

Supplementary information

Table S1: Overview of the number of pooled recipient guts per microbial sample

Genotype	Microbiome	Parasite	KNOxM	CxP	MxP	CxMxP	Replicate	Id	Guts
KNO	M1	P1	KNO_M1	C_P1	M1_P1	C_M1_P1	1	C_M1_P1_1	4
KNO	M1	P1	KNO_M1	C_P1	M1_P1	C_M1_P1	2	C_M1_P1_2	6
KNO	M1	P1	KNO_M1	C_P1	M1_P1	C_M1_P1	3	C_M1_P1_3	1
KNO	M1	P2	KNO_M1	C_P2	M1_P2	C_M1_P2	1	C_M1_P2_1	4
KNO	M1	P2	KNO_M1	C_P2	M1_P2	C_M1_P2	2	C_M1_P2_2	3
KNO	M1	P2	KNO_M1	C_P2	M1_P2	C_M1_P2	3	C_M1_P2_3	0
KNO	M1	MC	KNO_M1	C_PC	M1_PC	C_M1_PC	1	C_M1_PC_1	6
KNO	M1	MC	KNO_M1	C_PC	M1_PC	C_M1_PC	2	C_M1_PC_2	4
KNO	M1	MC	KNO_M1	C_PC	M1_PC	C_M1_PC	3	C_M1_PC_3	5
KNO	M2	P1	KNO_M2	C_P1	M2_P1	C_M2_P1	1	C_M2_P1_1	3
KNO	M2	P1	KNO_M2	C_P1	M2_P1	C_M2_P1	2	C_M2_P1_2	4
KNO	M2	P1	KNO_M2	C_P1	M2_P1	C_M2_P1	3	C_M2_P1_3	0
KNO	M2	P2	KNO_M2	C_P2	M2_P2	C_M2_P2	1	C_M2_P2_1	2
KNO	M2	P2	KNO_M2	C_P2	M2_P2	C_M2_P2	2	C_M2_P2_2	6
KNO	M2	P2	KNO_M2	C_P2	M2_P2	C_M2_P2	3	C_M2_P2_3	3
KNO	M2	MC	KNO_M2	C_PC	M2_PC	C_M2_PC	1	C_M2_PC_1	6
KNO	M2	MC	KNO_M2	C_PC	M2_PC	C_M2_PC	2	C_M2_PC_2	6
KNO	M2	MC	KNO_M2	C_PC	M2_PC	C_M2_PC	3	C_M2_PC_3	6
KNO	MC	P1	KNO_MC	C_P1	MC_P1	C_MC_P1	1	C_MC_P1_1	3
KNO	MC	P1	KNO_MC	C_P1	MC_P1	C_MC_P1	2	C_MC_P1_2	6
KNO	MC	P1	KNO_MC	C_P1	MC_P1	C_MC_P1	3	C_MC_P1_3	3
KNO	MC	P2	KNO_MC	C_P2	MC_P2	C_MC_P2	1	C_MC_P2_1	4
KNO	MC	P2	KNO_MC	C_P2	MC_P2	C_MC_P2	2	C_MC_P2_2	5
KNO	MC	P2	KNO_MC	C_P2	MC_P2	C_MC_P2	3	C_MC_P2_3	3
KNO	MC	MC	KNO_MC	C_PC	MC_PC	C_MC_PC	1	C_MC_PC_1	5
KNO	MC	MC	KNO_MC	C_PC	MC_PC	C_MC_PC	2	C_MC_PC_2	5
KNO	MC	MC	KNO_MC	C_PC	MC_PC	C_MC_PC	3	C_MC_PC_3	5
OM2	M1	P1	OM2_M1	OM2_P1	M1_P1	OM2_M1_P1	1	OM2_M1_P1_1	4
OM2	M1	P1	OM2_M1	OM2_P1	M1_P1	OM2_M1_P1	2	OM2_M1_P1_2	4

