To help assess Quality Assurance of this project, a QA summary is provided here:

All samples were processed in one day and in one batch to eliminate batch-to-batch variability. Processed along with the samples were:

- A seven-point matrix-matched calibration curve consisting of calf serum spiked with the analytes of interest. No samples fell outside the range of our calibration curve. Matrix-matched calibration curves have been shown to be more accurate than simply using pure standards with no matrix.
- Three method blanks which consisted of a blank extraction vial that was treated exactly the same as the samples but did not contain any sample matrix. Three of the 25 compounds of interest were detected at low levels in the blanks, two of which were subsequently excluded from data reporting. The third, PFNA, was found at very low levels in only one blank and thus was still included as long as samples contained at least three times the blank level.
- 4 certified reference material samples (NIST SRM 1957) that contained certified values for three analytes of interest. Measurements of these compounds in the SRM were within 20% of certified values and within 12% for the most predominant compound in the samples, PFOS.
- Replicates of three samples to assess precision. Replicate measurements were within 15%.

Further criteria for positive analyte identification included:

- Use of two MS/MS ion transitions for each ion – one for quantification and one for qualification
- The ratio of the two above ions were checked against the ratios found in standards
- A tight retention time window was applied (0.05 min)