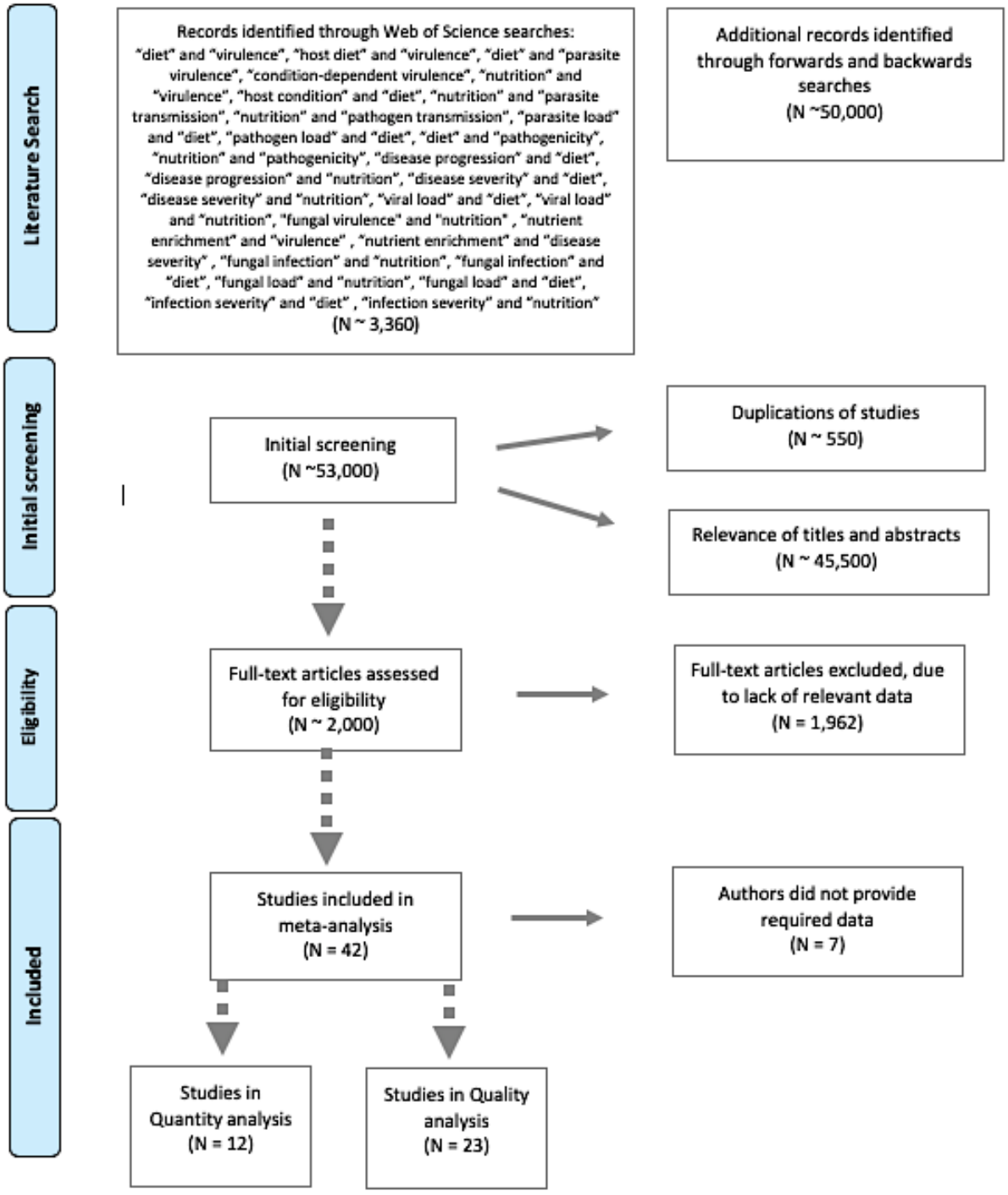
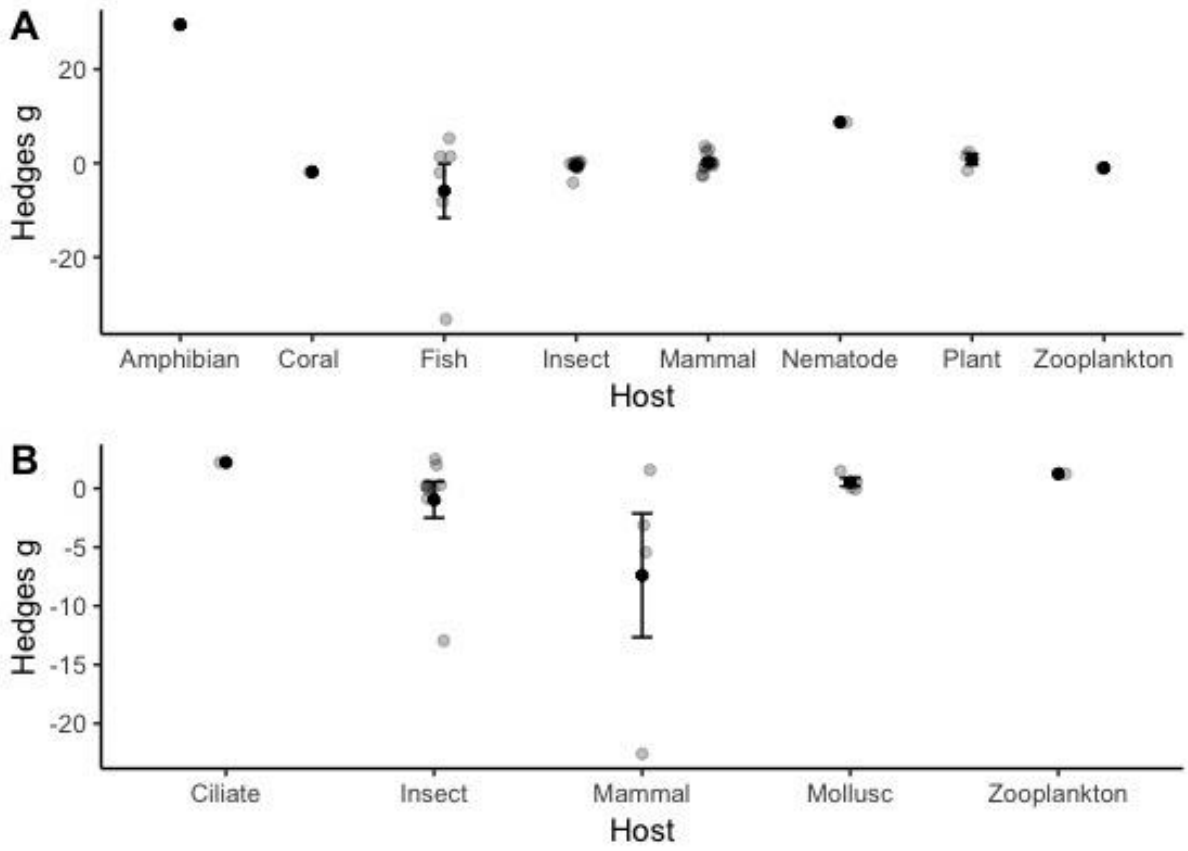