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OM2	M1	P1	OM2_M1	OM2_P1	M1_P1	OM2_M1_P1	3	OM2_M1_P1_3	6
OM2	M1	P2	OM2_M1	OM2_P2	M1_P2	OM2_M1_P2	1	OM2_M1_P2_1	5
OM2	M1	P2	OM2_M1	OM2_P2	M1_P2	OM2_M1_P2	2	OM2_M1_P2_2	5
OM2	M1	P2	OM2_M1	OM2_P2	M1_P2	OM2_M1_P2	3	OM2_M1_P2_3	5
OM2	M1	MC	OM2_M1	OM2_PC	M1_PC	OM2_M1_PC	1	OM2_M1_PC_1	5
OM2	M1	MC	OM2_M1	OM2_PC	M1_PC	OM2_M1_PC	2	OM2_M1_PC_2	4
OM2	M1	MC	OM2_M1	OM2_PC	M1_PC	OM2_M1_PC	3	OM2_M1_PC_3	5
OM2	M2	P1	OM2_M2	OM2_P1	M2_P1	OM2_M2_P1	1	OM2_M2_P1_1	4
OM2	M2	P1	OM2_M2	OM2_P1	M2_P1	OM2_M2_P1	2	OM2_M2_P1_2	5
OM2	M2	P1	OM2_M2	OM2_P1	M2_P1	OM2_M2_P1	3	OM2_M2_P1_3	5
OM2	M2	P2	OM2_M2	OM2_P2	M2_P2	OM2_M2_P2	1	OM2_M2_P2_1	5
OM2	M2	P2	OM2_M2	OM2_P2	M2_P2	OM2_M2_P2	2	OM2_M2_P2_2	6
OM2	M2	P2	OM2_M2	OM2_P2	M2_P2	OM2_M2_P2	3	OM2_M2_P2_3	5
OM2	M2	MC	OM2_M2	OM2_PC	M2_PC	OM2_M2_PC	1	OM2_M2_PC_1	5
OM2	M2	MC	OM2_M2	OM2_PC	M2_PC	OM2_M2_PC	2	OM2_M2_PC_2	5
OM2	M2	MC	OM2_M2	OM2_PC	M2_PC	OM2_M2_PC	3	OM2_M2_PC_3	6
OM2	MC	P1	OM2_MC	OM2_P1	MC_P1	OM2_MC_P1	1	OM2_MC_P1_1	4
OM2	MC	P1	OM2_MC	OM2_P1	MC_P1	OM2_MC_P1	2	OM2_MC_P1_2	6
OM2	MC	P1	OM2_MC	OM2_P1	MC_P1	OM2_MC_P1	3	OM2_MC_P1_3	5
OM2	MC	P2	OM2_MC	OM2_P2	MC_P2	OM2_MC_P2	1	OM2_MC_P2_1	6
OM2	MC	P2	OM2_MC	OM2_P2	MC_P2	OM2_MC_P2	2	OM2_MC_P2_2	5
OM2	MC	P2	OM2_MC	OM2_P2	MC_P2	OM2_MC_P2	3	OM2_MC_P2_3	5
OM2	MC	MC	OM2_MC	OM2_PC	MC_PC	OM2_MC_PC	1	OM2_MC_PC_1	5
OM2	MC	MC	OM2_MC	OM2_PC	MC_PC	OM2_MC_PC	2	OM2_MC_PC_2	4
OM2	MC	MC	OM2_MC	OM2_PC	MC_PC	OM2_MC_PC	3	OM2_MC_PC_3	5
T8	M1	P1	T8_M1	T8_P1	M1_P1	T8_M1_P1	1	T8_M1_P1_1	4
T8	M1	P1	T8_M1	T8_P1	M1_P1	T8_M1_P1	2	T8_M1_P1_2	4
T8	M1	P1	T8_M1	T8_P1	M1_P1	T8_M1_P1	3	T8_M1_P1_3	3
T8	M1	P2	T8_M1	T8_P2	M1_P2	T8_M1_P2	1	T8_M1_P2_1	5
T8	M1	P2	T8_M1	T8_P2	M1_P2	T8_M1_P2	2	T8_M1_P2_2	4
T8	M1	P2	T8_M1	T8_P2	M1_P2	T8_M1_P2	3	T8_M1_P2_3	3
T8	M1	MC	T8_M1	T8_PC	M1_PC	T8_M1_PC	1	T8_M1_PC_1	6
T8	M1	MC	T8_M1	T8_PC	M1_PC	T8_M1_PC	2	T8_M1_PC_2	5

