

S2 Table. Model summary outputs for within-host parameter estimation.***A. Summary of linear regression model to predict μ_R** **Formula:** *lm(mortality_rate~order, data = pan.dat)*; **Number observations:** 1060; **R²**=0.42

Term	Estimate	Lci-Uci	Statistic	P-value
Intercept (Diprotodontia)	0.11	0.08 - 0.14	T: 7.38	<0.001***
Rodentia	0.12	0.09 - 0.15	T: 7.1	<0.001***
Carnivora	-0.04	0-0.07	T: -2.58	0.01**
Cetartiodactyla	-0.05	0-0.07	T: -3.07	<0.001***
Primates	-0.06	0-0.07	T: -3.56	<0.001***
Afrosoricida	0.2	0.13 - 0.28	T: 5.07	<0.001***
Chiroptera	-0.02	0-0.07	T: -0.8	0.42
Dasyuromorphia	0.19	0.14 - 0.24	T: 8.02	<0.001***
Eulipotyphla	0.29	0.25 - 0.34	T: 12.82	<0.001***
Pilosa	0.01	0-0.19	T: 0.11	0.91
Didelphimorphia	0.24	0.17 - 0.3	T: 7.09	<0.001***
Cingulata	-0.05	0-0.18	T: -1.09	0.28
Perissodactyla	-0.08	0-0.14	T: -2.28	0.02*
Dermoptera	-0.05	0-0.34	T: -0.6	0.55
Hyracoidea	-0.03	0-0.24	T: -0.45	0.65
Microbiotheria	0.2	0-0.47	T: 1.7	0.09
Sirenia	-0.08	0-0.28	T: -1.16	0.25
Peramelemorphia	0.1	0.01 - 0.2	T: 2.2	0.03
Macroscelidea	0.18	0.08 - 0.28	T: 3.53	<0.001***
Proboscidea	-0.09	0-0.27	T: -1.35	0.18
Lagomorpha	0.04	0-0.14	T: 1.12	0.26
Pholidota	0.01	0-0.24	T: 0.12	0.9
Notoryctemorphia	0.56	0.32 - 0.79	T: 4.65	<0.001***
Monotremata	-0.08	0-0.27	T: -1.08	0.28
Tubulidentata	-0.07	0-0.47	T: -0.59	0.55
Scandentia	0.03	0-0.21	T: 0.63	0.53

B. Summary of linear mixed effect regression model to estimate T_{WR}

Formula: $\text{Imer}(\log10_max_lifespan_yrs \sim \log10mass_g + (1 | order), data = pan.dat)$ **Number observations:** 1060; **Groups:** 26

Term	Estimate	Lci-Uci	Statistic	P-value
(Intercept)	0.392	0.295-0.488	T: 7.96	<0.001***
log10mass (grams)	.199	0.185-0.214	T: 26.55	<0.001***
order (random effect)	Variance: 0.041	Std Dev: 0.202		

C. Summary of linear mixed effect regression model to estimate g_0

Formula: $\text{Imer}(\log10_neutrophil_count \sim \log10mass_g + BMR_W + (1 | order), data = pan.dat)$ **Number observations:** 144; **Groups:** 19

Term	Estimate	Lci-Uci	Statistic	P-value
(Intercept)	-0.245	-0.422 - -0.068	T: 2.72	0.008**
log10mass (grams)	0.212	0.168-0.255	T: 9.53	<0.001***
BMR (W)	-0.000368	-0.000103- -0.000633	T: -2.72	0.01*
order (random effect)	Variance: 0.041	Std Dev: 0.203		

D. Summary of generalized additive model to summarize α_s by order from literature

Formula: $\alpha \sim s(vFamily, bs = "re") + s(hOrder, bs = "re") + s(VirusPubs, k = 7, bs = "tp") + s(spill_type, bs = "re") + s(IsVectorBorne, bs = "re")$; **Deviance explained:** 88.2%; **R²:** 0.873; **N** = 75

Term	Estimate	Lci-Uci	Statistic	P-value	Effective degrees of freedom
Intercept	-4.55	[-6.15 – -2.95]	z: -5.57	<.001***	
smoothing:					
virus family			χ^2 : 612	.00387**	9.50
order			χ^2 : 1161	<.001***	4.74
virus spp. pub count			χ^2 : 5.77	.0163*	1.00
spillover type			χ^2 : 67.9	.00856**	0.867
vector-borne status			χ^2 : 98.9	.0249*	0.806

*Outputs from fitted linear and linear mixed effect regression models used to generate within-host parameter values. Projections for model A and order-level effects in B and C are visualized in main text Fig 3C. Order-level predictions for each parameter are visualized in S4 Fig and presented in S1 Table. Significance at $p < 0.001^{***}$, 0.01^{**} , 0.05^* .