CORRECTION

Correction: Correlative Gene Expression to Protective Seroconversion In Rift Valley Vaccinates

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Figs 6 and 7 are duplicates of Fig 5. Please view the correct Figs 6 and 7 below.

(A) Summary of Significantly Perturbed GO and Their Genes for Time shifted Data

	Time Pre-Serum Neutralization							
GO Terms (|Bayes Zscore| ≥ 2.24)	Day -7	Day -6	Day -5	Day -4	Day -3	Day -2	Day -1	Day 0
Bayes Zscore Significantly Activated	15	18	5	43	16	51	12	3
Bayes Zscore Significantly Repressed	15	30	17	82	42	30	38	15
Total Significantly Perturbed	30	48	22	125	58	81	50	18
Genes(|Bayes Zscore| ≥ 2.24)								
Bayes Zscore Significant Up Regulated	50	97	80	42	70	105	74	39
Bayes Zscore Significant Down Regulated	34	75	212	228	154	76	181	95
Total Significantly Perturbed	84	172	292	270	224	181	255	134

(B) Early Phase (Days -7, -6, -5, -4 pSN) Time Shifted Data GO Term Response
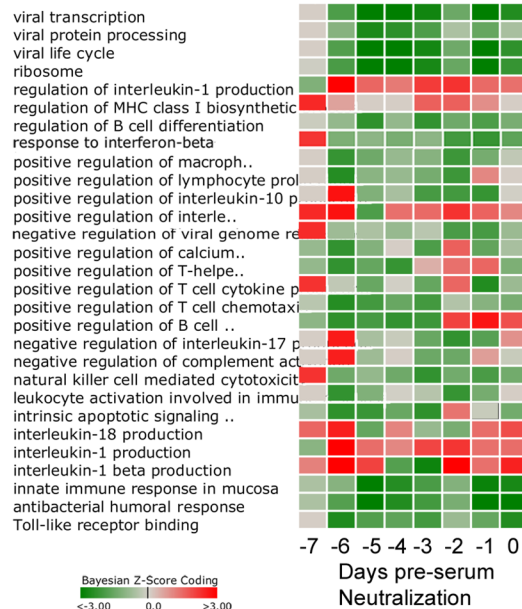
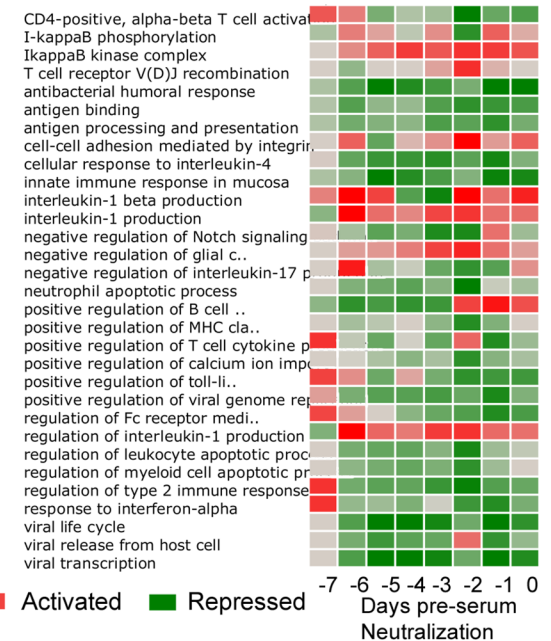### (C) Late Phase (Days -3, -2, -1, 0 pSN) Time Shifted Data GO Term Response

