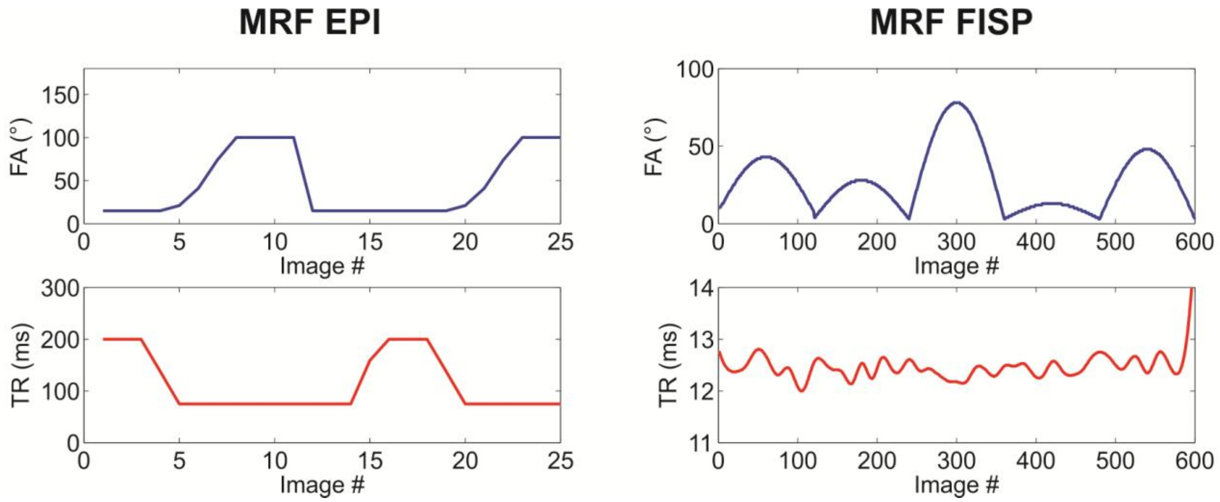
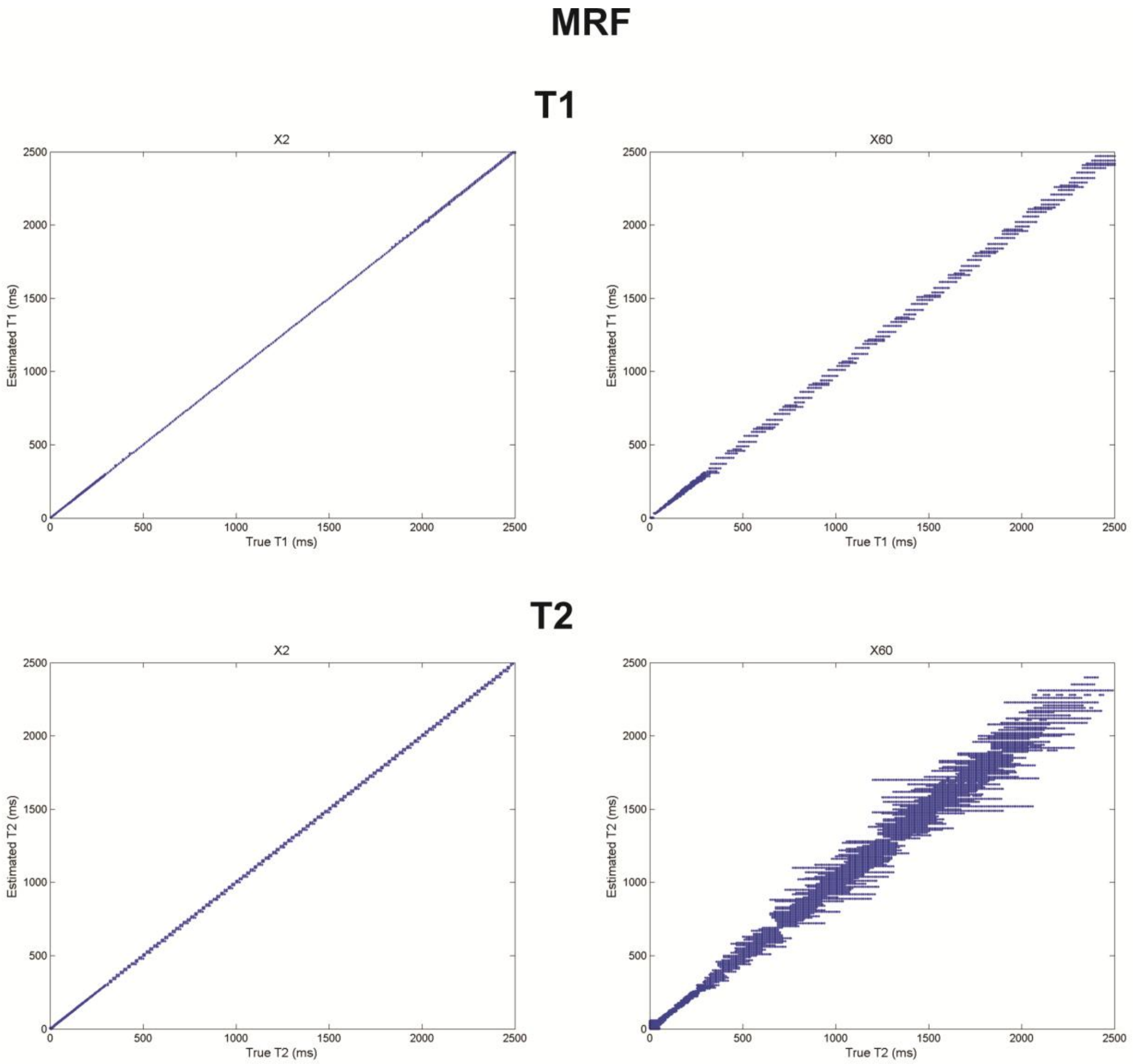
