Improved Pulmonary ^{129}Xe Ventilation Imaging via 3D-Spiral UTE MRI – Supporting Information

Additional FLORET Trajectory Information: Gradient waveform calculations in C have been previously released and hosted by ISMRM. Here, all trajectories for reconstruction were calculated using GPI (http://gpilab.com/). The software allows for investigation of the effect each parameter has on the sampling pattern, including undersampling. Additionally, as this software is open source, the code/logic can be viewed and modified as needed. For this particular study, the default SpiralCoords node/code was implemented, without modification, for trajectory calculation. The resulting FLORET trajectories used in this study can be seen in the figures below.

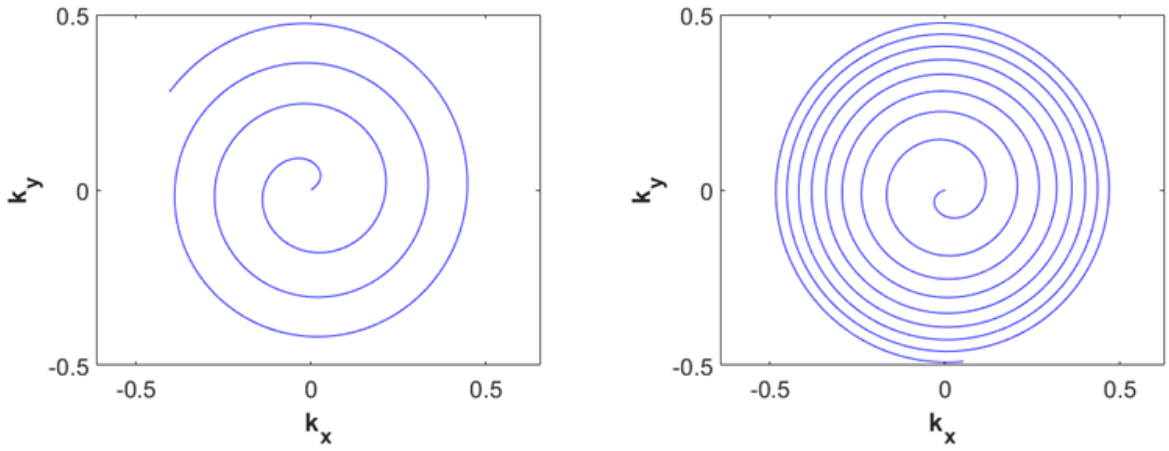

Figure S1: Base Fermat spirals ($k_z = 0$) for the comparative (left) and fully sampled (right) FLORET sequences. Note, the longer readout samples more of k-space within a single excitation/acquisition

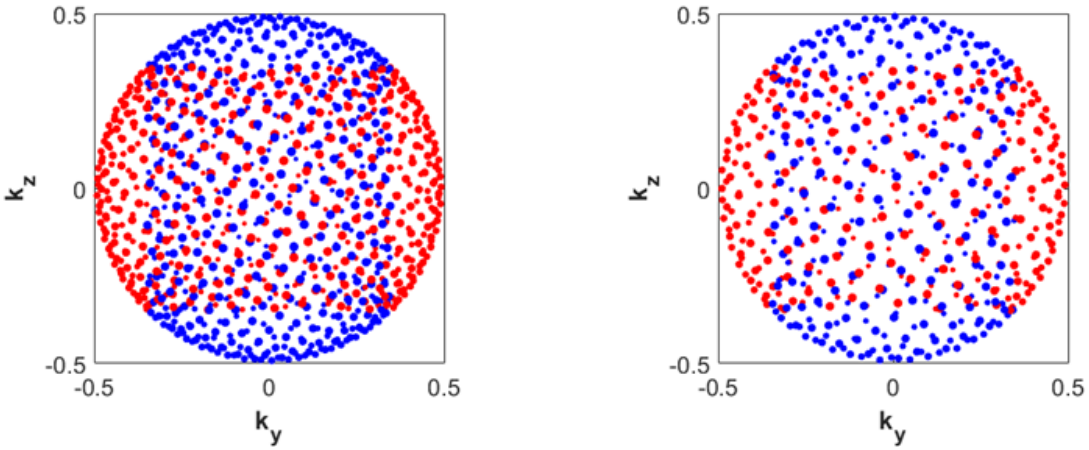

Figure S2: Trajectory endpoints for the comparative (left) and fully sampled (right) FLORET sequences. Each hub is colored differently, allowing them to be distinguished. Additionally, endpoints further away in the k_x dimension are smaller to provide depth. Despite the fully sampled nature of the sequence on the right, the left is denser due to its shorter read out duration

