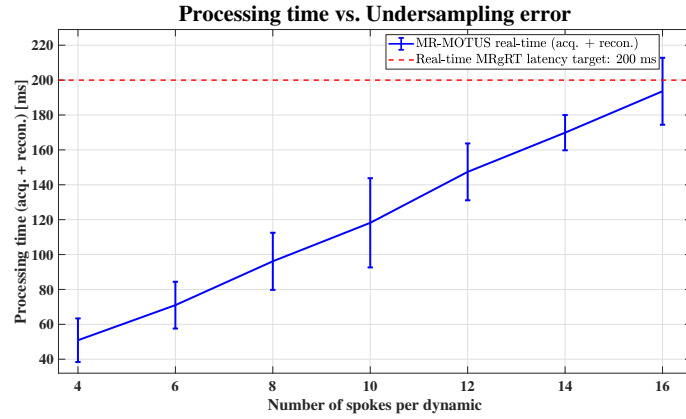


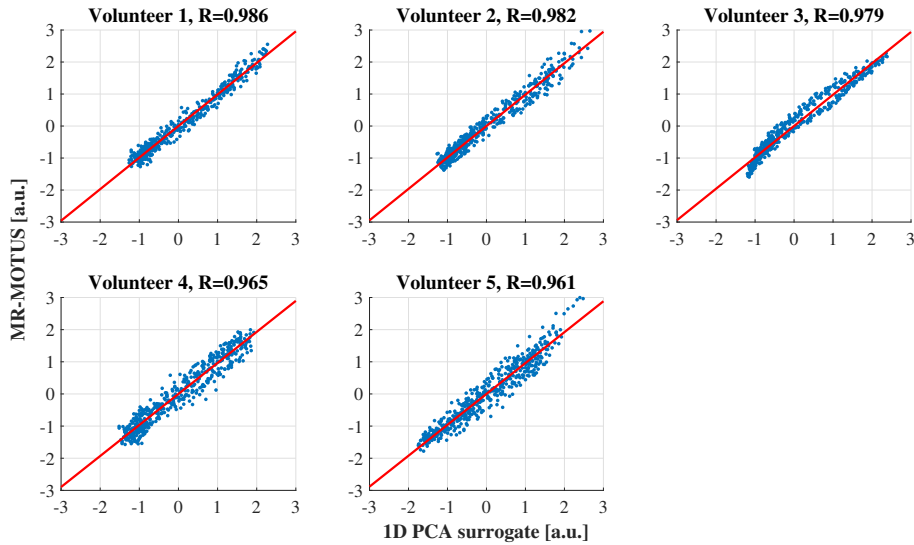
SupportingFigures.pdf

Supporting figures corresponding to the main article “Real-time non-rigid 3D respiratory motion estimation for MR-guided radiotherapy using MR-MOTUS”

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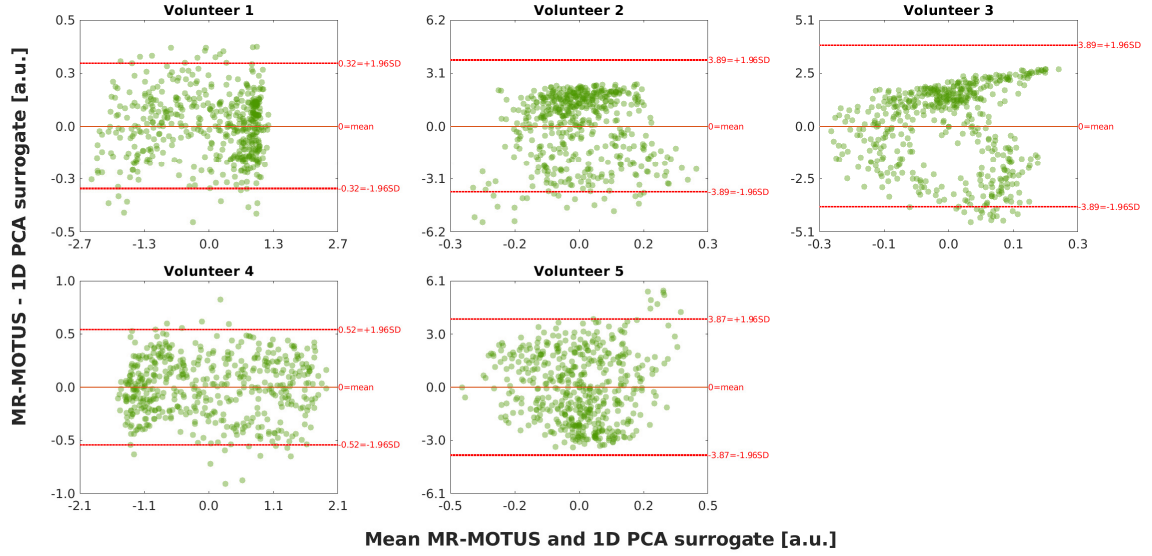


Supporting Information Figure S1: The dependency of the processing time (acquisition + reconstruction) on the number of spokes per dynamic. The solid blue line denotes the mean over 2000 real-time reconstructions for volunteer 4, and the vertical bars denote the standard deviations. We selected 14 spokes per dynamic, taking into account the fluctuations in the processing time, while maximizing the data per dynamic, and remaining below the real-time MR-guided radiotherapy target of 200 ms (dashed red line).