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T8	M1	MC	T8_M1	T8_PC	M1_PC	T8_M1_PC	3	T8_M1_PC_3	3
T8	M2	P1	T8_M2	T8_P1	M2_P1	T8_M2_P1	1	T8_M2_P1_1	3
T8	M2	P1	T8_M2	T8_P1	M2_P1	T8_M2_P1	2	T8_M2_P1_2	5
T8	M2	P1	T8_M2	T8_P1	M2_P1	T8_M2_P1	3	T8_M2_P1_3	5
T8	M2	P2	T8_M2	T8_P2	M2_P2	T8_M2_P2	1	T8_M2_P2_1	3
T8	M2	P2	T8_M2	T8_P2	M2_P2	T8_M2_P2	2	T8_M2_P2_2	1
T8	M2	P2	T8_M2	T8_P2	M2_P2	T8_M2_P2	3	T8_M2_P2_3	6
T8	M2	MC	T8_M2	T8_PC	M2_PC	T8_M2_PC	1	T8_M2_PC_1	4
T8	M2	MC	T8_M2	T8_PC	M2_PC	T8_M2_PC	2	T8_M2_PC_2	3
T8	M2	MC	T8_M2	T8_PC	M2_PC	T8_M2_PC	3	T8_M2_PC_3	5
T8	MC	P1	T8_MC	T8_P1	MC_P1	T8_MC_P1	1	T8_MC_P1_1	5
T8	MC	P1	T8_MC	T8_P1	MC_P1	T8_MC_P1	2	T8_MC_P1_2	2
T8	MC	P1	T8_MC	T8_P1	MC_P1	T8_MC_P1	3	T8_MC_P1_3	4
T8	MC	P2	T8_MC	T8_P2	MC_P2	T8_MC_P2	1	T8_MC_P2_1	3
T8	MC	P2	T8_MC	T8_P2	MC_P2	T8_MC_P2	2	T8_MC_P2_2	4
T8	MC	P2	T8_MC	T8_P2	MC_P2	T8_MC_P2	3	T8_MC_P2_3	4
T8	MC	MC	T8_MC	T8_PC	MC_PC	T8_MC_PC	1	T8_MC_PC_1	4
T8	MC	MC	T8_MC	T8_PC	MC_PC	T8_MC_PC	2	T8_MC_PC_2	4
T8	MC	MC	T8_MC	T8_PC	MC_PC	T8_MC_PC	3	T8_MC_PC_3	5

Table S2: Overview results for Pearson correlation between the number of guts per sample and OTU richness or Shannon entropy'. Raw and adjusted (adjusted for multiple comparisons through the control of the false discovery rate (FDR)) p-values are given.

		OTU richness				Shannon entropy'			
	DF	cor	t	p-value	Adjusted p-value	cor	t	p-value	Adjusted p-value
Genotype	1	0.917	2.294	0.262	0.366	0.992	7.841	0.081	0.330
Microbiome	1	-0.510	-0.593	0.659	0.769	-0.432	-0.478	0.716	0.716

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Parasite	1	0.957	3.295	0.188	0.328	0.889	1.942	0.303	0.424
CxM	7	0.549	1.737	0.126	0.328	0.494	1.504	0.176	0.411
CxP	7	0.502	1.537	0.168	0.328	0.590	1.935	0.094	0.330
MxP	7	0.055	0.146	0.888	0.888	-0.144	-0.384	0.712	0.716
CxMxP	25	0.268	1.391	0.177	0.328	0.211	1.080	0.290	0.424

Table S3: Overview forward and reverse primers used for the internal PCR.

