A.

Alpha-1AT

$y = 0.9927x + 0.0259$
$R^2 = 0.9984$

Measured Concentration (g/L)

Expected Concentration (g/L)

B.

Alpha-GP

$y = 1.0109x + 3E-05$
$R^2 = 0.9988$

Measured Concentration (g/L)

Expected Concentration (g/L)

C.

Lactate

$y = 0.9998x - 0.1589$
$R^2 = 0.9976$

Measured Concentration (mmol/L)

Expected Concentration (mmol/L)

Supplemental Figure 1: Assay linearity measured using five-part linearity dilution series. All data points are presented as the average of triplicate measurements. Line of best fit was determined by Deming regression for **A)** alpha-1-antitrypsin, **B)** alpha-1-glycoprotein, B) lactate.
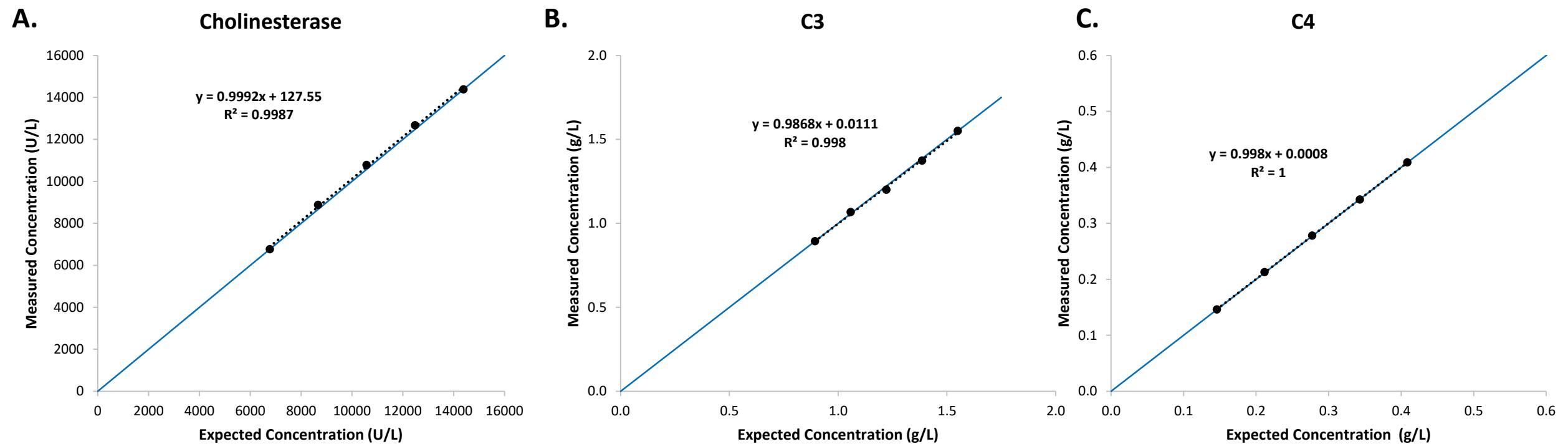
Supplemental Figure 2: Assay linearity measured using five-part linearity dilution series. All data points are presented as the average of triplicate measurements. Line of best fit was determined by Deming regression for **A)** cholinesterase, **B)** complement 3, **C)** complement 4.

A. Glucose

y = 1.0031x - 0.4577
R² = 0.9988

B. Haptoglobin

y = 0.9856x + 0.0113
R² = 0.9982

C. IgA

y = 0.9884x + 0.0321
R² = 0.9989
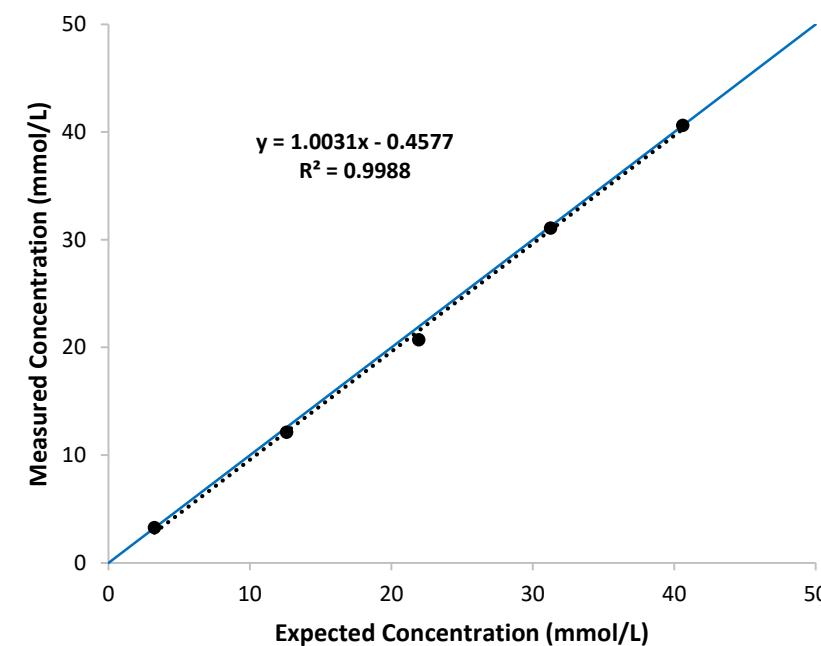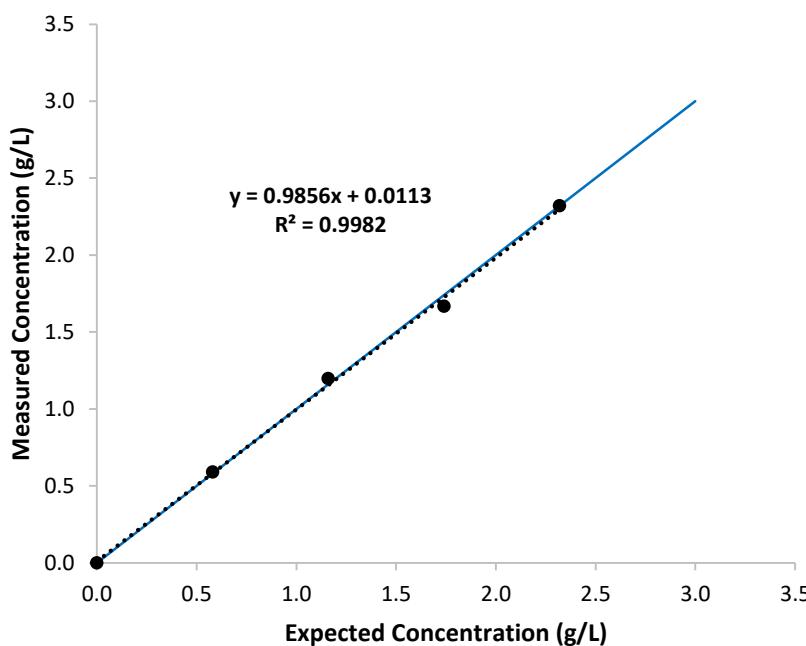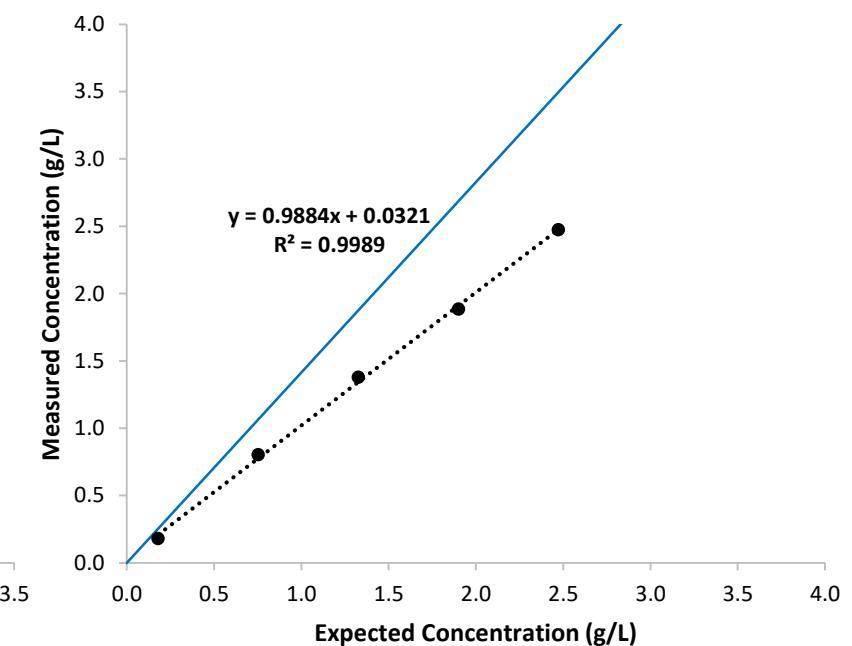
Supplemental Figure 3: Assay linearity measured using five-part linearity dilution series. All data points are presented as the average of triplicate measurements. Line of best fit was determined by Deming regression for **A)** glucose, **B)** haptoglobin, **C)** immunoglobulin A.