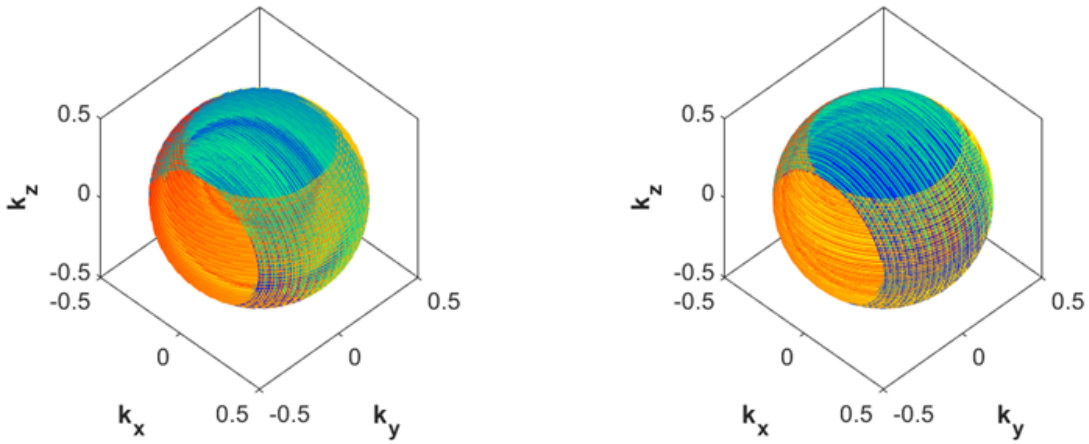

Figure S3: Complete trajectory sampling for the comparative (left) and fully sampled (right) FLORET sequences. Red-to-yellow indicates the first hub with the red indicating the first acquisition of the hub and yellow indicating the final acquisition of the hub. Similarly, the second hub is ordered blue-to-green. Note that the spirals are acquired relatively randomly in the cone dimension.

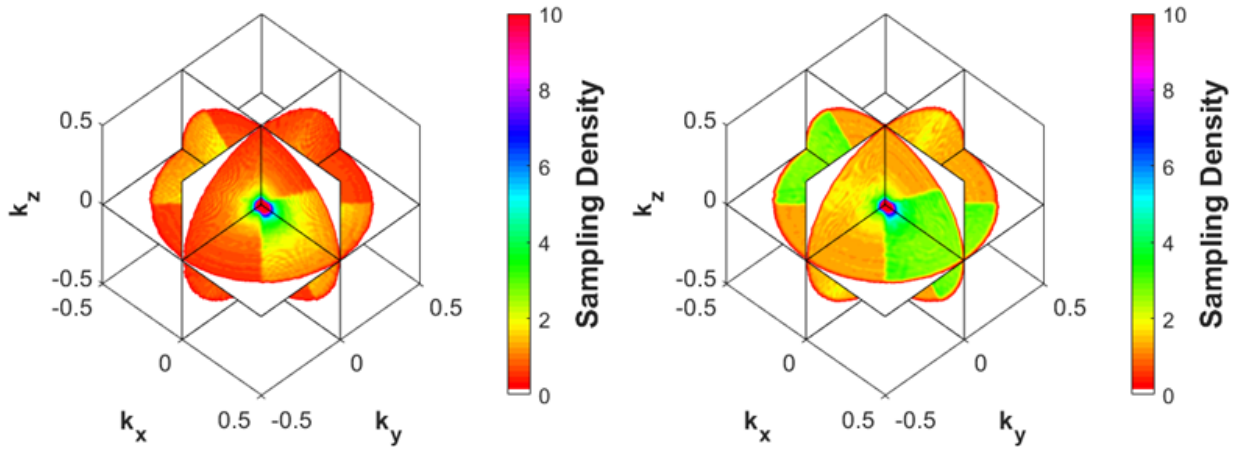

Figure S4: Approximate sampling density maps for the comparative (left) and fully sampled (right) FLORET sequences. Note the cones of increased sampling density due to the overlap of the hubs and the similar amount of undersampling in the cone and spiral dimensions. The minimum undersampling values (at the edges where no hub overlap occurs), is consistent with the reported sampling densities for each sequence.