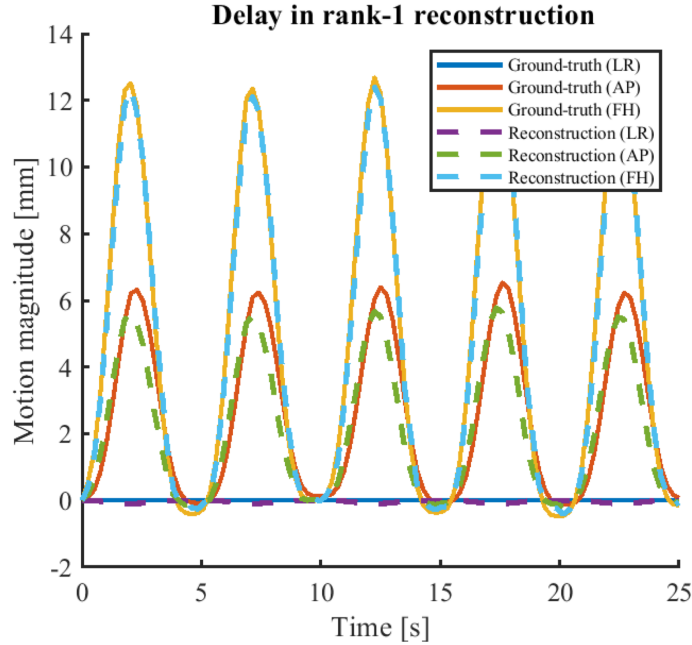


Supporting Information Figure S2: This figure visualizes for all volunteers scatter plots of the real-time reconstructed MR-MOTUS dynamic motion component Φ (y-axis), versus the 1D PCA motion surrogate (x-axis). Both quantities are normalized by subtracting the mean and dividing by the standard deviation. The red line shows the least-squares line through the samples. The slope is denoted by R , which directly corresponds to the Pearson correlation coefficient.

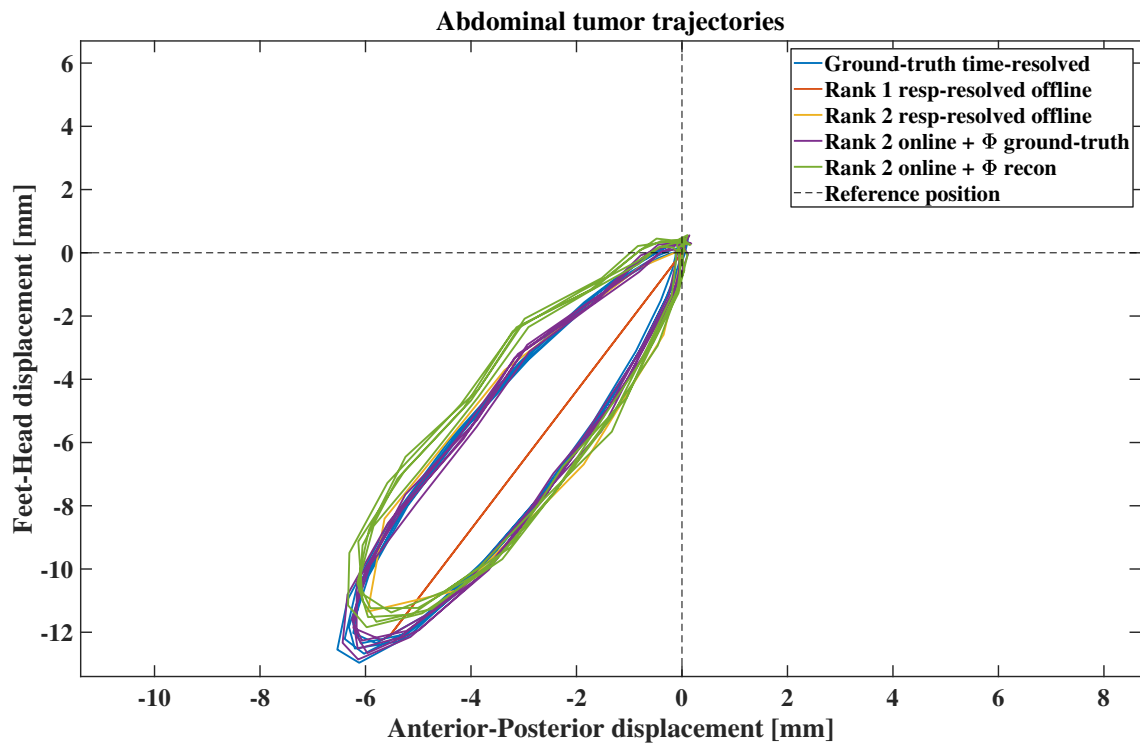
Bland-Altman analysis MR-MOTUS vs. 1D PCA surrogate



Supporting Information Figure S3: This figure visualizes Bland-Altman difference plots between the in-vivo real-time reconstructions and 1D PCA surrogate for all volunteers. Both the MR-MOTUS and 1D PCA surrogate were centered and scaled by their respective standard deviations in order to make this comparison possible.



Supporting Information Figure S4: Visualization of the delay in AP-direction caused by a rank-1 model applied to an XCAT model with hysteresis; this model will mostly capture the most dominant motion mode in FH direction (Supporting Figure S5), and thereby makes an error in the less dominant motion mode. Due to the phase delay between AP and FH components during hysteresis, this error manifests as a phase delay.



Supporting Information Figure S5: Analysis of the reconstructed tumor trajectories for different scenarios. This shows the expected elliptical trajectory. Moreover, the rank-1 seems to estimate the major axis of the ellipse, corresponding to the most dominant motion mode, whereas the rank-2 model is able to estimate the complete ellipse.