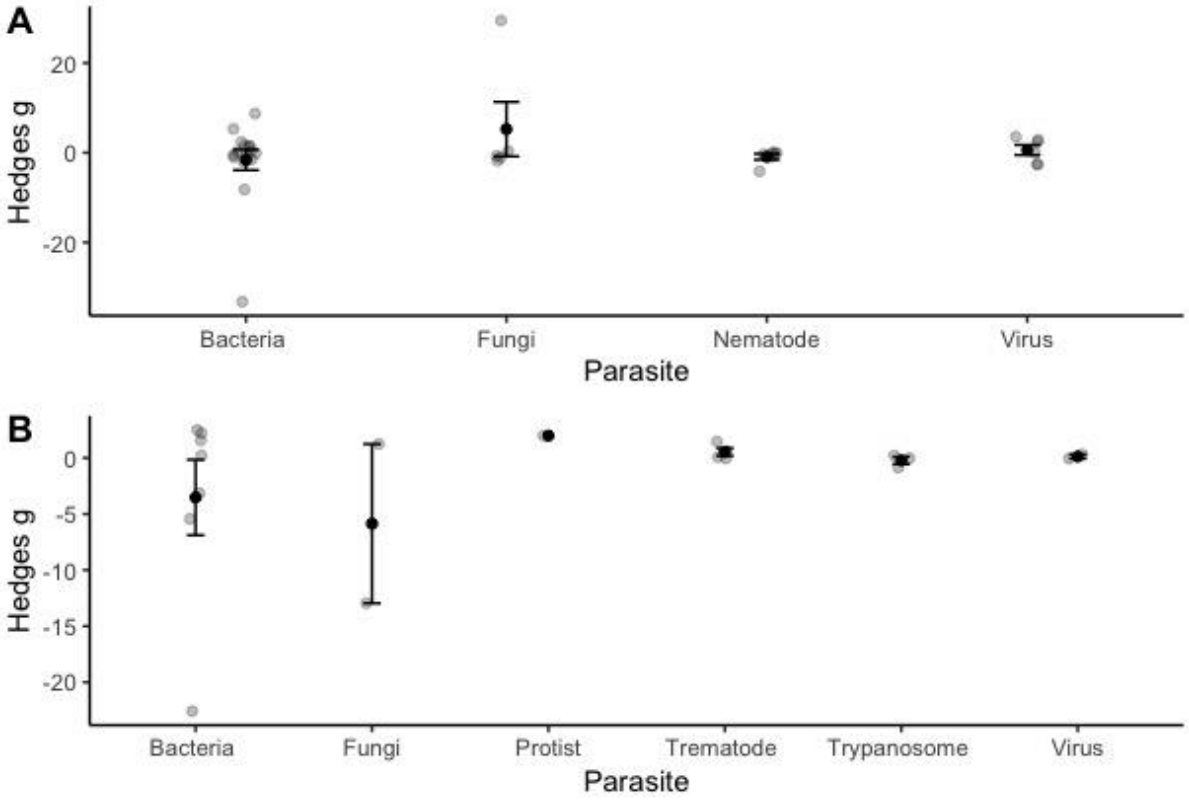


