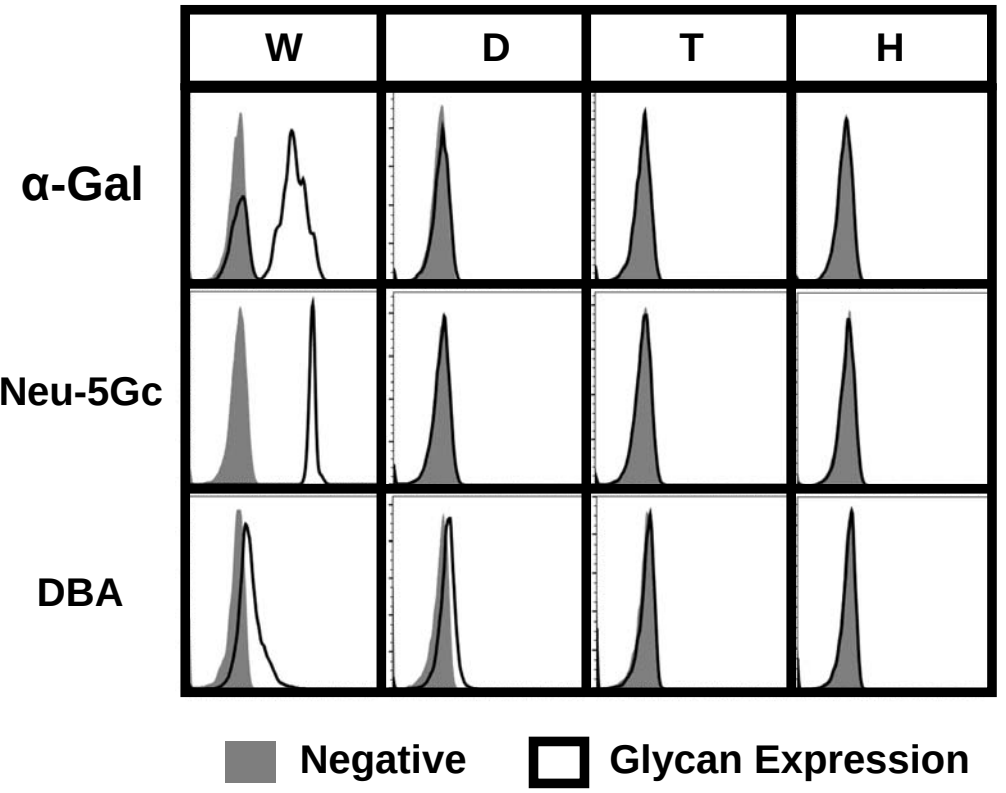
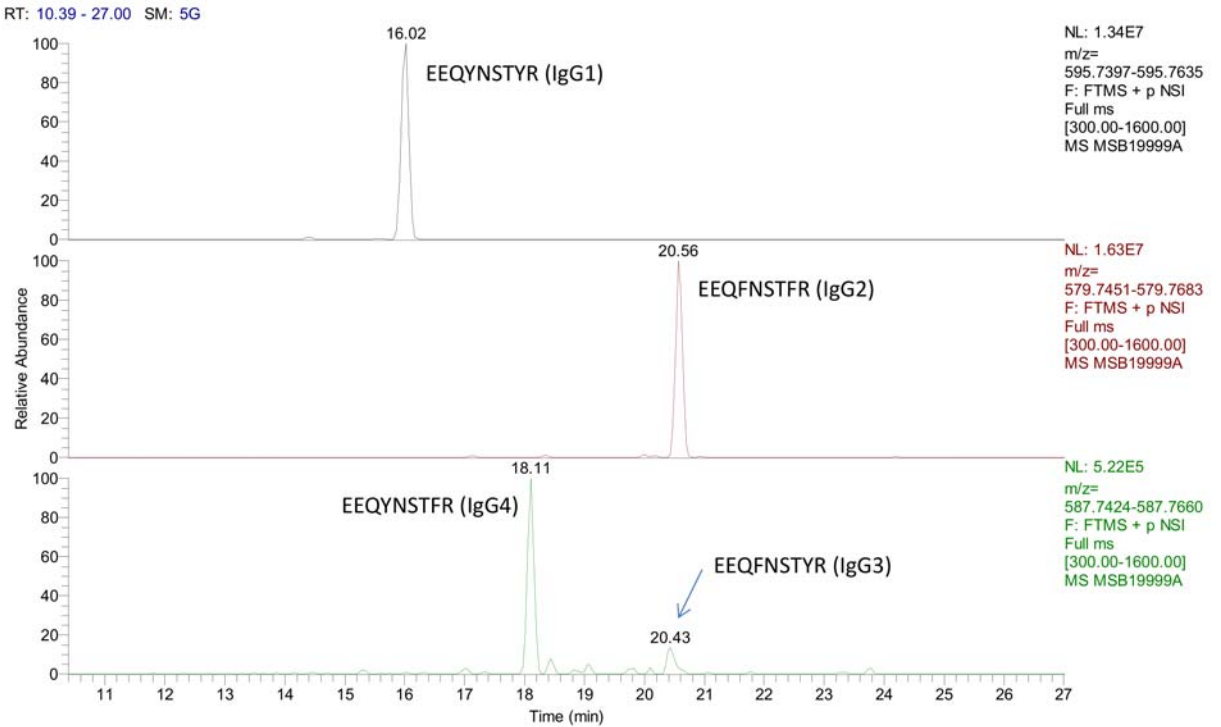
Supplementary Figure 1: RBC Phenotypes



