

Waugh, C. A. and Timms, P. 2019. A proposed roadmap for the control of infections in wildlife using *Chlamydia* vaccine development in koalas *Phascolarctos cinereus* as a template.
– Wildlife Biology 2019: wlb.00627

Appendix 1

Table A1. Estimate and standard error of the explanation variables in the minimum adequate model (M8) of the binary logistic regression. and Likelihood ratio test (LRT) of the minimum adequate model (M1) of the binary logistic regression. LP: Lymphocyte proliferation percent. Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

| Variable | Estimate | SE | df | LRT | p-value |
|------------|----------|--------|----|---------|----------------------------|
| Intercept | -1.2400 | 0.4835 | | | |
| LP | 1.3195 | 0.4312 | 1 | 100.173 | $<2.2 \times 10^{-16}$ *** |
| Wild (yes) | -3.9456 | 1.8040 | 1 | 11.895 | 0.0005629 *** |

Estimate and standard error of the explanation variables in the minimum adequate model (M8) of the binary logistic regression. and Likelihood ratio test (LRT) of the minimum adequate model (M1) of the binary logistic regression. Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1. IgG: Immunoglobulin G titer.

| Variable | Estimate | SE | df | LRT | p-value |
|-----------|--------------------------|-------------------------|----|--------|-----------------------------|
| Intercept | $-1.210 \times 10^{+00}$ | 2.400×10^{-01} | | | |
| IgG | 8.238×10^{-06} | 2.054×10^{-06} | 1 | 62.961 | 2.108×10^{-15} *** |

Estimated regression parameters, standard errors, t-values and p-values for the linear model represented in Eq. 1. LP (lymphocyte proliferation). Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

| Variable | Estimate | SE | df | LRT | p-value |
|------------|-----------|----------|----|--------|--------------------------|
| Intercept | -1.975884 | 0.589402 | | | |
| IVN | 0.056148 | 0.008584 | 1 | 80.231 | $<2 \times 10^{-16}$ *** |
| Wild (yes) | -1.368166 | 0.621882 | 1 | 5.569 | 0.01829 * |

Estimated regression parameters, standard errors, t-values and p-values for the linear model represented in Eq. 1. IgG (IgG titers in plasma). Signif. codes: 0 ‘****’ 0.001 ‘***’ 0.01 ‘**’ 0.05 ‘.’ 0.1 ‘ ’ 1

| Variable | Estimate | SE | <i>t</i> -value | p-value |
|-----------|----------|-------|-----------------|------------|
| Intercept | 2.817 | 3.667 | 0.768 | 0.44660 |
| Route | -6.294 | 3.977 | -1.582 | 0.00183 ** |
| Adjuvant | 13.214 | 3.977 | 3.322 | 0.12087 |

Estimated regression parameters, standard errors, t-values and p-values for the linear model represented in equ (1). IgG (IgG titers in plasma). Signif. codes: 0 ‘****’ 0.001 ‘***’ 0.01 ‘**’ 0.05 ‘.’ 0.1 ‘ ’ 1

| Variable | Estimate | SE | <i>t</i> -value | p-value |
|-----------|----------|-------|-----------------|----------------------------|
| Intercept | 72.989 | 8.381 | 8.709 | 2.35×10^{-12} *** |
| Antigen | 2.544 | 1.355 | 1.878 | 0.0651 |
| Route | 14.231 | 8.127 | 1.751 | 0.0849 |

Estimated regression parameters, standard errors, t-values and p-values for the linear model represented in equ (1). IVN (In vitro neutralization). Signif. codes: 0 ‘****’ 0.001 ‘***’ 0.01 ‘**’ 0.05 ‘.’ 0.1 ‘ ’ 1

| Variable | Estimate | SE | <i>t</i> -value | p-value |
|-----------|----------|-------|-----------------|----------------------------|
| Intercept | 89.985 | 9.717 | 9.261 | 1.99×10^{-13} *** |
| Antigen | -6.447 | 2.124 | -3.035 | 0.003476 ** |
| Adjuvant | 24.380 | 6.027 | 4.045 | 0.000143 *** |
| Route | -37.262 | 9.340 | -3.990 | 0.000173 *** |

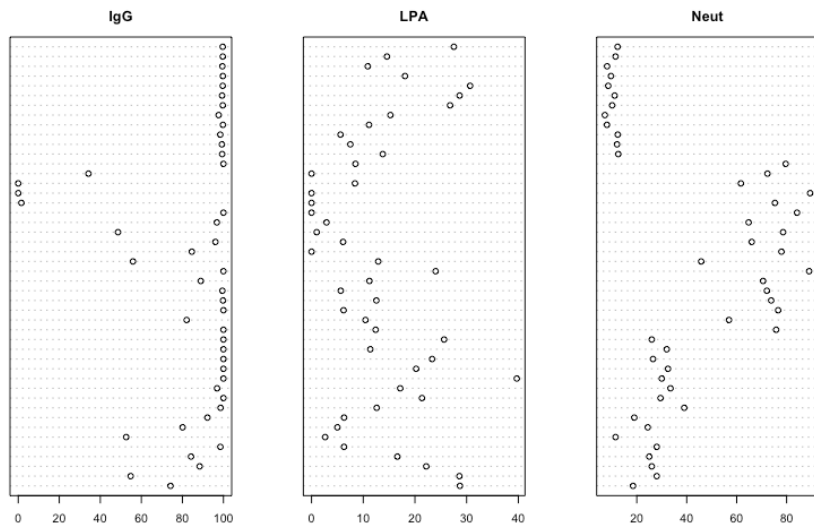


Figure A1. We used Cleveland dotplots (Fig. A1) to check for outliers (see figure below). We did not find any outliers for the explanatory variables. .

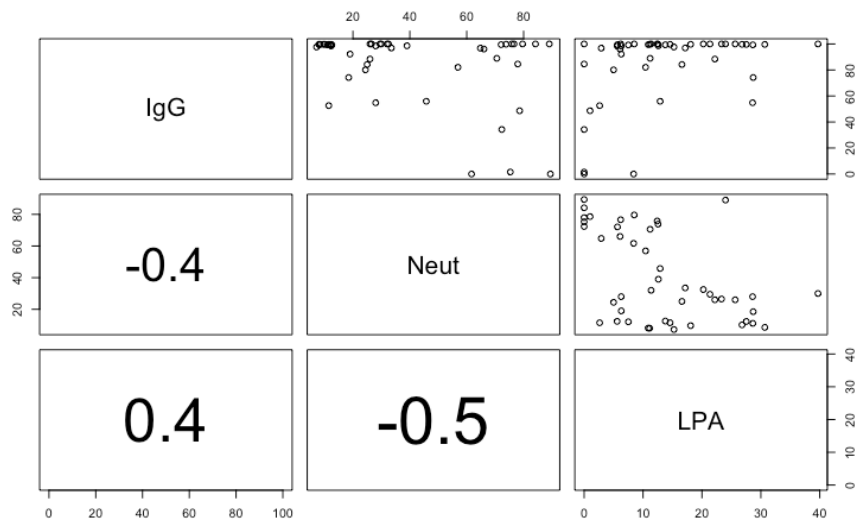


Figure A2. For the collinearity tests we used scatterplot correlations we did not find any collinearity between our explanatory variables.