Na me	p5-adapter	index(8 nt)	padF(10nt)	linkF(2nt)	gene-specificprimer	Full_primer_sequence
Forward						
F1	AATGATACGGCGACCACC GAGATCTACAC	ATCGT ACG	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACATCGTACGTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA
F2	AATGATACGGCGACCACC GAGATCTACAC	TAGCG AGT	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACTAGCGAGTTATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F3	AATGATACGGCGACCACC GAGATCTACAC	CGTGA GTG	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACCGTGAGTGTATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F4	AATGATACGGCGACCACC GAGATCTACAC	GATCG TGT	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACGATCGTGTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA
F5	AATGATACGGCGACCACC GAGATCTACAC	ACGAC GTG	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACACGACGTGTATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F6	AATGATACGGCGACCACC GAGATCTACAC	ATATA CACc	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACATATACACTATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F7	AATGATACGGCGACCACC GAGATCTACAC	GCTCT AGTt	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACGCTCTAGTTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA
F8	AATGATACGGCGACCACC GAGATCTACAC	GACact ga	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACGACACTGATATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F9	AATGATACGGCGACCACC GAGATCTACAC	AAGCA GCA	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACAAGCAGCATATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F10	AATGATACGGCGACCACC GAGATCTACAC	CGATC TAC	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACCGATCTACTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA

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F11	AATGATACGGCGACCACC GAGATCTACAC	TGCGT CAC	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACTGCGTCACTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA
F12	AATGATACGGCGACCACC GAGATCTACAC	AGAGT CAC	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACAGAGTCACTATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F13	AATGATACGGCGACCACC GAGATCTACAC	ACGCG TGA	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACACGCGTGATATGGT AATTGTGTGCCAGCMGCCGCGGTAA
F14	AATGATACGGCGACCACC GAGATCTACAC	GTCTA GTG	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACGTCTAGTGTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA
F15	AATGATACGGCGACCACC GAGATCTACAC	TCTAC ACT	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACTCTACACTTATGGTA ATTGTGTGCCAGCMGCCGCGGTAA
F16	AATGATACGGCGACCACC GAGATCTACAC	GGAGA CTA	TATGGT AATT	GT	GTGCCAGCMGCC GCGGTAA	AATGATACGGCGACCACCGAGATCTACACGGAGACTATATGGT AATTGTGTGCCAGCMGCCGCGGTAA
Reverse						
R1	CAAGCAGAAGACGGCATA CGAGAT	ACTAT GTC	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATACTATGTCAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R2	CAAGCAGAAGACGGCATA CGAGAT	AGTAG CGT	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATAGTAGCGTAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R3	CAAGCAGAAGACGGCATA CGAGAT	CGTAC TCA	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATCGTACTCAAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R4	CAAGCAGAAGACGGCATA CGAGAT	TAGCA GAC	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATTAGCAGACAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R5	CAAGCAGAAGACGGCATA CGAGAT	TCATA GAC	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATTCATAGACAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R6	CAAGCAGAAGACGGCATA CGAGAT	AGCTG CTA	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATAGCTGCTAAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R7	CAAGCAGAAGACGGCATA CGAGAT	CTCGT TAC	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATCTCGTTACAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R8	CAAGCAGAAGACGGCATA CGAGAT	GCGCA CGT	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATGCGCACGTAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R9	CAAGCAGAAGACGGCATA CGAGAT	CTAGC TCG	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATCTAGCTCGAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R10	CAAGCAGAAGACGGCATA CGAGAT	GTATG ACG	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATGTATGACGAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT
R11	CAAGCAGAAGACGGCATA CGAGAT	TACAC AGT	AGTCAG TCAG	CC	GGACTACNVGGG TWTCTAAT	CAAGCAGAAGACGGCATAACGAGATTACACAGTAGTCAGTCAGC CGGACTACNVGGGTWTCTAAT

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	CAAGCAGAAGACGGCATA	TCAGC	AGTCAG		GGACTACNVGGG	CAAGCAGAAGACGGCATA	CGAGATTCAGCGTTAGTCAGTCAGC
R12	CGAGAT	GTT	TCAG	CC	TWTCTAAT	CGGACTACNVGGGTWTCTAAT	

RESULTS

Table S4: Results of post-hoc analyses on body size, survival, OTU richness, Shannon entropy' and microbial community composition for the significant results of the statistical analysis (see Table 1). Raw and adjusted (adjusted for multiple comparisons through the control of the false discovery rate (FDR)) p-values are given for the results on *Daphnia* gut microbial communities.