A.

IgE

y = 1.0053x + 5.3499
R² = 0.9981

Y-axis: Measured Concentration (IU/mL)
X-axis: Expected Concentration (IU/mL)

B.

IgG

y = 0.9959x + 0.201
R² = 0.9984

Y-axis: Measured Concentration (g/L)
X-axis: Expected Concentration (g/L)

C.

IgM

y = 1.0021x + 0.0038
R² = 0.9999

Y-axis: Measured Concentration (g/L)
X-axis: Expected Concentration (g/L)
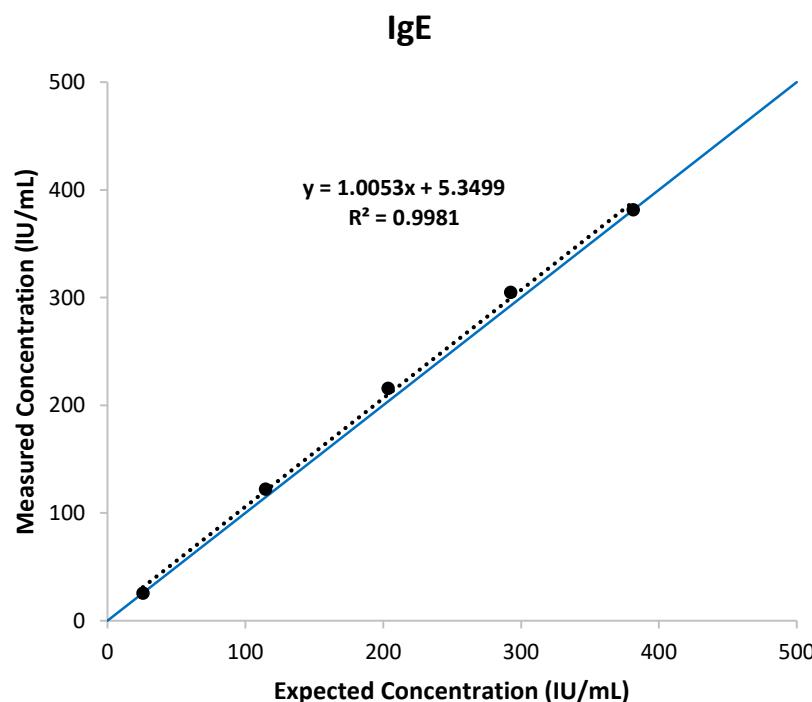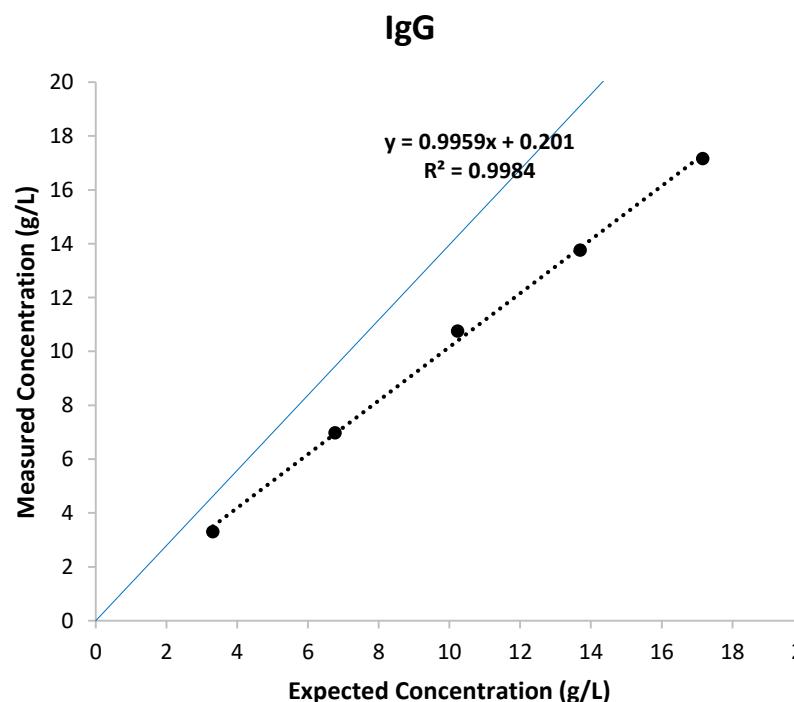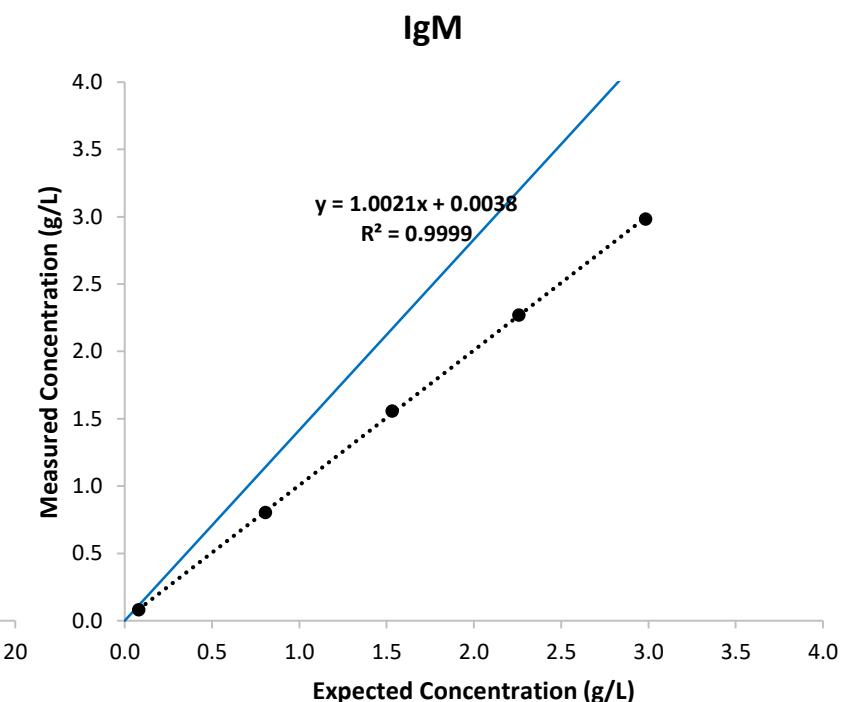
Supplemental Figure 4: Assay linearity measured using five-part linearity dilution series. All data points are presented as the average of