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 Bao1,2,3, Stefani Spranger4,5, Kyle Hernandez6,7, Yuanyuan Zha7 Peter Pytel8, Jason J. Luke2,3, Thomas F. Gajewski7,8, Samuel L. Volchenboum1, Susan L. Cohn1, Ami V. Desai1,*

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. \( \rho \) = Spearman’s correlation coefficient. \( P \) = \( p \)-value.