			DF	Body size		Survival		OUT richness			Shannon entropy'			Microbial community composition		
				p-value	z-value	p-value	z-value	p-value	Adjusted p-value	z-value	p-value	Adjusted p-value	z-value	p-value	Adjusted p-value	R ²
Genotype	KNO vs OM2	1			0.001	3.31	<u><0.001</u>	0.003	3.588	0.002		3.347	0.003			
	KNO vs T8	1			0.634	-0.48	0.275	0.275	1.530	0.111		1.992	0.006	0.009	0.069	
	OM2 vs T8	1					0.052		-	0.195		-1.718	0.092	0.009	0.073	
					<u><0.001</u>	-4.54		0.078	2.325		0.195			0.092	0.092	0.035
Microbiome	M1 vs M2	1		-												
		1			0.031	2.529										
	M1 vs MC				0.633	0.912										
	M2 vs MC	1			0.227	1.654										
Parasite	P1 vs P2	1			0.567	-0.57										
	P1 vs PC	1			0.007	3.26										
	P2 vs PC	1			0.001	2.61										
Genotype x Microbiome	Within KNO	M1 vs M2	1					1.000	1.000	0.459	0.999	1.000	0.708			
			1					1.000		-	1.000					
		M1 vs MC							1.000	0.018		1.000	0.375			
			1					1.000		-	1.000					
		M2 vs MC							1.000	0.461		1.000	-0.337			
			1					0.997		-	0.999					
	M1 vs M2								1.000	0.802		1.000	-0.673			

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Genotype x Parasite	Within T8	M1 vs MC	1				0.024	-3.40	0.018		
			1				0.142	3	0.164	-3.395	
		M2 vs MC	1				0.142	-	0.070		
								0.639	0.315	-2.957	
		M1 vs M2	1				0.998	1.000	0.998	1.000	0.720
		M1 vs MC	1				0.764	1.000	0.773	1.000	1.632
		M2 vs MC	1				0.987	1.000	0.985	1.000	0.995
		KNO vs OM2	1				0.008		0.013		
								0.142	0.164	-3.395	
		KNO vs T8	1				1.000		0.993		
								1.000	1.000	0.895	
		OM2 vs T8	1				0.018	-	0.065		
								0.142	0.315	-2.985	
	Within M1	KNO vs OM2	1				0.297		0.293		
								1.000	1.000	2.354	
		KNO vs T8	1				1.000		0.997		
								1.000	1.000	0.788	
	Within M2	OM2 vs T8	1				0.375	-	0.513		
								1.000	1.000	-2.014	
		KNO vs OM2	1				1.000		1.000		
								1.000	1.000	0.106	
	Within MC	KNO vs T8	1				0.634		0.543		
								1.000	1.000	1.974	
		OM2 vs T8	1				0.860		0.471		
								1.000	1.000	2.077	
	Within KNO	P1 vs P2	1		0.894	0.13					
		P1 vs PC	1		<0.001	3.52					
		P2 vs PC	1		<0.001	3.69					
	Within OM2	P1 vs P2	1		0.134	-1.50					
		P1 vs PC	1		0.699	0.39					
		P2 vs PC	1		0.206	-1.26					

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		Within T8	P1 vs P2	1		0.907	0.12				
			P1 vs PC	1		0.232	1.20				
			P2 vs PC	1		0.217	1.24				
			KNO vs	1							
			OM2			0.013	2.48				
			KNO vs	1							
		Within P1	T8			0.504	0.67				
			OM2 vs	1							
			T8			0.023	-2.28				
			KNO vs	1							
			OM2			<.0001	4.08				
			KNO vs	1		0.484	0.70				
	Within P2		T8								
			OM2 vs	1							
			T8			<0.001	-3.96				
			KNO vs	1							
			OM2			0.255	-1.14				
			KNO vs	1							
		Within PC	T8			0.019	-2.35				
			OM2 vs	1							
			T8			0.116	-1.57				
			P1 vs P2	1				1.000	1.000	0.008	
			P1 vs PC	1				0.898	1.000	1.390	
		Within M1	P2 vs PC	1				0.970	1.000	1.120	
			P1 vs P2	1				1.000	1.000	-0.587	
			P1 vs PC	1				0.664	1.000	-1.815	
		Within M2	P2 vs PC	1				0.931	1.000	-1.293	

