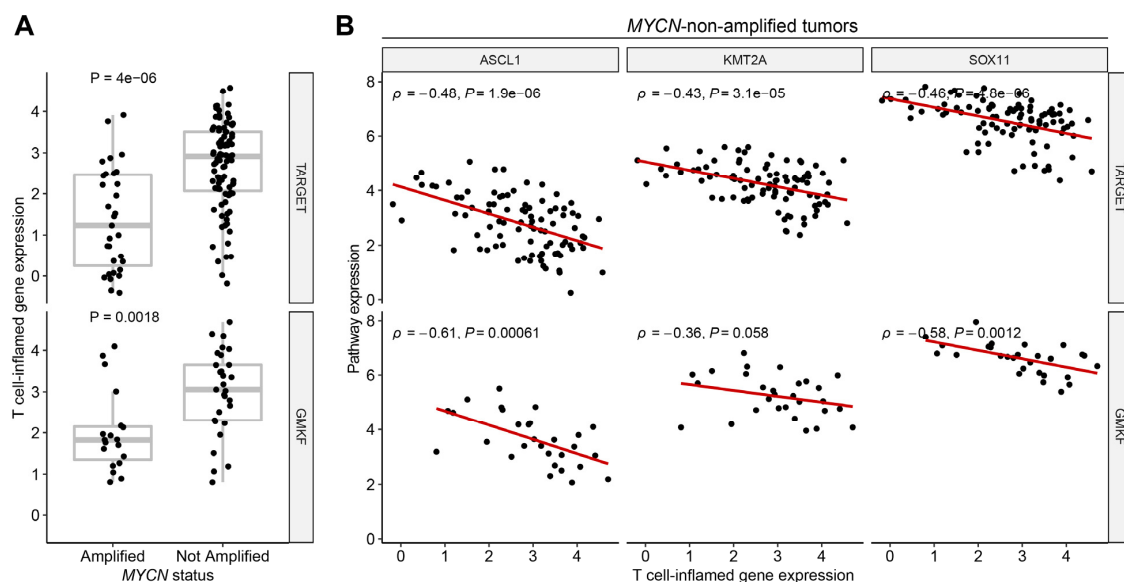
This document contains **Supplementary Figures 1 to 3. Supplementary Tables 1 and 2** are provided separately as an Excel Spreadsheet file.



Supplementary Figure 1: Correlation of DC gene expression with *CD8A* gene expression in T cell-inflamed, intermediate, and non-T cell-inflamed tumors. Spearman's correlation of expression levels of *BATF3*, *IRF8*, *THBD* (*CD141*), and *CD1C* are shown for the TARGET ($n=123$ high-risk patients) and GMKF ($n=48$ high-risk patients) cohorts. ρ = Spearman's correlation coefficient. P = p-value.



Supplementary Figure 2. Partially exclusive activation of the four pathways in non-T cell-inflamed tumors. Numbers represents the number of tumors that harbor activation of each pathway or multiple pathways.



Supplementary Figure 3. Neuroblastoma-intrinsic oncogenic pathway activation correlates with non-T cell-inflamed tumor microenvironment in the discovery (TARGET) and validation (GMKF) cohorts. (A) T cell-inflamed gene expression is significantly higher in *MYCN* non-amplified tumors compared to *MYCN* amplified tumors. $n=123$ and 48 tumors from high-risk patients in TARGET and GMKF are shown, respectively. **(B)** Correlation between T cell-inflamed gene expression and pathway activation score of *ASCL1*, *KMT2A* and *SOX11*. $n=91$ and 29 *MYCN* non-amplified tumors from high-risk patients in TARGET and GMKF are shown, respectively. Two-sided Welch Two Sample *t*-test was used in **A**. Spearman's correlation was used in **B**. ρ = Spearman's correlation coefficient. P = p-value.