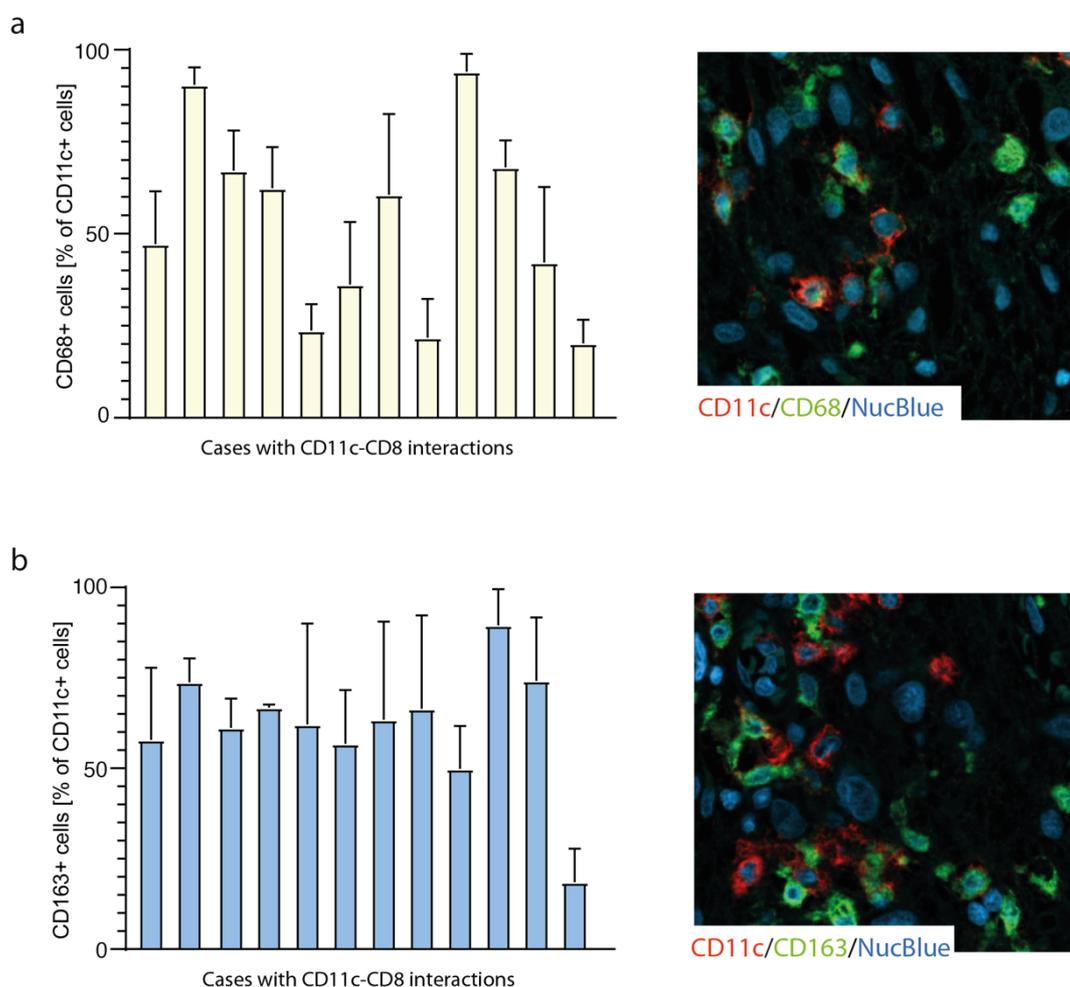


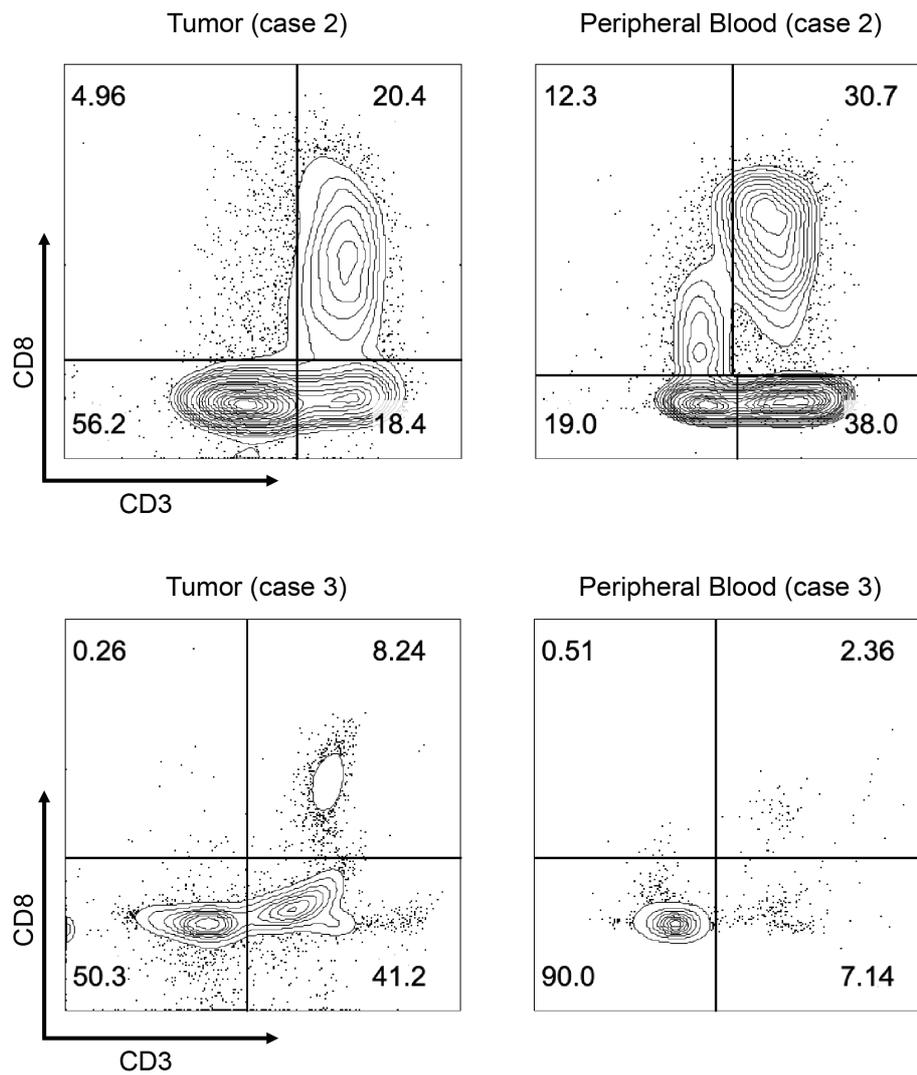
Supplementary Materials

CD11c-CD8 Spatial Cross Presentation: A Novel Approach to Link Immune Surveillance and Patient Survival in Soft Tissue Sarcoma

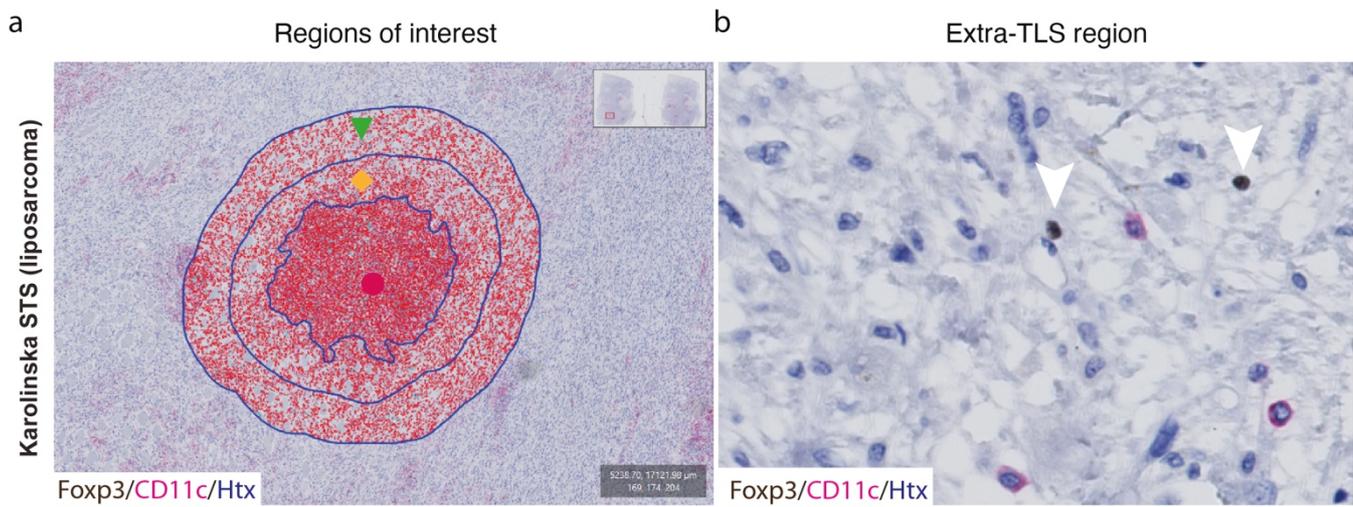
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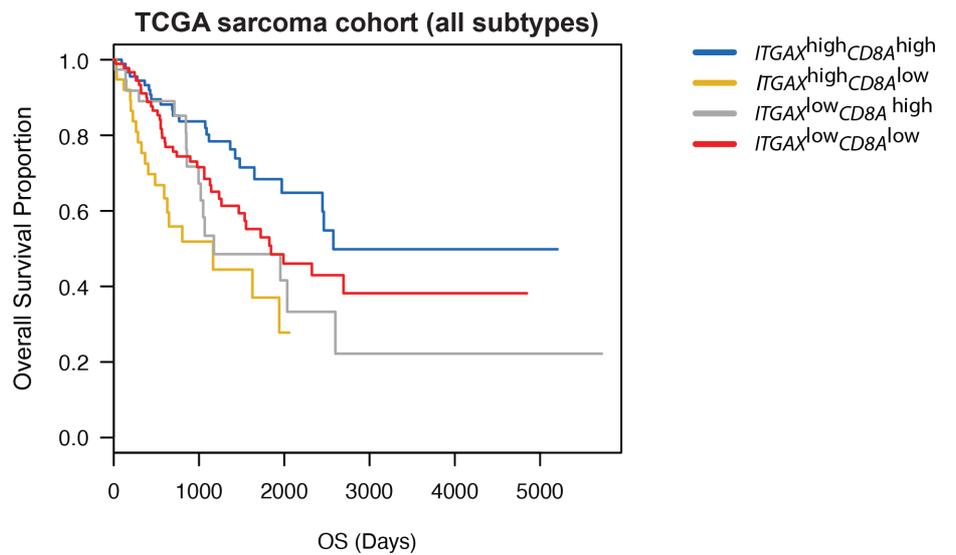
Supplementary Figure S1. A subpopulation of CD11c+ cells expresses macrophage markers. (a) QuPath digital image quantification of CD11c+ cells expressing the macrophage marker CD68 in STS cases with CD11c-CD8 interactions. Each bar represents an individual case displaying CD11-CD8 interactions; (b) QuPath digital image quantification of CD11c+ cells expressing the macrophage marker CD163 in STS cases with CD11c-CD8 interactions. Each bar represents an individual case displaying CD11-CD8 interactions.