triplicate measurements. Line of best fit was determined by Deming regression for **A)** immunoglobulin E, **B)** immunoglobulin G, **C)** immunoglobulin M
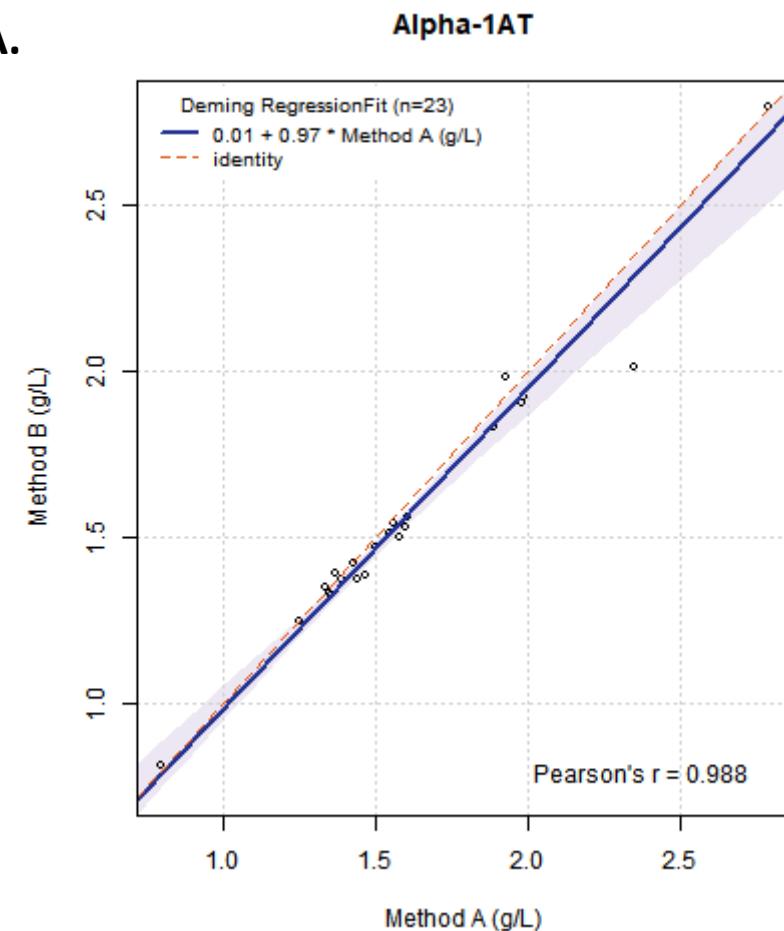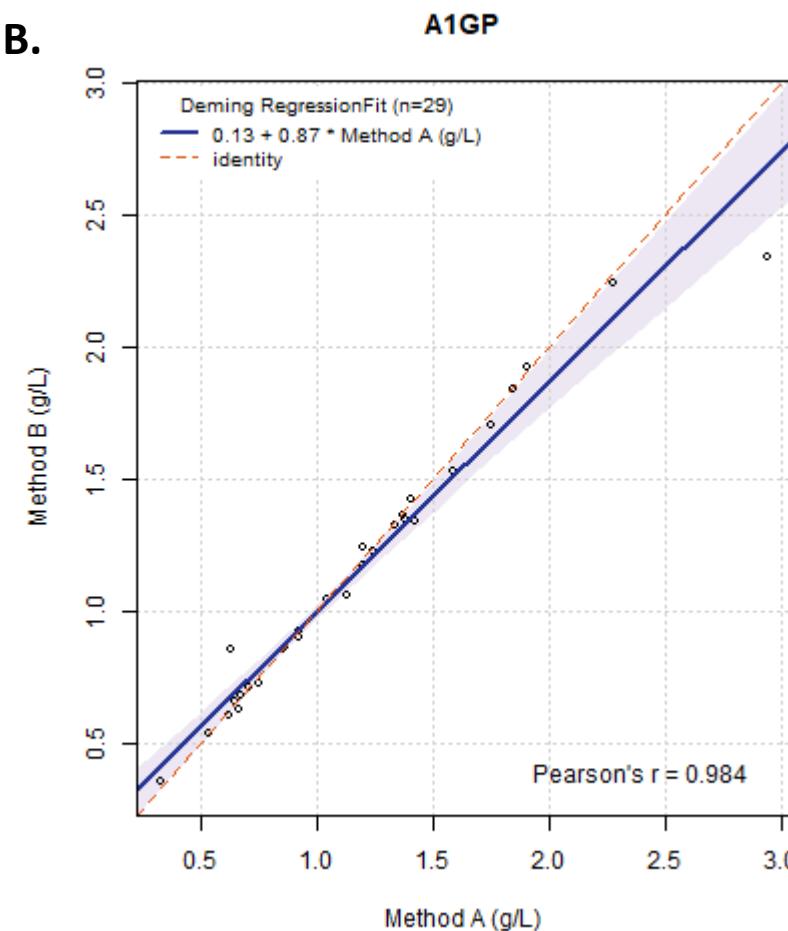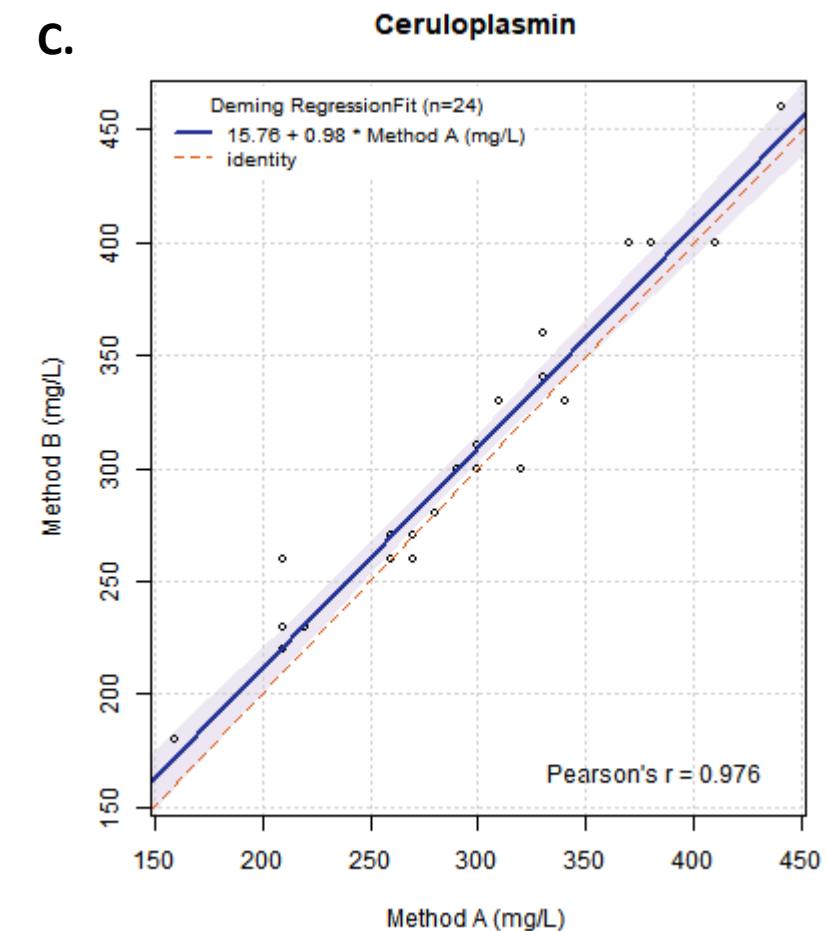
Supplemental Figure 5: Method comparison analysis for assays measured by Abbott ARCHITECT (x-axis) and Alinity (y-axis) systems. The dashed red line indicates the line of perfect agreement (y=x) and the solid blue line indicates the Deming regression line. **A)** Alpha-1-antitrypsin, **B)** Alpha-1-glycoprotein, **C)** Ceruloplasmin.

