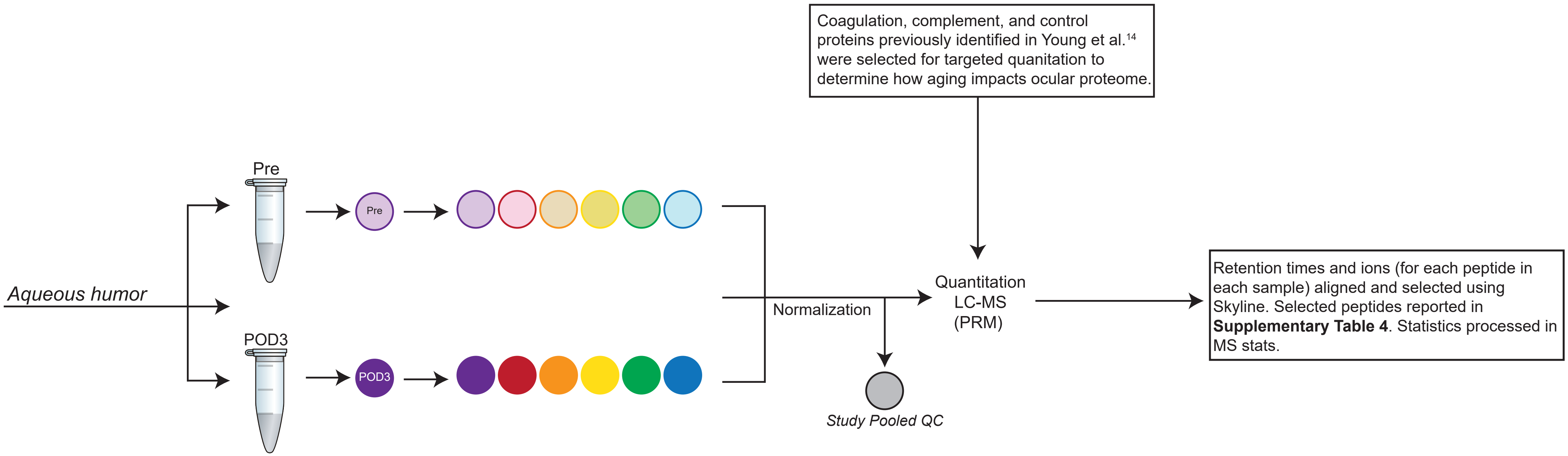

Supplemental Figure 1. AH sample collection and proteomics workflow. Pre and POD 3 samples were collected from the rabbits, and each sample was normalized to the lowest measured peptide quantity among the three samples. Proteins (and the resulting peptides) from previous work were selected for targeted quantitation by parallel reaction monitoring (PRM). Retention times for each sample (and each peptide) were analyzed in Skyline.