Supporting Information

Supplementary Table S1. Patient information. The table summarizes patient diagnosis, survival status and the time of biopsy collection following radiotherapy. All patients received only neo-adjuvant radiotherapy (RT) and underwent surgery as part of their standard treatment regimen. N: number of patients, MPNST: malignant peripheral nerve sheath tumor, NOS: not otherwise specified.

Supplementary Table S2. TaqMan Assays.

Supplementary Table S3. IHC quantification of Cancer Testis antigen and MHC-I expression in sarcoma patients before and after radiotherapy.

Supplementary Figure S4. Summary of radiotherapy-induced changes of immune response-related gene expression in human sarcoma. Retrospective analysis of 37 paired samples before/after radiotherapy by qRT-PCR for (A) immune effector molecules (B) immune suppressor molecules (C) cytokines (D) CT-antigens and (E) transcription factors. The horizontal bars on the bar graphs represent the median. Statistical analysis was performed for each transcript between the cohort before (open bars) and after (stippled bars) radiotherapy using the two-tailed bivariate analysis (Graphpad-Prism) on the ΔCt values after normalization to β-actin. The p-values of statistically different groups are displayed in the graph. The data for individual patients are shown in Fig. 1.

Supplementary Figure S5. Summary of radiotherapy-induced changes in human sarcoma at protein level. IHC analysis of paired sarcoma samples before/after radiotherapy for (A) CD3 (B) CD4 (C) CD8 (D) MHC-I (E) CT7 and (F) NY-ESO-1. The horizontal bars on the bar graphs represent the median. Statistical analysis was performed for each target gene between the
cohort before and after radiotherapy using the two-tailed bivariate analysis (Graphpad-Prism). The p-values of statistically different groups are displayed in the graph. The data for individual patients are shown in Fig. 2. ** Correlation is significant at the 0.01 level, *** Correlation is significant at the 0.001.

**Supplementary Figure S6. Correlation between different immune response-related transcripts following radiotherapy in sarcoma patients.** (A) Scatter dot plots demonstrating the significance of a bivariate correlation analysis (2-tailed). Each symbol represents an individual patient. Only correlations with a significant P value are represented in the figure. The solid line represents linear regression.

**Supplementary Table S7. Correlation analysis of radiotherapy-induced immunological changes in sarcoma patients.** qRT-PCR analysis was performed on 37 pairs of FFPE human sarcomas for (A) immune effector cells/ molecules, (B) immune suppressor cells/ molecules, (C) effector cytokines, (D) suppressor cytokines, (E) transcription factors and (F) CT-antigens . The ΔΔCt values were computed for each of the target genes against each other. A bivariate correlation analysis was performed and is given by the Spearman`s rho correlation coefficient (ρ) and the significance by the two-tailed P value. * Correlation is significant at the 0.05 level, ** Correlation is significant at the 0.01 level. All correlations with a significant P value are in bold.