

## Supplementary data:

Supplementary Table 1: Detailed patient sample information.

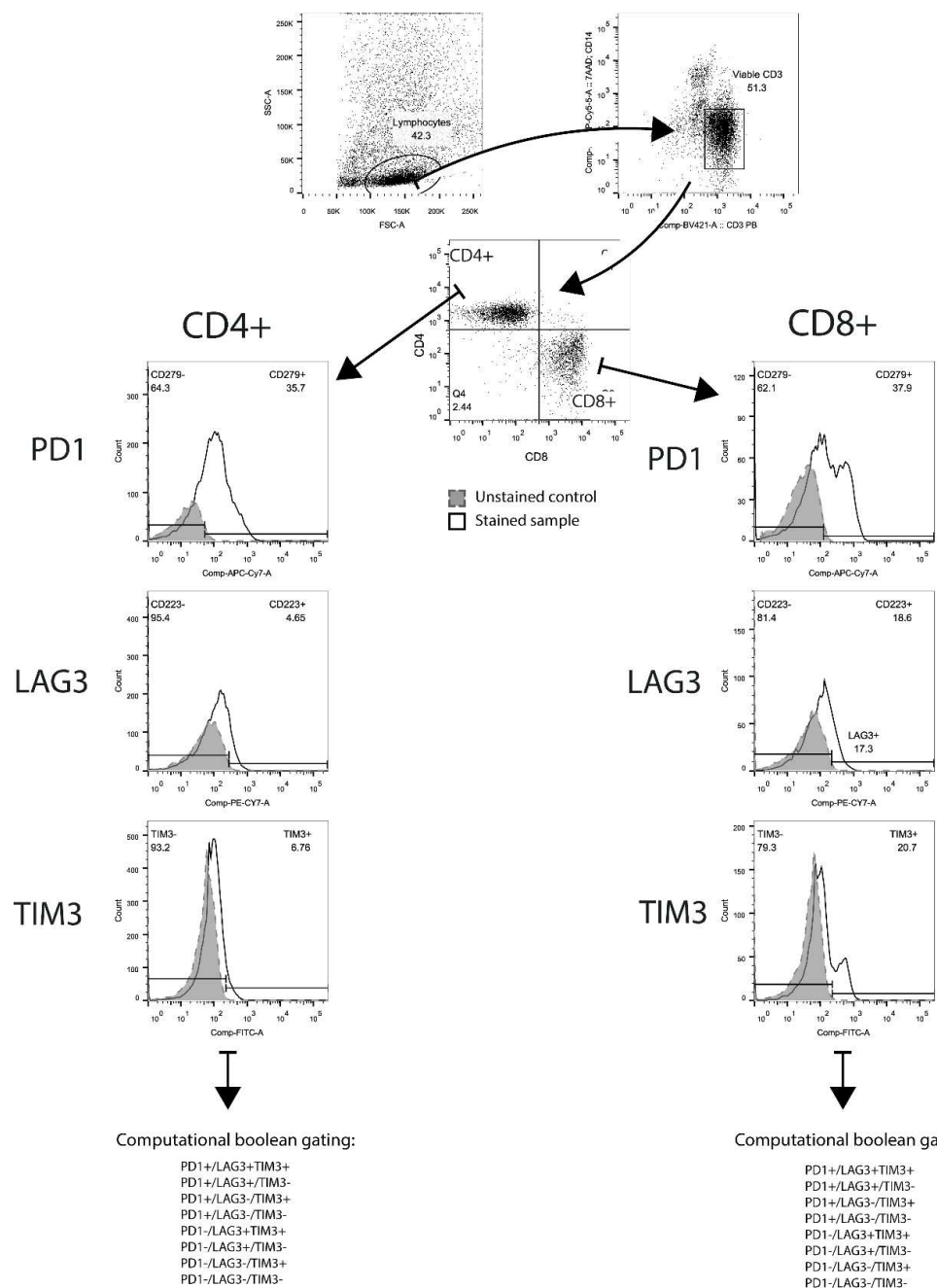
HISTOLOGY	GENDER	AGE	ORIGIN RESECTION	PREVIOUS TREATMENT
GIST	Female	72	Abdomen	Imatinib
GIST	Male	82	Abdomen	Imatinib
GIST	Female	78	Abdomen	Imatinib
GIST	Male	46	Abdomen	Imatinib
GIST	Male	29	Pelvis	Imatinib
GIST	Male	63	Abdomen	None
GIST	Male	66	Abdomen	None
GIST	Female	54	Abdomen	None
GIST	Male	69	Abdomen	None
LEIOMYOSARCOMA	Female	72	Abdomen	None
LEIOMYOSARCOMA	Male	58	Abdomen	None
LEIOMYOSARCOMA	Female	61	Abdomen	None
LEIOMYOSARCOMA	Female	62	Extremities	None
LEIOMYOSARCOMA	Female	53	Extremities	None
LEIOMYOSARCOMA	Male	81	Extremities	None
LEIOMYOSARCOMA	Male	80	Extremities	None
LIPOMA	Female	86	Abdomen	None
LIPOMA	Male	49	Extremities	None
LIPOMA	Female	35	Extremities	None
LIPOMA	Male	54	Head	None
LIPOMA	Male	60	Retroperitoneal	None
LIPOMA	Male	42	Trunk	None
LIPOSARCOMA DEDIFFERENTIATED	Male	63	Abdomen	None
LIPOSARCOMA DEDIFFERENTIATED	Male	81	Abdomen	None
LIPOSARCOMA MYXOID	Male	36	Abdomen	None
LIPOSARCOMA MYXOID	Male	62	Abdomen	None
LIPOSARCOMA MYXOID	Male	61	Extremities	None
LIPOSARCOMA MYXOID	Male	25	Extremities	None