A. Cholinesterase

Deming RegressionFit (n=6)
— -314.1 + 0.98 * Method A (U/L)
-- identity

Pearson's r = 1

Method B (U/L) vs Method A (U/L)

B. C3

Deming RegressionFit (n=29)
— -0.01 + 1.07 * Method A (g/L)
-- identity

Pearson's r = 0.995

Method B (g/L) vs Method A (g/L)

C. C4

Deming RegressionFit (n=27)
— 0 + 1.05 * Method A (g/L)
-- identity

Pearson's r = 0.991

Method B (g/L) vs Method A (g/L)
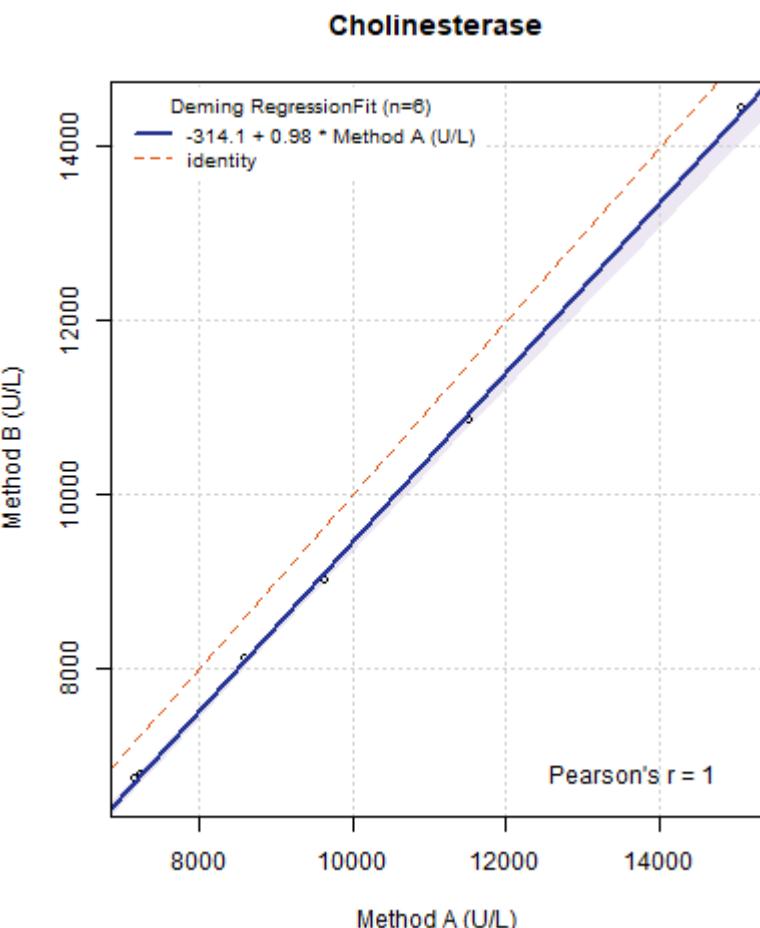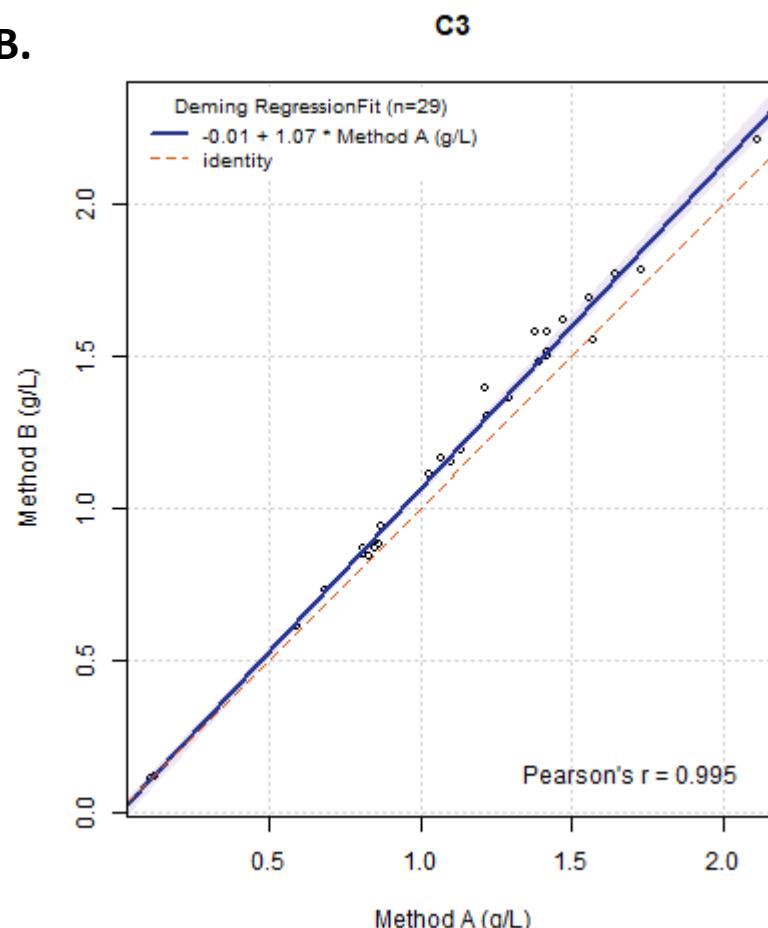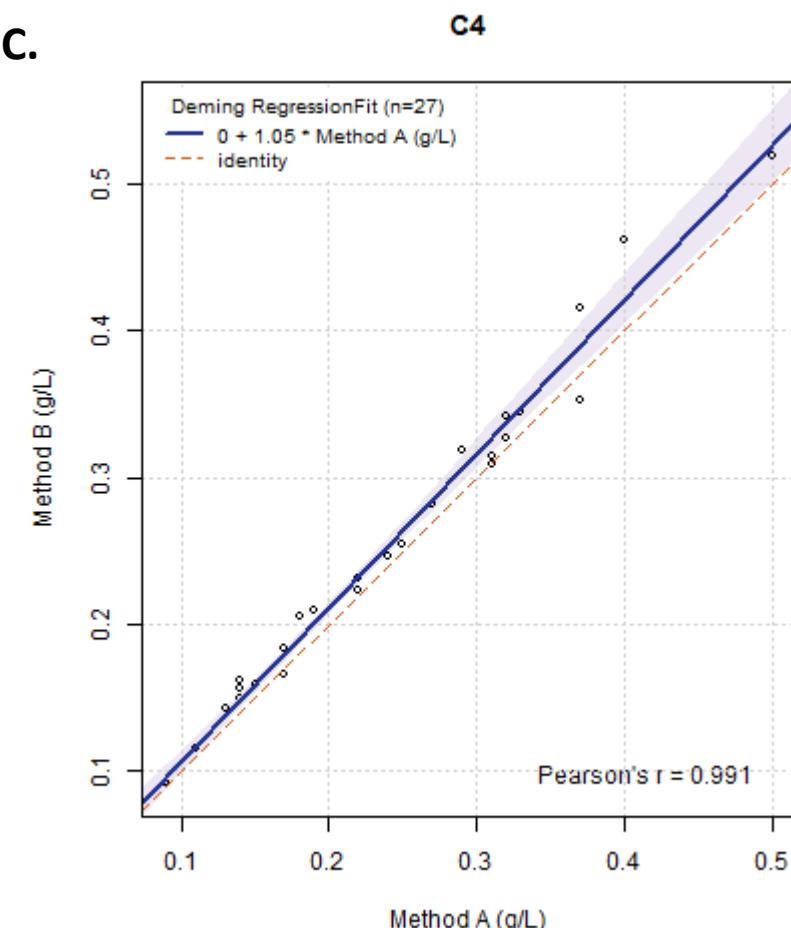
Supplemental Figure 6: Method comparison analysis for assays measured by Abbott ARCHITECT (x-axis) and Alinity (y-axis) systems. The dashed red line indicates the line of perfect agreement (y=x) and the solid blue line indicates the Deming regression line. **A)** cholinesterase, **B)** complement C3, **C)** complement C4.