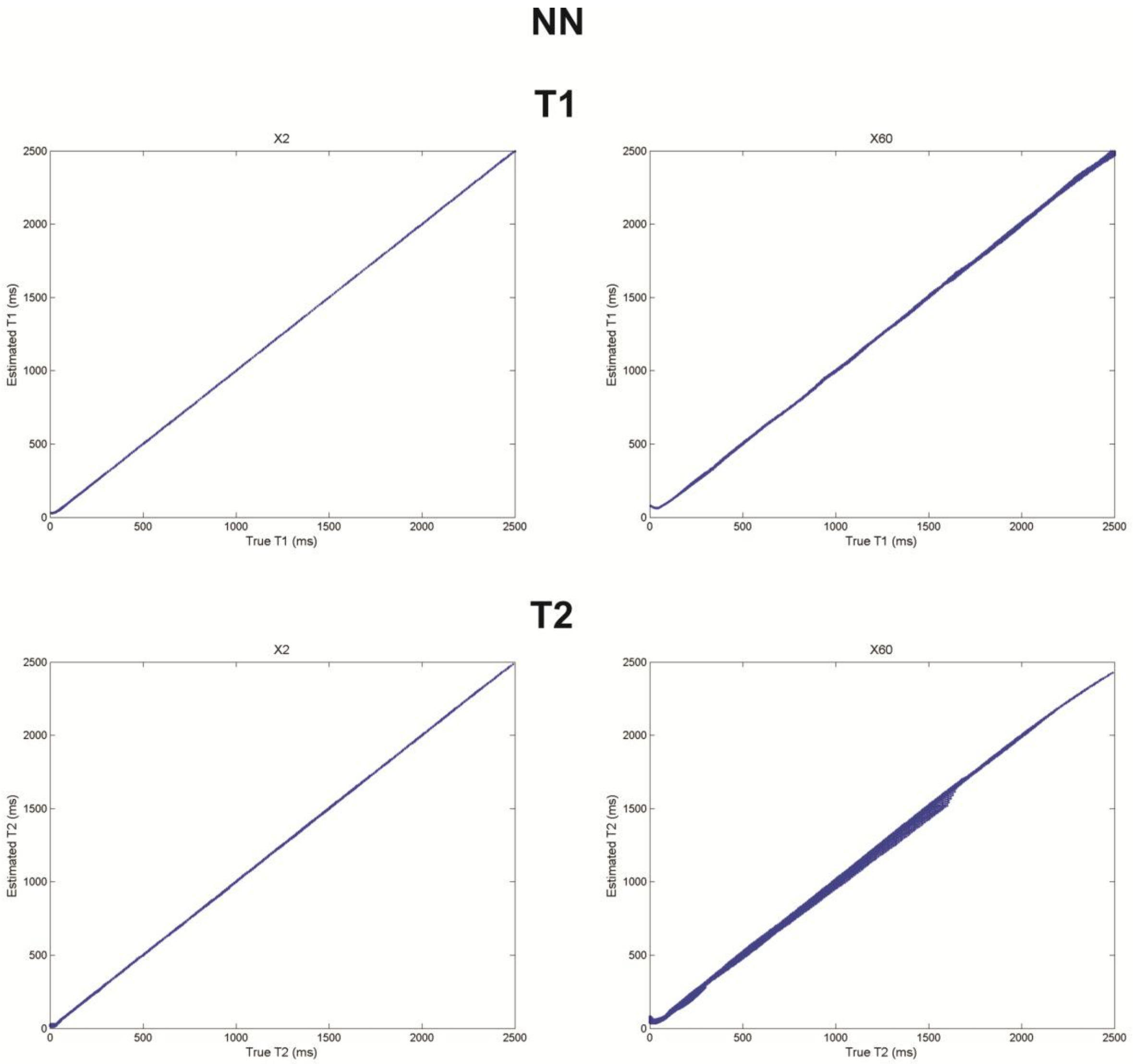


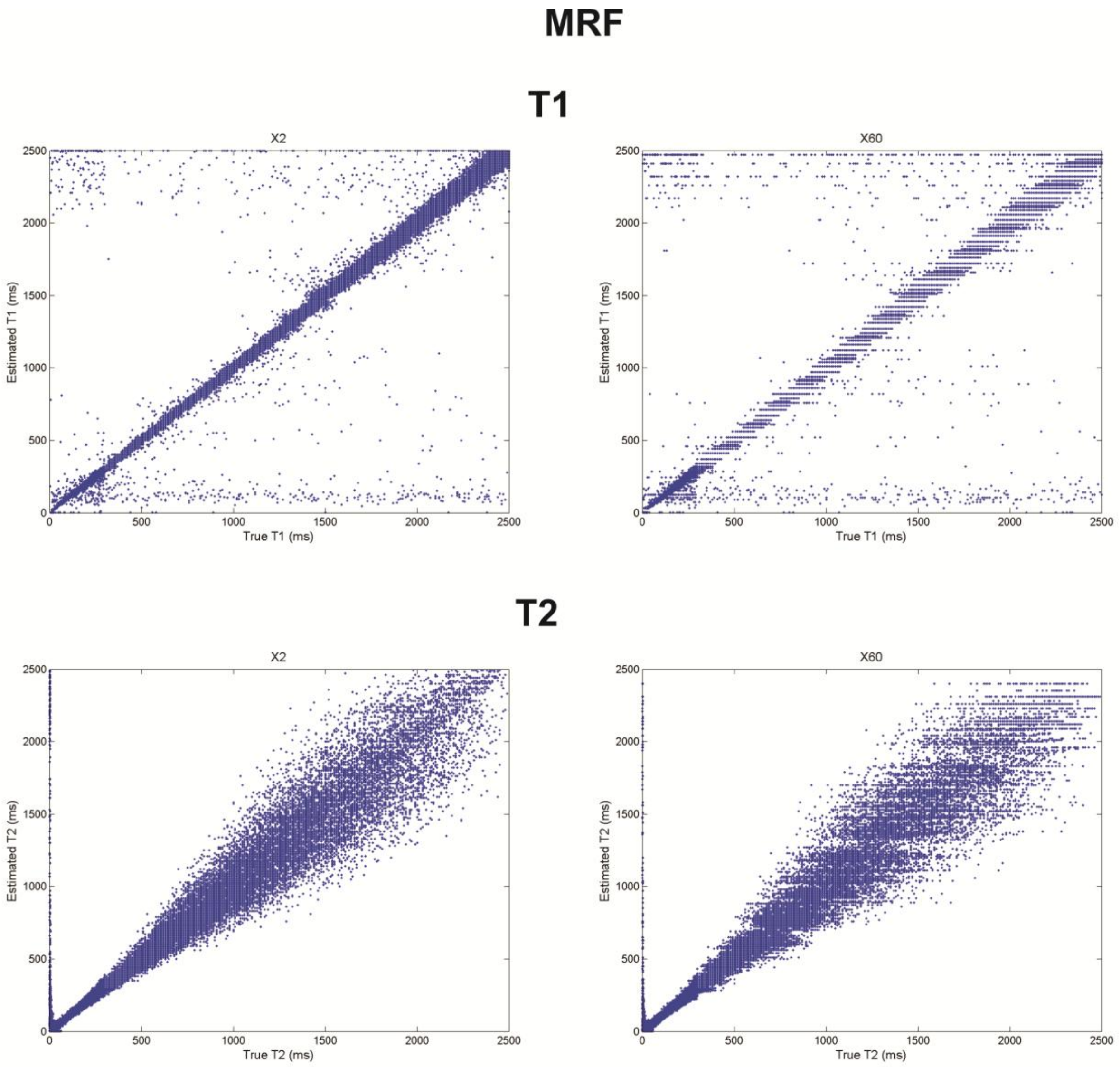
Supporting Fig. S1. Schedule of FA and TRs used for the optimized MRF EPI and MRF FISP sequences.