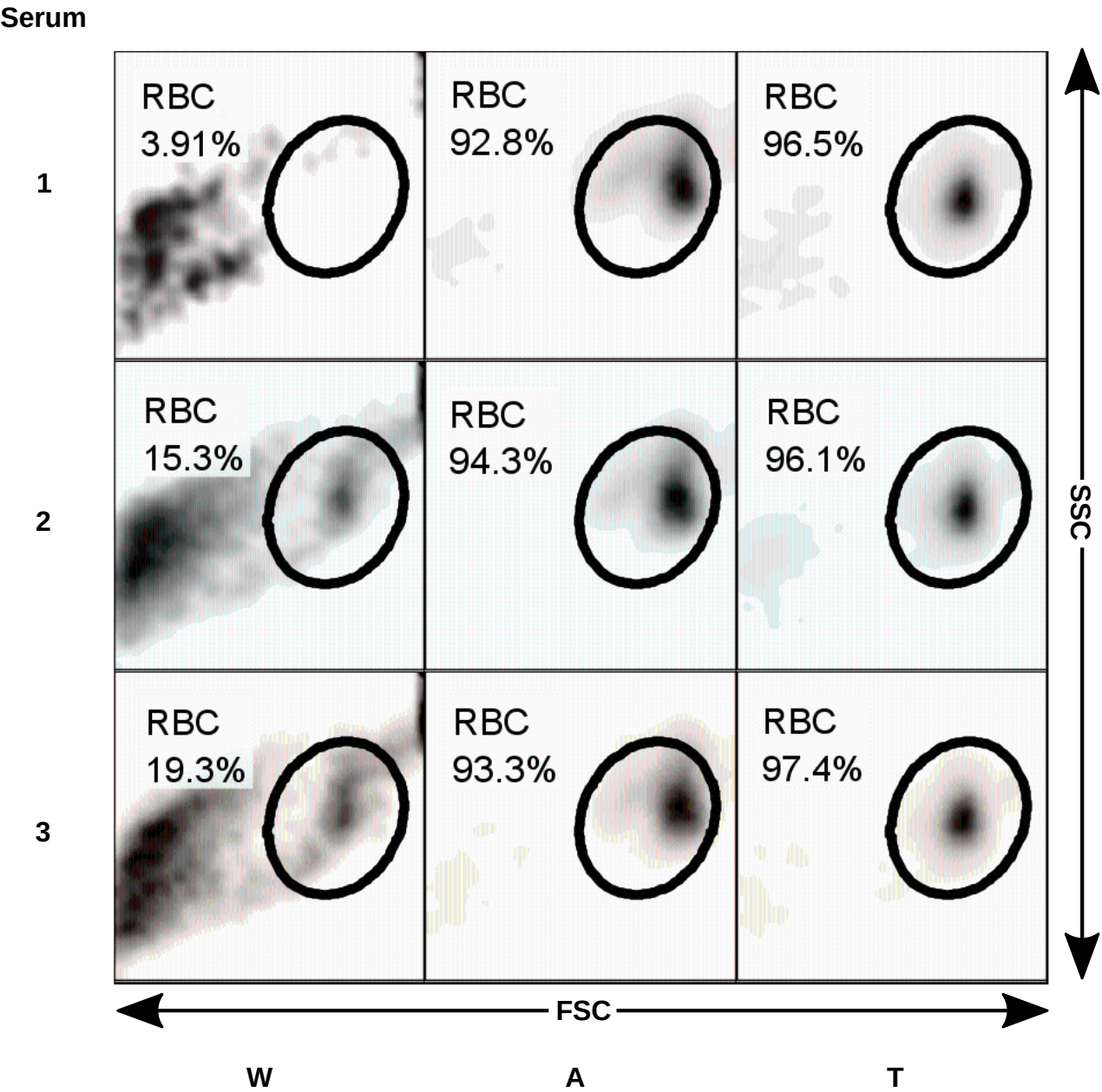
	AUC per Isotype				Total (AUC)		%IgG1	%IgG2	%IgG3	%IgG4
	IgG1	IgG2	IgG3	IgG4	IgG	IgM				
Number of values	3	3	3	3	3	3	3	3	3	3
Minimum	253000000	1370000000	669000	40100000	1660000000	42500000	15	72	0	2.41
25% Percentile	253000000	1370000000	669000	40100000	1660000000	42500000	15	72	0	2.41
Median	377000000	1510000000	975000	65000000	1950000000	42700000	19	77	0	3
75% Percentile	843000000	2620000000	1290000	176000000	3640000000	63400000	23	82	0.06	5
Maximum	843000000	2620000000	1290000	176000000	3640000000	63400000	23	82	0.06	5
Mean	491000000	1833000000	978000	93700000	2417000000	49530000	19	77	0.02	3.47
Std. Deviation	311100000	684900000	310511	72350000	1069000000	12010000	4	5	0.03464	1.357
Std. Error of Mean	179600000	395400000	179274	41770000	617400000	6934000	2.309	2.887	0.02	0.7837

Supplementary Figure 2: Serum from a single donor and RBC from a single triple knockout pig were incubated together. After washing antibodies were eluted and relative bound amounts determined by mass spectroscopy. Three identical experiments were performed.

Supplementary Figure 3: Representative Mass Spectroscopy Chromatogram of Immunoglobulin-Derived Peptides



Supplementary Figure 4: Gating and Fate of RBC Incubated with Different Sera



Three human sera were incubated with RBC from wild type pigs (W), autologous human RBC (A), and RBC from pigs lacking the GGTA1/CMAH/B4GalNT2 genes (T). After incubating with fluorescent secondary antibodies to report bound human immunoglobulin, cells were analyzed by flow cytometry. Forward scatter (FSC, x-axis) and side scatter (SSC, y-axis) were used to identify RBC. Black ovals represent gates used to select RBC for analysis. The percentages shown next to each gate represents the fraction of total events that resided within the gate. Human sera disrupted wild type swine RBC as seen by an increase in debris and the reduction in RBC falling in the gated regions.