Fig 6. DBGGA GO term analysis on time-shifted data. (**A**) Summary table of GO Terms and component gene perturbation by time pre-seroconversion. Only GO terms and their genes with Bayesian score ≥|2.24| are included in analysis. (**B-C**) Heat maps of perturbed GO terms described by time pre-seroconversion and identified from the Early Phase (time −6, −5, −4, −3 pSN) (**B**) and the Later Phase (time −2, −1, 0, 1 pSN) (**C**). Red color indicates activation, green color indicates repression. Intensity of color represents amplitude of perturbation. The list of GO terms shown represent a subset of all perturbed terms that were selected as being most relevant to innate and adaptive immune response.
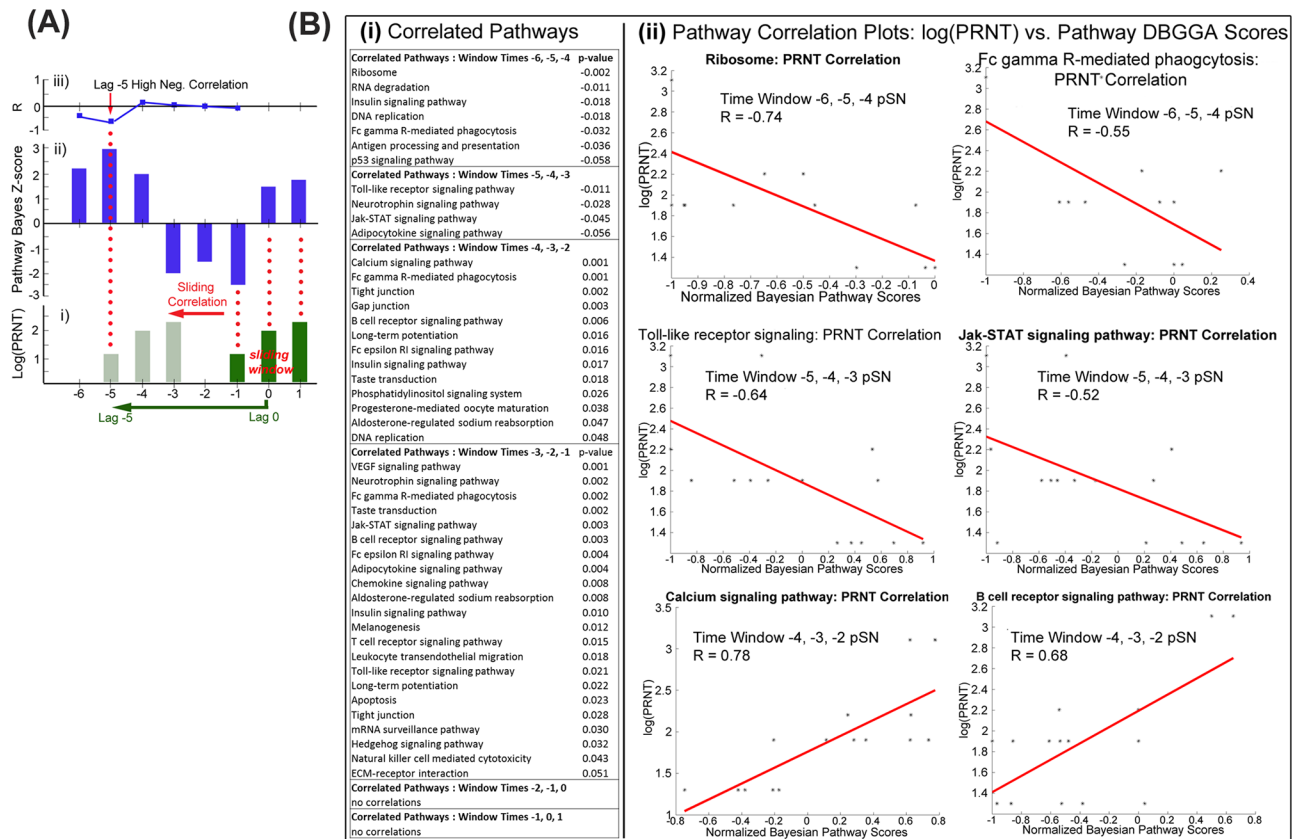
Fig 7. Sliding window correlation (SWC) to identify pathways associated with serum neutralization titers. (**A**) Visualization of sliding window correlation approach. (**i**) Hypothetical Log10(PRNT$_{80}$) data taken from time points capturing neutralizing antibody levels during time period in which animals reached threshold for protection (log10 = 1.903) (dark green bars). (**i-ii**)The trajectory of the Log10(PRNT$_{80}$) data is applied to other time points prior to serum neutralization (light green bars) to identify pathway with complementary or antithetical trajectories (**A-ii** for hypothetical Pathway Bayesian Z-score data, dark blue bars). (**iii**) Graphical representation of the R correlation coefficient value between Log10(PRNT$_{80}$) and Pathway Bayesian Z-score. (**B**) Pathways correlated to PRNT$_{80}$values at the time of seroconversion listed by pathway at incremented window times (each consisting of three time points), with significant correlation p-values (**i**), or plotted as log(PRNT$_{80}$) vs normalized Bayesian Z-score (**ii**) for six selected pathways having highest correlations.

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Reference

1. Laughlin RC, Drake KL, Morrill JC, Adams LG (2016) Correlative Gene Expression to Protective Sero-conversion in Rift Valley Fever Vaccinates. PLoS ONE 11(1): e0147027. doi: 10.1371/journal.pone.0147027 PMID: 26783758