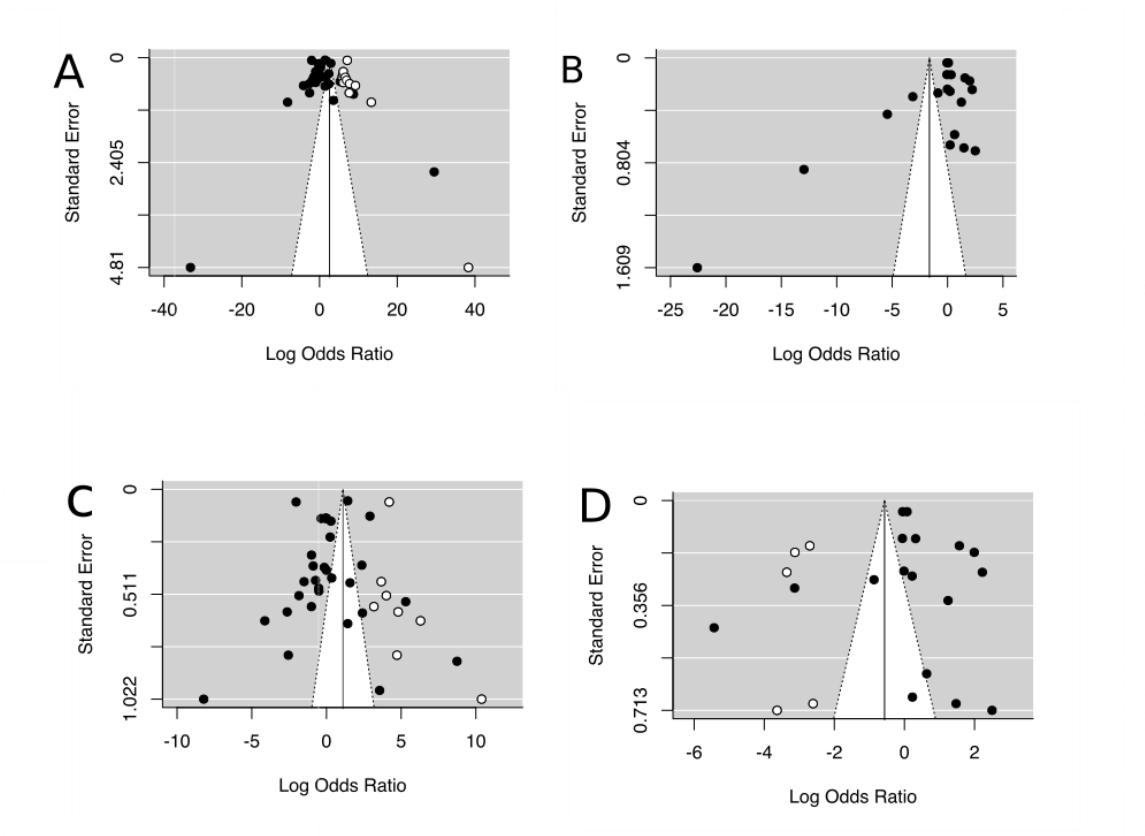
Supplementary Figure 1: PRISMA flow chart detailing data collection.