LIPOSARCOMA MYXOID	Male	59	Extremities	Radiotherapy
LIPOSARCOMA MYXOID	Male	36	Retroperitoneal	Radiotherapy
LIPOSARCOMA WELL DIFFERENTIATED	Male	54	Abdomen	None
LIPOSARCOMA WELL DIFFERENTIATED	Female	68	Extremities	None
LIPOSARCOMA WELL DIFFERENTIATED	Male	66	Extremities	None
LIPOSARCOMA WELL DIFFERENTIATED	Male	48	Extremities	None
LIPOSARCOMA WELL DIFFERENTIATED	Male	61	Extremities	None
LIPOSARCOMA WELL DIFFERENTIATED	Male	57	Retroperitoneal	None
LIPOSARCOMA WELL DIFFERENTIATED	Female	46	Retroperitoneal	None
MELANOMA	Male	81	Abdomen	None
MELANOMA	Female	57	Extremities	None
MELANOMA	Male	71	Extremities	None
MELANOMA	Male	82	Head	None
MYXOFIBROSARCOMA	Male	83	Extremities	None
MYXOFIBROSARCOMA	Male	72	Extremities	None
MYXOFIBROSARCOMA	Female	70	Extremities	None
MYXOFIBROSARCOMA	Male	67	Extremities	None
MYXOFIBROSARCOMA	Male	60	Trunk	None
MYXOFIBROSARCOMA	Female	70	Extremities	Radiotherapy
MYXOFIBROSARCOMA	Male	84	Extremities	Radiotherapy
MYXOFIBROSARCOMA	Male	81	Extremities	Radiotherapy
PLEOMORPHIC SARCOMA	Male	75	Abdomen	None
PLEOMORPHIC SARCOMA	Male	50	Extremities	None
PLEOMORPHIC SARCOMA	Male	40	Extremities	None
PLEOMORPHIC SARCOMA	Female	64	Extremities	None