A.

Glucose

Deming RegressionFit (n=40)
—— -0.93 + 0.98 * Method A (mmol/L)
-- - identity

Method B (mmol/L)

Method A (mmol/L)

Pearson's r = 0.995

B.

Haptoglobin

Deming RegressionFit (n=26)
—— 0 + 1.02 * Method A (g/L)
-- - identity

Method B (g/L)

Method A (g/L)

Pearson's r = 0.999

C.

IgA

Deming RegressionFit (n=24)
—— -0.03 + 1.04 * Method A (g/L)
-- - identity

Method B (g/L)

Method A (g/L)

Pearson's r = 0.999
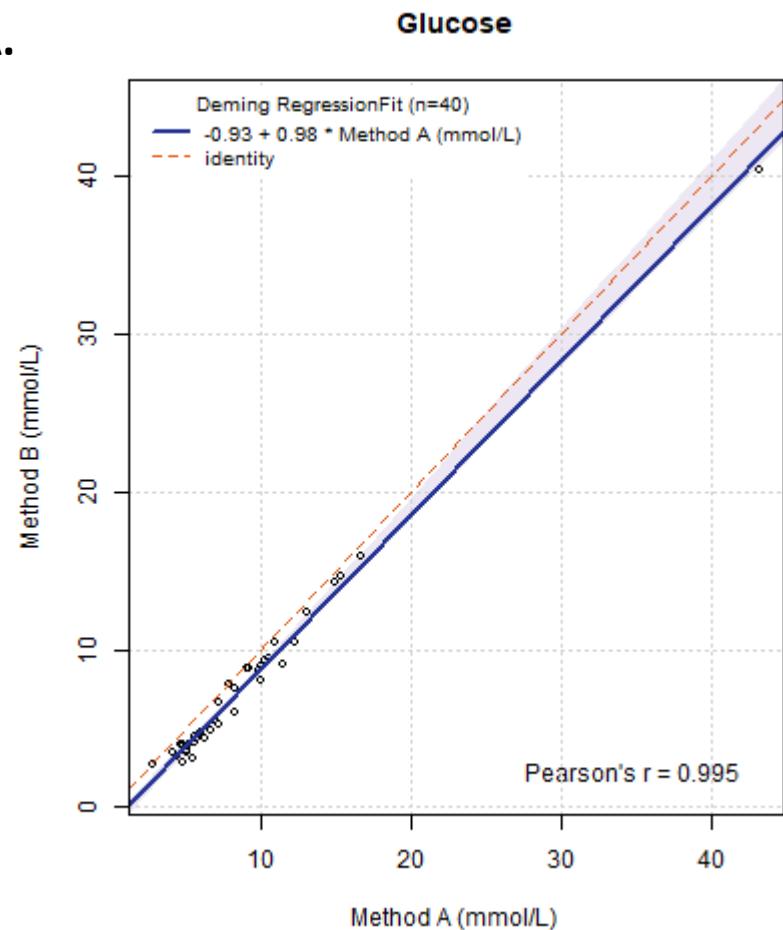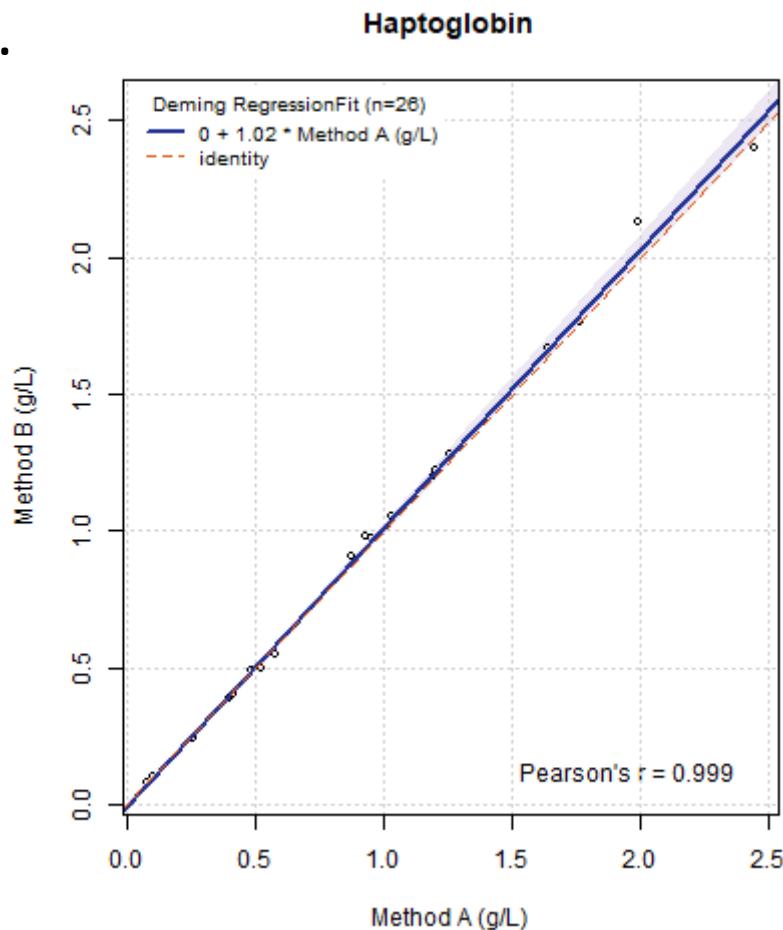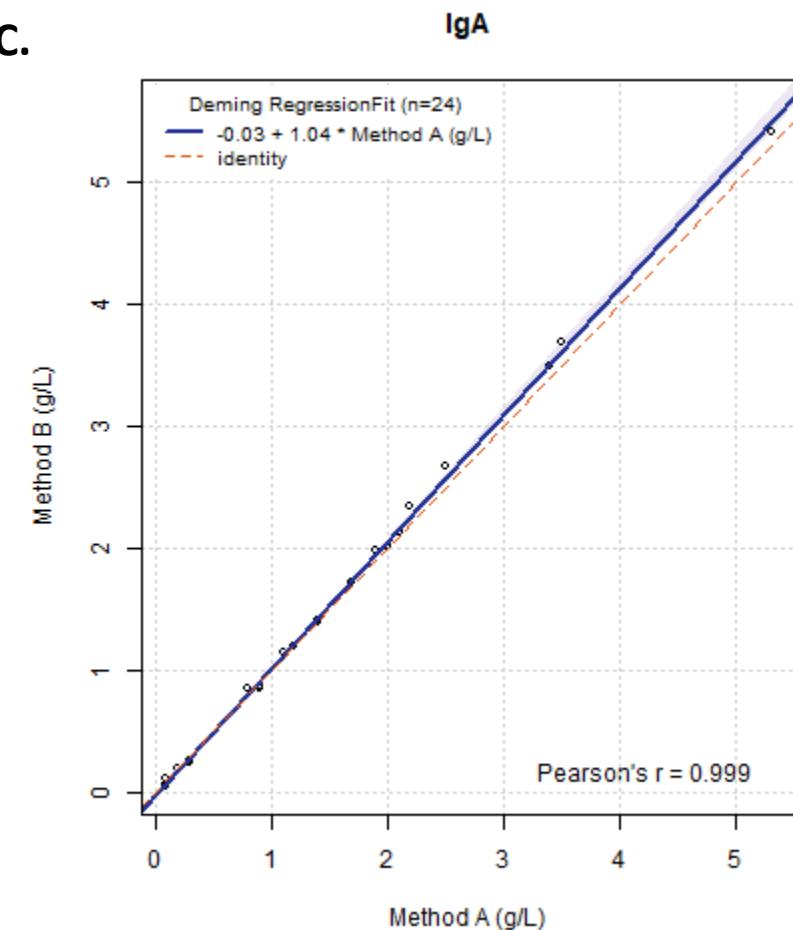
