oncogenic pathways was also assessed. The performance of previously identified immune signatures as the Immunologic Constant of Rejection (2,3), which captures an active Th1/cytotoxic response associated with favorable prognosis and responsiveness to immunotherapy, was also checked within each tumor subtype.

Results We found 5 main modules, in agreement with results obtained in adult solid tumors: Wound Healing, TGF-B signaling, IFN-G signaling, Macrophages and Lymphocytes (figure 1). These 5 modules clustered pediatric patients into 6 immune subtypes S1-S6 with distinct survival (S2 vs S4, p = 0.0044, adjusted for cancer type). S2 cluster has the best overall survival and characterized by low enrichment of wound healing signature, high Th1, low Th2 and high expression of HLA1 and HLA2, while the opposite holds true for cluster S4 with the worst survival and highest enrichment of wound healing signature, high Th2, and low Th1. The S6 cluster is characterized by highest enrichment of lymphocyte signature, the highest expression of immune checkpoints accompanied by elevated expression of exhaustion markers, and an unpolarized immune response with high abundance of macrophages. Additionally, pan-cancer, the upregulation of WNT-Beta catenin pathway is associated with adverse outcome and lack of T-cell infiltration. In the per-cancer analysis, ICR is associated with better survival in osteosarcoma and with worse survival in Wilms’ tumors, similarly with what observed in adult kidney’s cancer despite the different embryological origin.

Conclusions We demonstrated that pediatric solid cancers can be classified according to their immune disposition, unveiling unexpected similarity with adults’ tumors. Immunological parameters might be explored to refine diagnostic and prognostic biomarkers and to identify potential immune responsive tumors. This is the first pan-cancer immunogenic analysis in children.

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522 METABOLIC REQUISITES FOR T CELL PROTEIN TRANSLATION IN TUMORS
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Background T cells are a secretory immune subset with the capacity to control solid tumors. Protein translation is of paramount importance in CD8 T cells, controlling proliferation, stimulation and lineage fate.

Methods Herein, we used both the fluorescent analogue of methionine homopropargylglycine (HPG) incorporation assay and O-propargyl-puromycin (OPP) method which enters the nascent polypeptide chains to monitor protein synthesis in mouse and human tumors. Moreover, we employed label free quantitative proteomics (LFQ), lipidomics, metabolic analysis, and in vivo animal modeling to elucidate mechanisms of protein translation in antitumor immunity.

Results We found that canonical protein synthesis is restricted in endogenous CD8 tumor infiltrating lymphocytes (TILs) by the tumor microenvironment (TME). Proteomic analysis revealed that gluconeogenesis and B-oxidation of fatty acids (FAO) were upregulated in CD8 T cells under tumor stress but these metabolic sources were unable to support translation in the TME. Further, we discovered that glucose metabolism and mammalian target of rapamycin complex 1 (mTORC1) preferentially hinder protein synthesis in CD8 TILs. These data enabled the discovery that proteasomal protein...