<b>PLEOMORPHIC SARCOMA</b>	Male	41	Extremities	None
<b>PLEOMORPHIC SARCOMA</b>	Male	60	Extremities	None
<b>PLEOMORPHIC SARCOMA</b>	Male	76	Extremities	Radiotherapy
<b>PLEOMORPHIC SARCOMA</b>	Male	45	Extremities	Radiotherapy
<b>PLEOMORPHIC SARCOMA</b>	Male	51	Extremities	Radiotherapy
<b>PLEOMORPHIC SARCOMA</b>	Male	71	Trunk	Radiotherapy

Supplementary Table 2: number of samples retrieved from publicly available data sets.

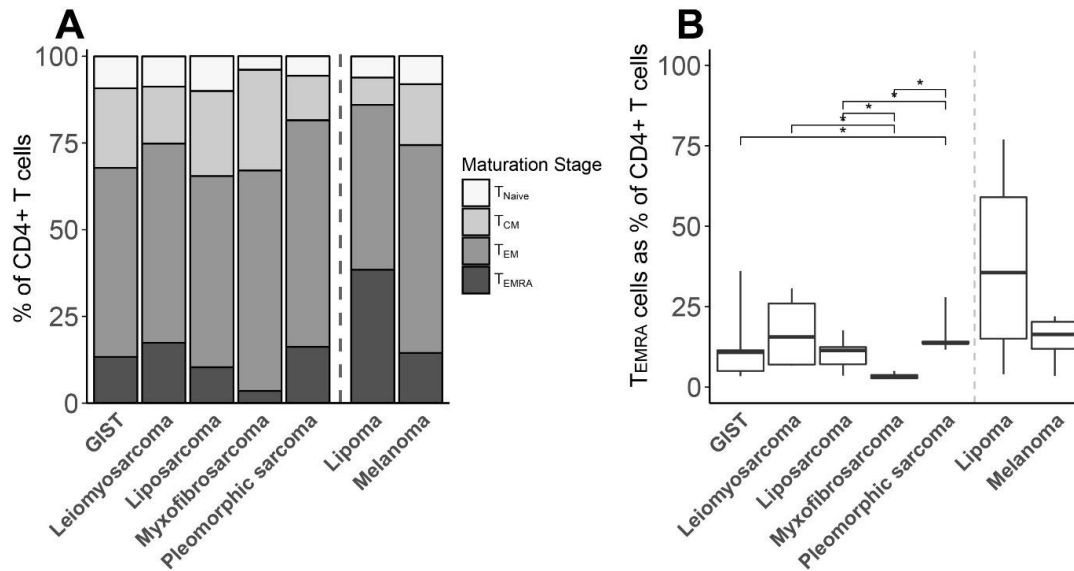
	RNAseq (GSE71121)	Microarray (GSE71121)	DNaseq (TCGA)
GIST	10	29 <sup>A</sup>	9 <sup>B</sup>
Leiomyosarcoma	36	89	98
Liposarcoma	18	45	56
Myxofibrosarcoma	15	43	22
Pleomorphic sarcoma	42	89	50

<sup>A</sup>GSE17743, <sup>B</sup>SRP042250



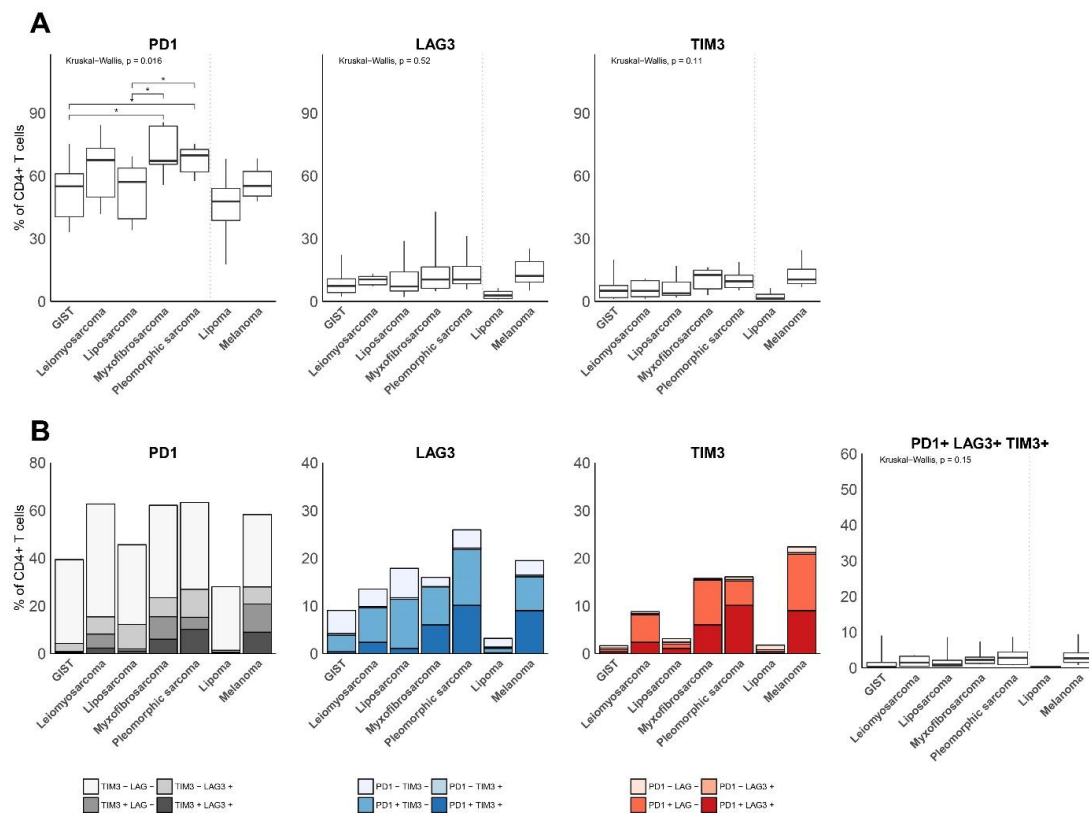
### Supplementary Figure S1: Flow cytometry gating strategy.

