Transcriptomic Signatures of Influenza Vaccine Responses

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Analysis Approach. Subjects will be randomly assigned to vaccine type. For all laboratory assays, randomized complete or incomplete block designs that include technical replicates and laboratory controls will be utilized to ensure sample and assay processing are balanced with respect to collection date, vaccine, and sex, keeping specimens from the same subject adjacent to one another. Data will be scrutinized to identify potential biases, batch effects, or failed assays. We will normalize mRNA-sequence data by Conditional Quantile Normalization (CQN), adjusting for library size, gene length, and GC content. Our primary aim is to test the hypotheses that vaccine type (Fluad vs Fluzone) is associated with the change in immune response as measured by hemagglutination inhibition (HAI) Antibody titer. To test this hypothesis, we will use the Wilcoxon Rank Sum test to test for differences between the vaccine types in the change from baseline HAI to Day 28 HAI Ab titers.