Supplemental Figure 7: Method comparison analysis for assays measured by Abbott ARCHITECT (x-axis) and Alinity (y-axis) systems. The dashed red line indicates the line of perfect agreement (y=x) and the solid blue line indicates the Deming regression line. **A)** glucose, **B)** haptoglobin, **C)** immunoglobulin A.
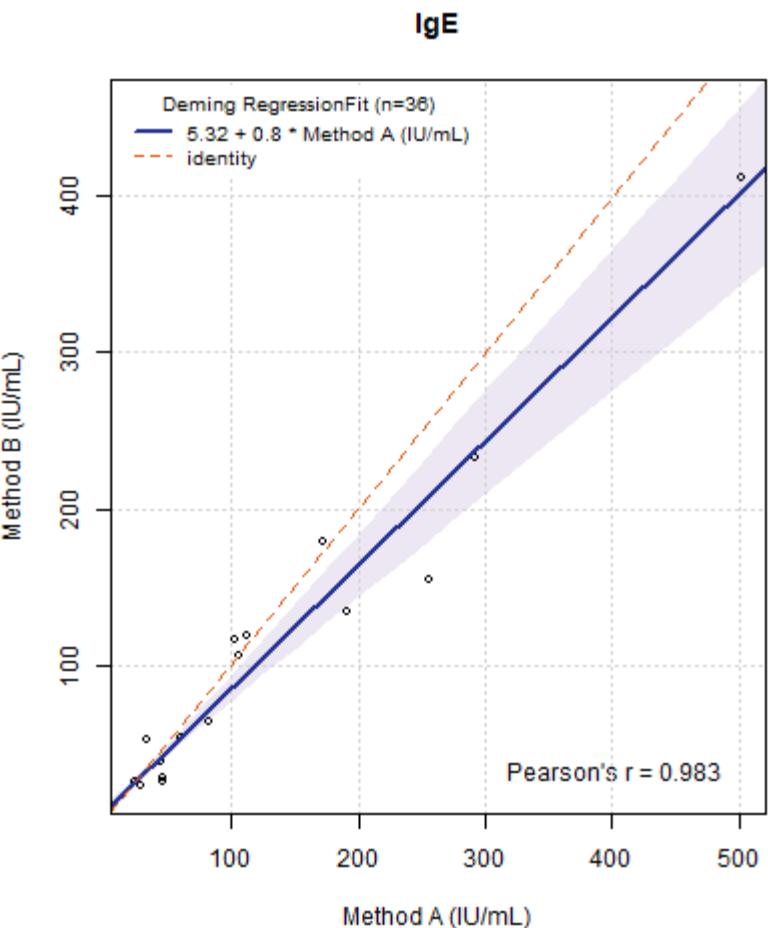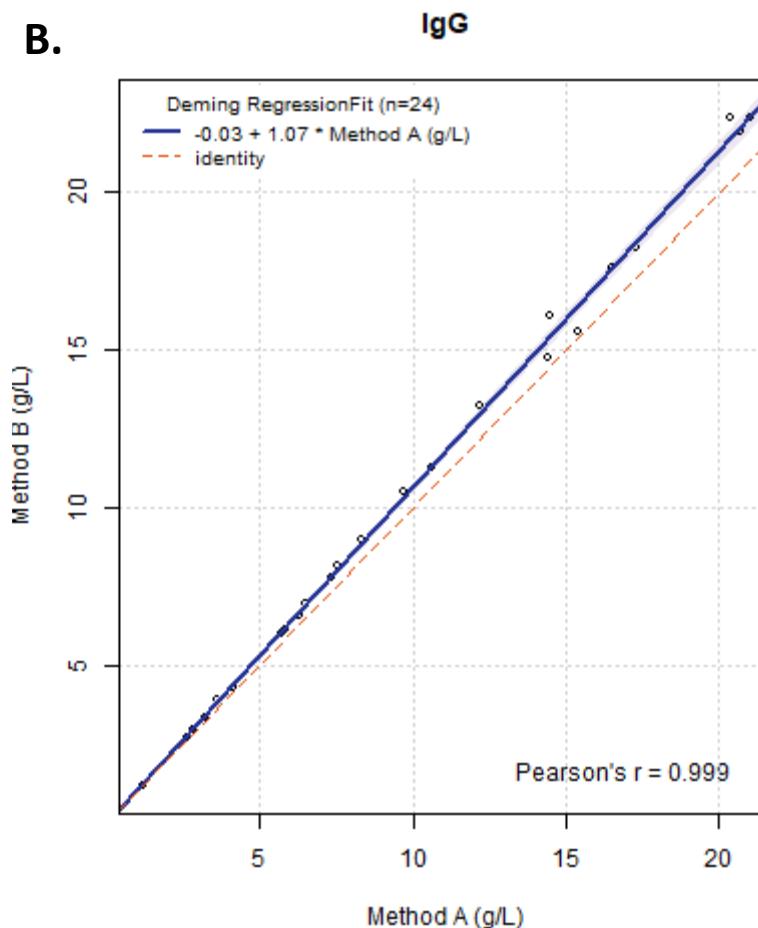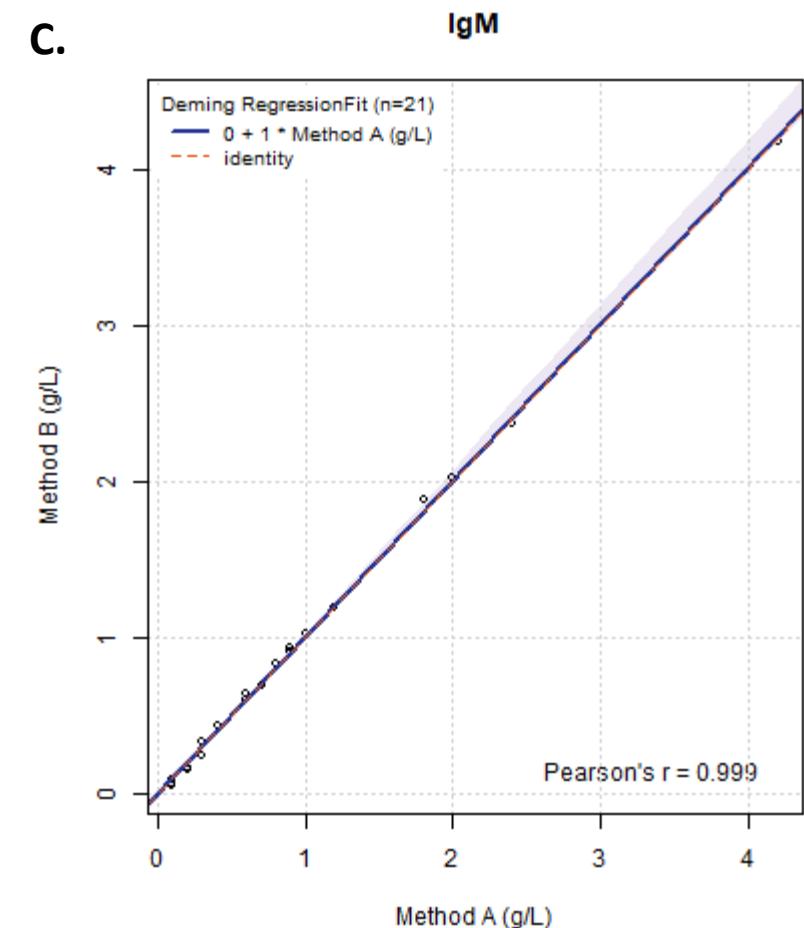