Supplementary Figure 2: Virulence effect size (Hedge's g) for different host types for treatments affecting nutrient quality (A) and quantity (B). Black points represent mean values +/- 1 S.E. Raw data are shown as jittered points.



Supplementary Figure 3: Virulence effect size for different pathogen types for treatments affecting nutrient quality (A) and quantity (B). Black points represent mean values +/- 1 S.E.. Raw data are shown as jittered points.



Supplementary Figure 4: Trim and fill plots for the nutrient quality (A, C) and quantity (B, D) meta-analyses, with outliers included (A and B) and removed (C and D).

1

Supplementary Table 1: A table showing the studies used in the nutrient quality meta-analysis.' * ' denote outliers.

Host (vertebrate (V)/invertebrate (In)/plant (P))	Pathogen	Treatment type	Specific change to nutrition	Change in virulence (+ increase, - decrease, = no change)	Hedge's g	Refs
Caenorhabditis elegans (In)	Staphylococcus aureus (E)	High v Control	Glucose	+	8.739	(64)
Mus sp (V)	Coxsackievirus B3	High v Low	Vitamin E	+	-2.553	(32)
Mus sp (V)	Staphylococcus aureus (E)	High v Control	Manganese	+	3.559	(47)
		Control v Low	Manganese	+	-1.002	
Plutella xylostella (In)	Metarhizium anisopliae (E)	High v Control	Carbon and Nitrogen	-	-0.732	(65)
		Control v Low	Carbon and Nitrogen	-	0.352	
Mus sp (V)	Coxsackievirus B3	Control v Low	Selenium	-	-2.630	(14)
Mus sp (V)	Citrobacter rodentium (E)	Control v Low	Selenium	-	-0.518	(55)
Tenebrio molitor (In)	Heterorhabditis indica (E)	High v Control	Lipid	+	-0.352	(66)
			Protein	-	0	
Tenebrio molitor (In)	Steinernema riobrave (E)	High v Control	Lipid	=	-0.075	(66)

			Protein	=	-4.128	
Manduca sexta (In)	Heterorhabditis sonorensis (E)	Control v Low	Lower quality feed	=	-0.886	(67)
Manduca sexta (In)	Steinernema carpocapsae (E)	Control v Low	Lower quality feed	+	1.424	(67)
Ictalurus punctatus (V)	Flavobacterium columnare (E)	High v Low	Lower $CuSO_4$ supplementation	-	-2.033	(68)
			Higher $CuSO_4$ supplementation	=	0.247	
Apis mellifera (In)	Melissococcus plutonius (E)	High v Low	Potassium	=	0.247	(69)
Daphnia dentifera (In)	Metschnikowia bicuspidate (E)	High v Low	Environmental nutrients	=	-1.007	(50)
Morone saxatilis (V)	Mycobacterium marinum (Int)	High v Low	Lower quality feed	+	5.306	(70)
Macaca mulatta (V)	Simian Immunodeficiency Virus (SIV) (Int)	High v Low	Micronutrient supplements	+	-0.002	(46)
Homo sapien (V)	Mycobacterium tuberculosis (Int)	High v Control	Vitamin A and Zinc	=	0.298	(71)