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Within MC	P1 vs P2	1				1.000	1.000	0.192	
	P1 vs PC	1				0.979	1.000	1.057	
	P2 vs PC	1				0.992	1.000	0.913	
	M1 vs M2	1				0.789	1.000	1.618	
	M1 vs MC	1				1.000	1.000	-0.368	
	M2 vs MC	1				0.635	1.000	-1.856	
	M1 vs M2	1				0.995	1.000	0.855	
	M1 vs MC	1				1.000	1.000	-0.163	
	M2 vs MC	1				0.951	1.000	-1.214	
	M1 vs M2	1			-	0.794	1.000	-1.609	
	M1 vs MC	1				0.999	1.000	-0.639	
	M2 vs MC	1				0.984	1.000	1.009	

Table S5: Overview of relative abundances of the 40 most common OTUs in *Daphnia* guts from the microbiome transplant experiment. Abundances were calculated on rarefied data. Sd: standard deviation.

Class	Order	Family	Genus	OTU	Mean	Sd
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>NA</i>	OTU_1_Burkholderiaceae	29.94%	28.01%
Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	<i>Methylobacterium</i>	OTU_2_Methylobacterium_sp.	6.59%	15.64%
Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>	OTU_4_Streptococcus_sp.	6.09%	13.60%
Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	OTU_3_Acinetobacter_sp.	5.43%	14.72%
Alphaproteobacteria	Rickettsiales	Rickettsiales_Incertae_Sedis	<i>Candidatus_Hepatincola</i>	OTU_6_Candidatus_Hepatincola_sp.	3.48%	6.23%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Hydrogenophaga</i>	OTU_9_Hydrogenophaga_sp.	2.63%	5.56%
Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Shinella</i>	OTU_5_Shinella_sp.	2.60%	9.35%
Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	OTU_7_Acinetobacter_sp.	2.25%	5.68%

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Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	OTU_10_ <i>Flavobacterium</i> _sp.	1.97%	6.65%
Actinobacteria	Micrococcales	Microbacteriaceae	<i>Candidatus_Limnoluna</i>	OTU_13_ <i>Candidatus_Limnoluna</i> _sp.	1.89%	3.04%
Bacteroidia	NA	NA	NA	OTU_12_Bacteroidia	1.76%	3.55%
Gammaproteobacteria	Betaproteobacteriales	T34	NA	OTU_11_Betaproteobacteriales	1.65%	5.84%
Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	<i>Escherichia/Shigella</i>	OTU_15_ <i>Escherichia/Shigella</i> _sp.	1.53%	2.67%
Actinobacteria	Micrococcales	Microbacteriaceae	<i>Candidatus_Planktoluna</i>	OTU_19_ <i>Candidatus_Planktoluna</i> _sp.	1.28%	2.20%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA	OTU_8_Burkholderiaceae	1.26%	1.67%
Bacteroidia	Cytophagales	Cyclobacteriaceae	<i>Algoriphagus</i>	OTU_14_ <i>Algoriphagus</i> _sp.	1.14%	2.60%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Polynucleobacter</i>	OTU_22_ <i>Polynucleobacter</i> _sp.	1.13%	1.91%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Rhodoferrax</i>	OTU_16_ <i>Rhodoferrax</i> _sp.	1.06%	2.66%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA	OTU_18_Burkholderiaceae	0.86%	1.97%
Bacteroidia	Flavobacteriales	Weeksellaceae	<i>Empedobacter</i>	OTU_24_ <i>Empedobacter</i> _sp.	0.86%	1.35%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Polynucleobacter</i>	OTU_27_ <i>Polynucleobacter</i> _sp.	0.79%	4.82%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA	OTU_30_Burkholderiaceae	0.79%	3.00%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Burkholderia-Caballeronia-Paraburkholderia</i>	OTU_34_ <i>Burkholderia-Caballeronia-Paraburkholderia</i> _sp.	0.74%	1.87%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA	OTU_21_Burkholderiaceae	0.67%	1.42%
Gammaproteobacteria	Betaproteobacteriales	T34	NA	OTU_17_Betaproteobacteriales	0.64%	2.81%
Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	OTU_26_ <i>Flavobacterium</i> _sp.	0.62%	2.50%
Gammaproteobacteria	Betaproteobacteriales	T34	NA	OTU_20_Betaproteobacteriales	0.53%	2.37%
Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	OTU_38_ <i>Acinetobacter</i> _sp.	0.53%	1.22%
Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	OTU_23_ <i>Flavobacterium</i> _sp.	0.46%	3.95%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Polynucleobacter</i>	OTU_39_ <i>Polynucleobacter</i> _sp.	0.46%	0.85%
Mollicutes	Mycoplasmatales	Mycoplasmataceae	<i>Candidatus_Bacilloplasma</i>	OTU_50_ <i>Candidatus_Bacilloplasma</i> _sp.	0.46%	3.47%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA	OTU_45_Burkholderiaceae	0.45%	1.00%
Gammaproteobacteria	Betaproteobacteriales	NA	NA	OTU_54_Betaproteobacteriales	0.41%	2.95%
Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Massilia</i>	OTU_25_ <i>Massilia</i> _sp.	0.40%	3.45%
Actinobacteria	Micrococcales	Microbacteriaceae	<i>Aurantimicrobium</i>	OTU_41_ <i>Aurantimicrobium</i> _sp.	0.38%	0.51%
Bacilli	Bacillales	Staphylococcaceae	<i>Staphylococcus</i>	OTU_40_ <i>Staphylococcus</i> _sp.	0.36%	1.01%
Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	OTU_29_ <i>Acinetobacter</i> _sp.	0.35%	1.09%