Supplemental Figure 8: Method comparison analysis for assays measured by Abbott ARCHITECT (x-axis) and Alinity (y-axis) systems. The dashed red line indicates the line of perfect agreement (y=x) and the solid blue line indicates the Deming regression line. **A)** immunoglobulin E, **B)** immunoglobulin G, **C)** immunoglobulin M.
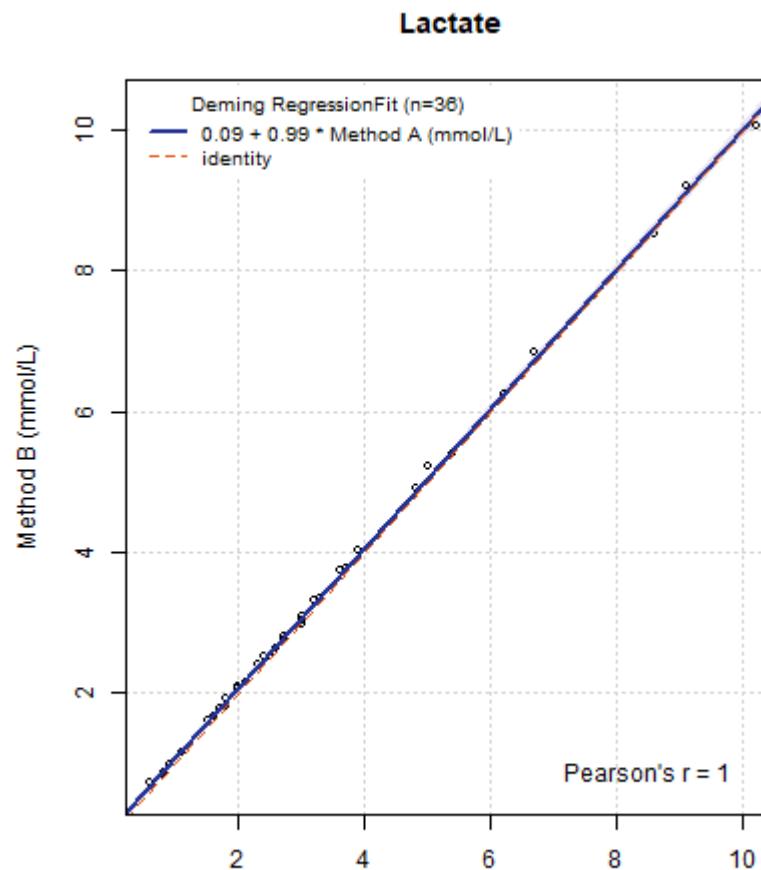
Supplemental Figure 9: Method comparison analysis for lactate measured by Abbott ARCHITECT (x-axis) and Alinity (y-axis) systems. The dashed red line indicates the line of perfect