**Supplementary Figure S1. Illustration of utility of companion canine spontaneous cancer model to address the complexities in preclinical in vivo radiobiological assays. This example demonstrates the aspect of heterogeneity in gene expression response and apparent diffusion coefficient of companion canine tumors in response to thermoradiotherapy.** A, the transcriptional response of individual canine tumors to thermoradiotherapy, 24 h after the first treatment day was derived by subtracting pre-treatment from post-treatment expression values of 16 companion dogs with soft tissue sarcomas. 2712 probe sets were selected that showed at least 2-fold changes. They are arranged by hierarchical clustering. The vertical red bar marks a cluster of genes induced in almost all samples, the vertical yellow and orange bars mark gene clusters induced only in the samples in group I. The vertical green bar marks a cluster of genes repressed in almost all samples. The clustering bars were color-coded to indicate their histopathology diagnosis. B, the gene clusters were expanded to show the names of representative genes on the right side. C, the differences in gene expression reveal markers of inflammation that are upregulated in those tumors in which the MRI diffusion coefficient was increased by treatment. The difference in the apparent diffusion coefficient between the two subgroups with different gene expression response to thermoradiotherapy was significant. Reprinted from Chi and colleagues (1).

Abbreviations: FSA, fibrosarcoma; HPC, hemangiopericytoma, PNST, peripheral nerve sheath tumor.

**Reference**

1. Chi JT, Thrall DE, Jiang C, Snyder S, Fels D, Landon C, et al. Comparison of genomics and functional imaging from canine sarcomas treated with thermoradiotherapy predicts therapeutic response and identifies combination therapeutics. Clin Cancer Res 2011;17:2549–60.