Homo sapien (V)	Human immunodeficiency virus HIV-1 (Int)	High v Control	Vitamin E and C	-	2.368	(54)
Mus sp (V)	Clostridium difficile (E)	Control v Low	Protein	=	-0.505	(53)
Cucumis melo (P)	Acidovorax citrulli (E)	High v Low	Potassium	-	2.409	(72)
Lycopersicon esculentum (P)	Ralstonia solanacearum (E)	Control v Low	Calcium	-	1.579	(33)
		High v control	Calcium	-	-1.500	
Homo sapien (V)	Human immunodeficiency virus HIV-1 (Int)	High v Low	Micronutrient supplements	-	2.910	(48)
Dicentrarchus labrax (V)	Vibrio pelagius	High v Control	Shrimp protein hydrolysate	-	1.424	(73)
Oncorhynchus mykiss (V)	Flavobacterium columnare	High v Low	Growth medium (Shieh broth)	+	-33.212 *	(74)
Danio rerio (V)	Flavobacterium columnare	High v Low	Growth medium (Shieh broth)	+	-8.219	(74)
Gorgonia ventalina (In)	Aspergillus sydowii	High v Control	Fertilizer	+	-1.839	(75)
Pseudacris regilla (V)	Batrachochytrium dendrobatidis	High v Control	Nitrogen and Phosphorus	-	29.498 *	(76)

Supplementary table 2:	A table showing all of the studies used in the nutrient quantity meta-analysis. ' * ' denote outliers				
Host (Vertebrate (V)/ Invertebrate (In))	Pathogen	Treatment type	Change in virulence (+ increase, - decrease, = no change)	Hedge's g	Study
Mus sp (V)	*Staphylococcus aureus* (E)	Control v Low	+	1.568	(77)
Paramecium caudatum (ciliate)	*Holospora undulata* (Int)	High v Low	+	2.224	(78)
Aedes aegypti (In)	*Vavraia culicis*	High v Low	+	-12.959*	(8)
Potamopyrgus antipodarum (In)	*Microphallus sp* (E)	High v Control	=	-0.051	(79)
Potamopyrgus antipodarum (In)	*Notocotylus gippyensis* (E)	High v Control	+	0.075	(79)
Bombus impatiens (In)	*Crithidia sp* (E)	High v Low	-	-0.013	(51)
Trichoplusia ni (In)	Autographa californica multiple nucleopolyhedrovirus AcMNPV (Int)	Control v Low	+	0.319	(15)
		High v Control	+	-0.058	
Bombus terrestris (In)	*Crithidia bombi*	High v Control	-	0.219	(80)
		Control v Low	-	-0.868	
Mus sp (V)	*Listeria monocytogenes* (Int)	High v Control	-	-3.133	(81)
Cavia porcellus (V)	*Listeria monocytogenes* (Int)	High v Control	-	-22.580*	(81)
		Control v Low	-	-5.431	
Anopheles stephensi (In)	*Plasmodium yoelii yoelii* (Int)	Control v Low	+	1.992	(82)
	Microphallus sp (E)	Control v Low	+	1.474	(83)

Potamopyrgus antipodarum (In)					
		High v Control	+	0.634	
Daphnia magna (In)	*Glugoides intestinalis* (Int)	Control v Low	-	1.245	(20)
Drosophila melanogaster (In)	*Lactococcus lactis* (E)	Control v Low	=	0.229	(52)
	Pseudomonas entomophila (E)	Control v Low	-	2.500	

Supplementary Table 3: Outlier analysis for overall effect size

Meta-analysis	Outliers	Overall Effect size (Hedge's g)	Standard error	K	T-value	P-value
Quality	Included	1.086	1.349	33	0.805	0.427
	Removed	0.187	0.575	31	0.325	0.748
Quantity	Included	-1.353	1.470	19	-0.929	0.307
	Removed	0.406	0.546	17	0.743	0.468

Supplementary Table 4: Outlier analysis for moderator variables

Meta-analysis	Moderator	Outliers	F – Value	P – Value
Quality	Treatment type	Included	0.429	0.616
		Removed	0.632	0.544
	Vertebrate vs Invertebrate	Included	0.044	0.957
		Removed	0.053	0.948
	Host Type (Broad Grouping)	Included	0.317	0.813
		Removed	0.276	0.842
	Pathogen Type (Broad Grouping)	Included	0.782	0.514
		Removed	0.456	0.716
Quantity	Treatment type	Included	2.060	0.164
		Removed	0.249	0.783
	Vertebrate vs Invertebrate	Included	2.646	0.102
		Removed	0.199	0.174
	Host Type (Broad Grouping)	Included	0.233	0.796
		Removed	0.918	0.426
	Pathogen Type (Broad Grouping)	Included	0.233	0.796
		Removed	0.042	0.959

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