**Supporting Protocol S1**

The R2\* distribution of the entire histogram was obtained by calculating the values from all tumor slices of each group with intervals of three slices. Then, the pixel percentage of the R2\* values greater than the mean + SD (mean plus standard deviation), mean + 2SDs and mean + 3SDs values of each group was obtained by dividing the number of pixels with the values corresponding to mean + SD, mean + 2SDs and mean + 3SDs in the tumor histograms of each group by the number of pixels in all of the histograms and subsequently multiplying that number by 100. The mean + SD, mean + 2SDs and mean + 3SDs pixel percentages of each group were calculated (data not shown), and the mean + 3SDs value that best represented the skewedness of the FTH-BCSC Doc tumors was defined as the threshold.