Representative gating strategy to analyze immune checkpoint-positive CD4 or CD8 T cells in tumors via flow cytometry. Using FlowJo software (Ashland, Oregon, USA), viable lymphocytes were gated via SSC and FSC, followed by T cells that were gated via 7AAD and CD14 negativity and CD3 positivity. Next, T cell subsets were gated via CD4 or CD8 positivity, after which immune checkpoint-positive CD4 or CD8 T cells were gated via PD1, LAG3 and/or TIM3 positivity. Unstained controls were taken along for every sample and used to set thresholds for the corresponding stained samples. The PD1, LAG3 and TIM3-positive and negative populations were analyzed in an integrated manner to assess all possible combinations and compute the fractions of these populations within CD4 or CD8 T cells.



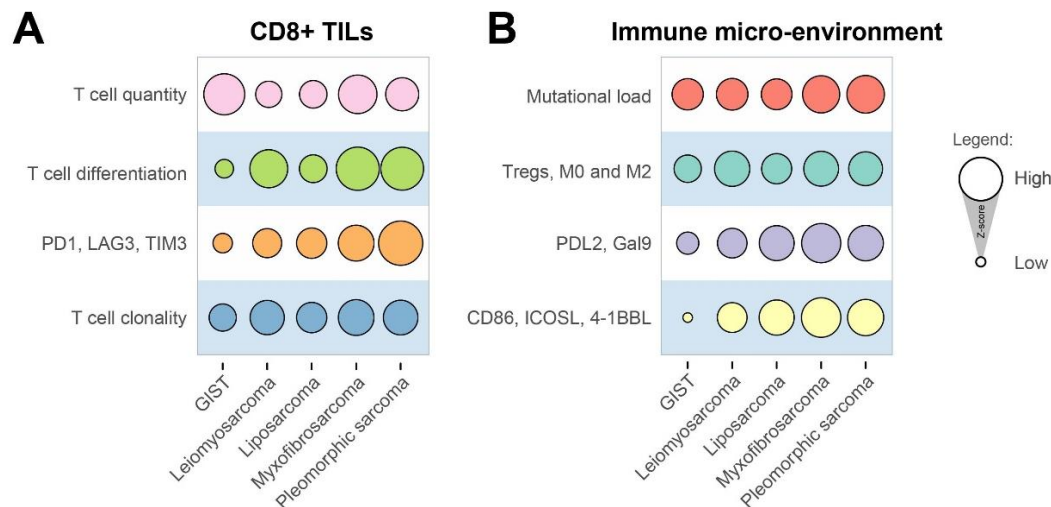
Supplementary Figure S2: Differential fractions of CD4+ T<sub>EMRA</sub> in STS subtypes.

**(A)** FCM analysis of maturation stages of CD4+ T cells in different STS subtypes based on definitions as described in legend of Figure 2. **(B)** T<sub>EMRA</sub> cells as percentage of CD4+ T cells represented by box-and whisker plots. See legend to Figure 2 for patient numbers. \*represents p-value <0.05 according to Mann-Whitney U test.



**Supplementary Figure S3: GIST and Liposarcoma show relatively low fractions of PD1-positive CD4+ T cells compared to other STS subtypes**

**(A)** FCM analysis of fractions of PD1, LAG3, and TIM3-expressing CD4+ T cells in different STS subtypes. **(B)** FCM analysis of fractions of CD4+ T cells co-expressing PD1, LAG3 and/or TIM3 in different STS subtypes. FCM analysis was only performed on samples with at least 200 CD4+ T cells. See legend to Figure 3 for patient numbers. \*represents  $p$ -value  $< 0.05$  according to Mann-Whitney U test.



#### Supplementary Figure S4: Overview of immune parameters of different STS subtypes.

Immune analyses of different STS subtypes are schematically summarized according to two sets of parameters, those that reflect intra-tumoral CD8 T cells (**A**) as well as those that reflect the immune micro-environment (**B**). CD8 T cell-related parameters include: T cell quantity (i.e., number of T cells per gram as presented in Figure 1A); T cell differentiation (fraction of TEM, Figure 2B); Co-inhibitory receptors (fraction of T cells co-expressing PD1, LAG3 and TIM3, Figure 3B) and T cell clonality (fraction of 10 most dominant clones, Figure 4B). Parameters related to immune micro-environment include: mutational load (mutations per Mb, Figure 5A); Inhibitory immune cells (fractions of regulatory T cells, and M0 and M2 macrophages, Figure 6A-C); Co-inhibitory ligands (expression of PDL2 and Galectin9 genes, Figure 6D-F; and co-stimulatory ligands (expression of CD86, ICOSL and 4-1BBL genes, Figures 6G-K). The listed parameters were utilized to compute Z-scores\*. Circle sizes represent mean Z scores that are normalized (range: -0.82 to 0.83) for all parameters per STS subtype. \*Z-scores were calculated as follows:  $(X - \mu) / \sigma$  where X is the value of the parameter,  $\mu$  is the population mean,  $\sigma$  is the standard deviation.