agreement (y=x) and the solid blue line indicates the Deming regression line.
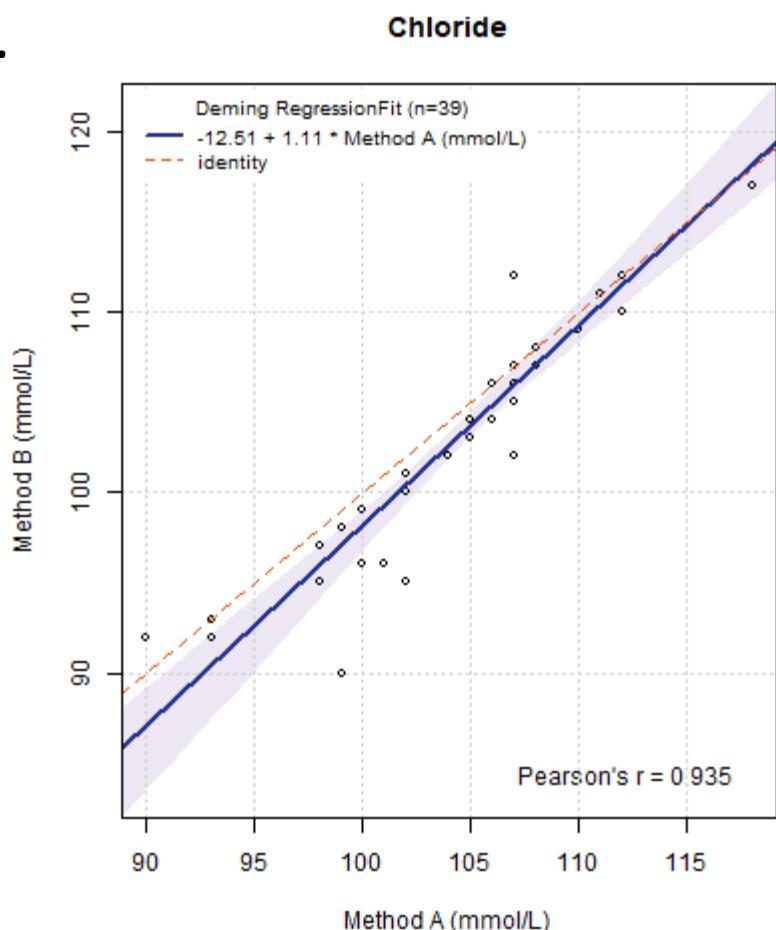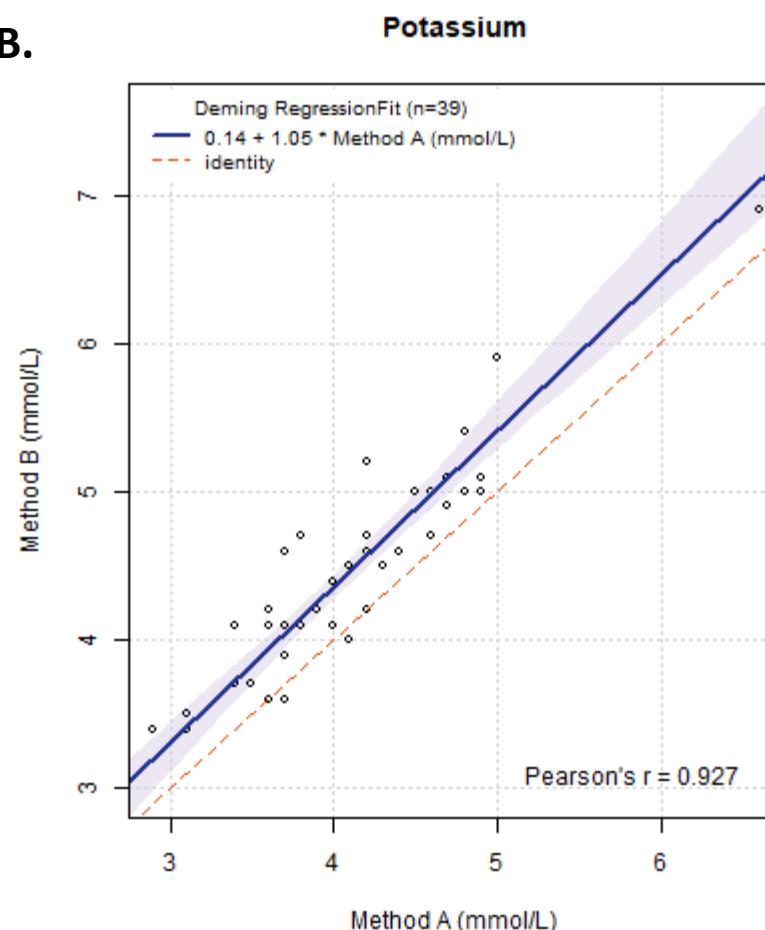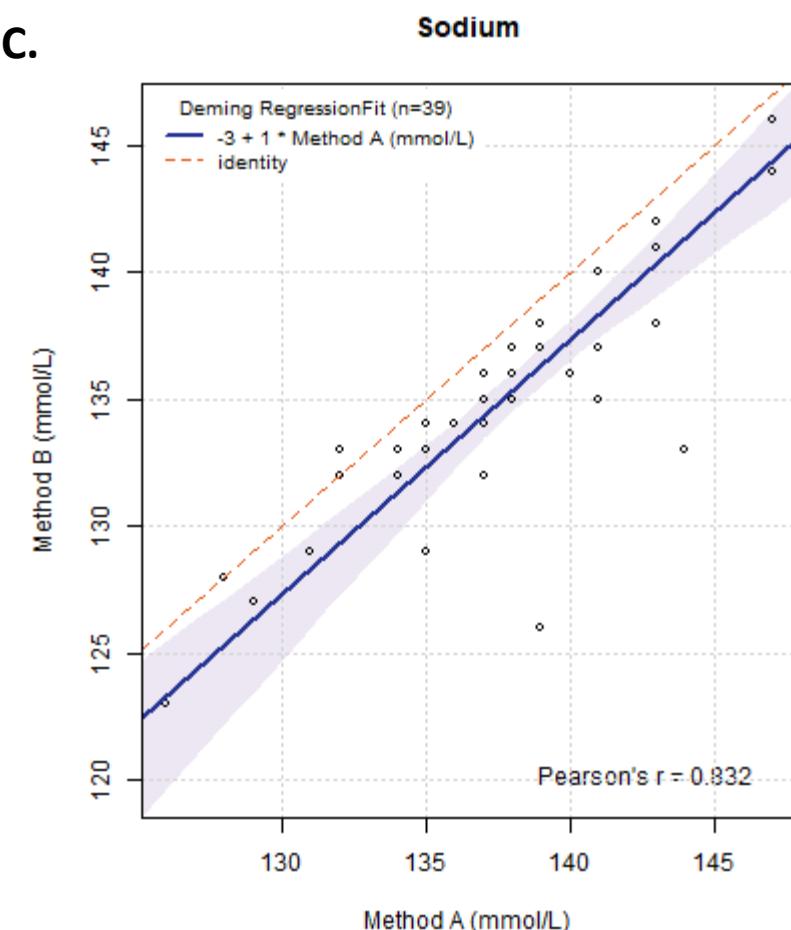
Supplemental Figure 10: Method comparison analysis for electrolytes measured by Abbott ARCHITECT (x-axis) and Alinity (y-axis) systems. The dashed red line indicates the line of perfect agreement (y=x) and the solid blue line indicates the Deming regression line. **A)** Chloride, **B)** Potassium, **C)** Sodium