Supplementary Figure S2. The majority of the isolated CD8⁺ cells from primary tumors express CD3. Flow cytometry for CD8 and CD3 in preparations of freshly isolated CD45⁺ cells from two different patients. Case 2 is a dedifferentiated liposarcoma, G3 from a 56-year-old male (top), and case 3 is a UPS, G3 from a 59-year-old female (bottom).

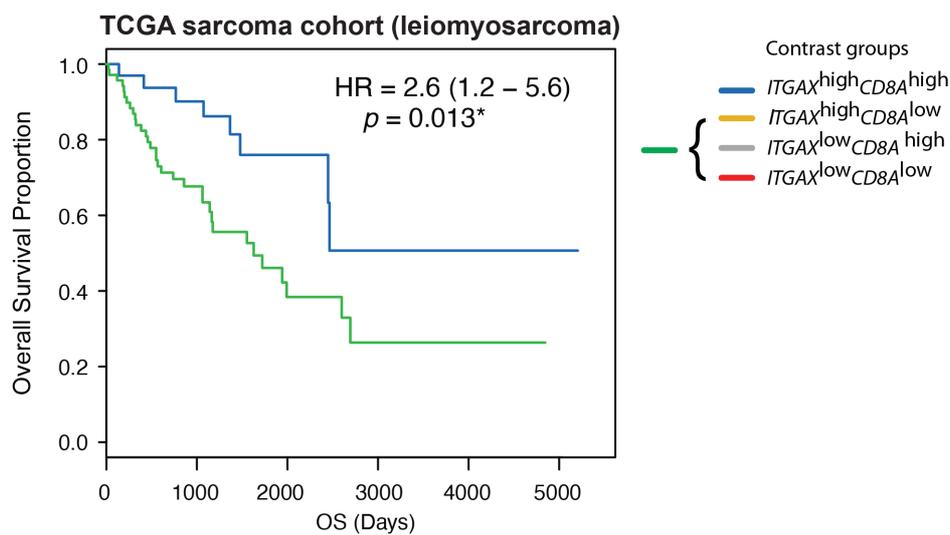


Supplementary Figure S3. Digital image analysis of Foxp3+ cells in relation to presence of TA-TLSs. (a) Representative example of how regions of interest were selected for digital image analysis of Foxp3+ cells residing primarily within a TA-TLS (intra-TLS, red label) and not in the peri-TLS region (yellow label) or in the extra-TLS region (green label) (b) Representative image of an extra-TLS region with sparsely distributed Foxp3+ cells.



Number at risk

91	50	18	6	1	1
38	11	3	0	0	0
38	15	6	2	2	1
92	47	19	8	3	0



Number at risk

33	24	9	4	1	1
71	32	10	4	1	0

Supplementary Figure S4. *ITGAX-CD8A* expression levels are prognostic in STS. (a) Contrast group analysis of gene expression levels of *ITGAX* (CD11c) and *CD8A* (CD8) in the TCGA sarcoma cohort. (b) Contrast group analysis of gene expression levels of *ITGAX* (CD11c) and *CD8A* (CD8) in leiomyosarcoma subgroup analysis.