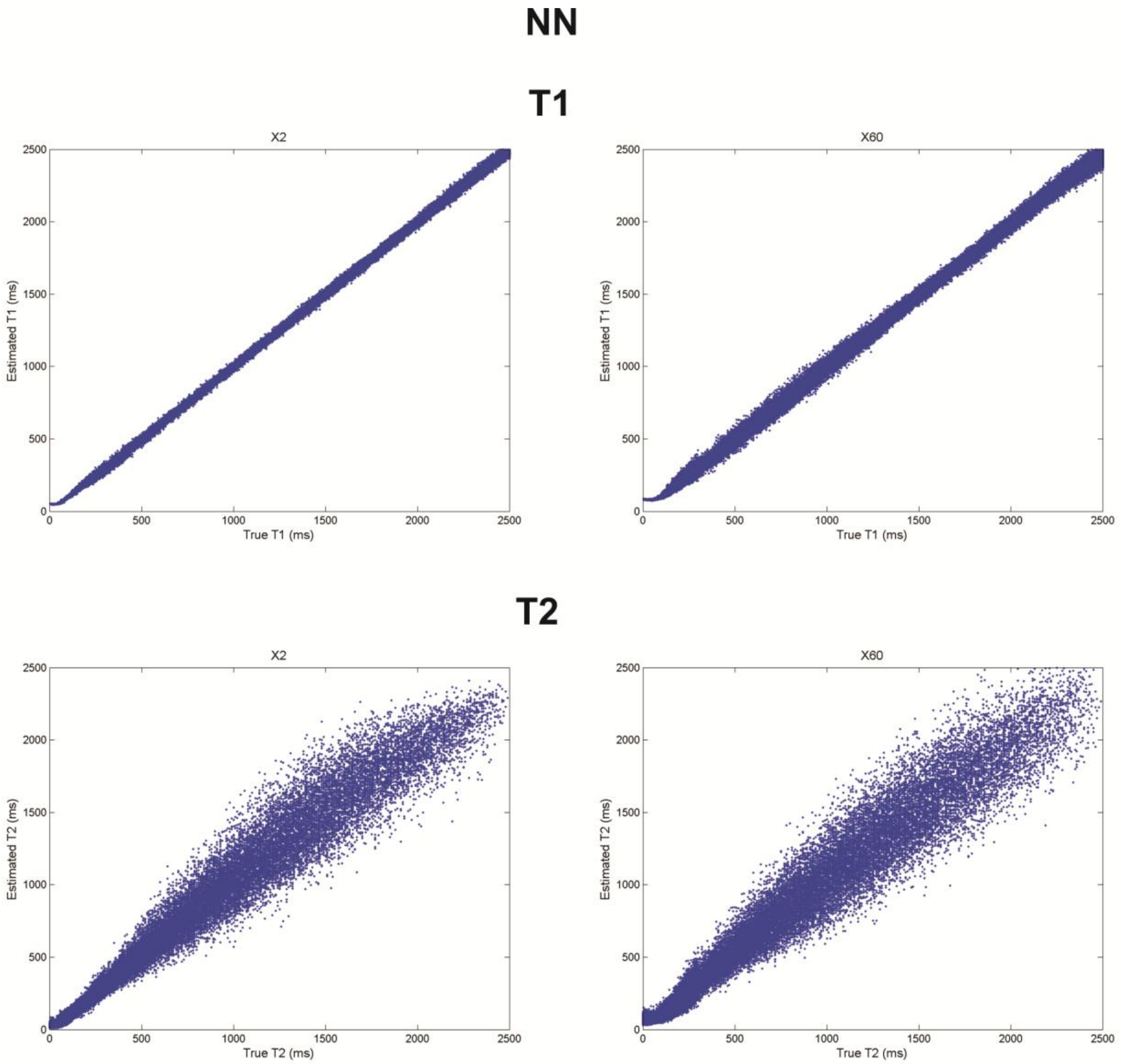
Supporting Fig. S2. MRF dictionary matching reconstruction of the noiseless T_1 and T_2 values tested in comparison to the true values for the lightly undersampled (X2) and 60-fold undersampled (X60) training dictionaries.



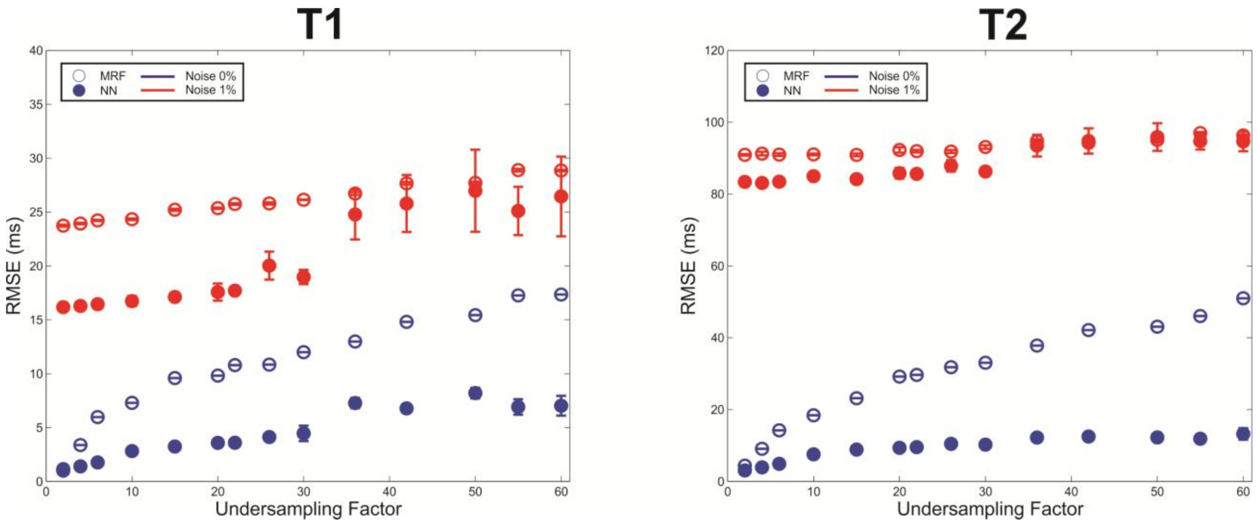
Supporting Fig. S3. NN reconstruction of the noiseless T_1 and T_2 values tested in comparison to the true values for the lightly undersampled (X2) and 60-fold undersampled (X60) training dictionaries.



Supporting Fig. S4. MRF dictionary matching reconstruction of the T_1 and T_2 values corrupted by 1% Gaussian noise in comparison to the true values for the lightly undersampled (X2) and 60-fold undersampled (X60) training dictionaries. The dictionary matching of noisy data was particularly susceptible to short (<11 ms) T_2 values for the noise level tested resulting in large errors.



Supporting Fig. S5. NN reconstruction of the T_1 and T_2 values corrupted by 1% Gaussian noise in comparison to the true values for the lightly undersampled (X2) and 60-fold undersampled (X60) training dictionaries. Because the NN reconstruction was trained on noisy data it was more robust to the effects of noise.



Supporting Fig. S6. RMSE of the MRF dictionary matching (open circles) and NN reconstruction (closed circles) for the different undersampling factors and noise levels tested. For the noiseless acquisition (blue curves) the error in the NN reconstruction was 2 fold smaller for T_1 and 4 fold smaller for T_2 at the largest undersampling factor tested. For the noisy acquisition (red curves) only tissues with T_2s > 11 ms were included in the error calculation for the MRF dictionary matching whereas all tissues were included in the NN reconstruction error. Nevertheless, the NN reconstruction error was still smaller or equal to the MRF error for all undersampling factors tested.