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Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	NA	OTU_35_Burkholderiaceae	0.33%	0.72%
Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	OTU_28_ <i>Acinetobacter</i> _sp.	0.33%	1.02%
Bacilli	Bacillales	Family_XI	<i>Gemella</i>	OTU_47_ <i>Gemella</i> _sp.	0.30%	2.03%

Table S6: Results Deseq analysis on class level and OTU level between main effects.

	Genotype			Microbiome			Parasite		
	KNO VS OM2	KNO VS T8	OM2 VS T8	M1 vs M2	M2 vs MC	M1 vs MC	P1 vs P2	P2 vs PC	P1 vs PC
Class level									
Gammaproteobacteria	0.001				<0.001				
Alphaproteobacteria	0.002	0.003	<0.001		<0.001	<0.001			<0.001
Bacilli				0.012	0.010	0.003	0.034		
Bacteroidia	0.002	0.004			<0.001	<0.001			
Actinobacteria				0.025					
OTU level									
OTU_2_Methylobacterium_sp.	<0.001		<0.001	0.003	<0.001	0.001		0.005	<0.001
OTU_3_Acinetobacter_sp.	<0.001	0.014					<0.001	0.003	
OTU_4_Streptococcus_sp.			0.006	0.013		<0.001			
OTU_5_Shinella_sp.					0.036	<0.001			
OTU_6_Candidatus_Hepatincola_sp.		0.018	0.002	0.010		<0.001			
OTU_7_Acinetobacter_sp.	<0.001	<0.001		0.026			<0.001	0.001	
OTU_10_Flavobacterium_sp.	0.048	0.002							
OTU_11_Betaproteobacteriales	<0.001	<0.001				0.007			
OTU_12_Bacteroidia	<0.001	<0.001							
OTU_13_Candidatus_Limnoluna_sp.		<0.001	0.002			0.001			
OTU_14_Algoriphagus_sp.	<0.001	<0.001							
OTU_15_Escherichia/Shigella_sp.				0.031		0.012			
OTU_16_Rhodoferax_sp.	<0.001	<0.001		0.021		0.001		0.027	
OTU_17_Betaproteobacteriales				0.010		<0.001			
OTU_18_Burkholderiaceae			0.005			0.026			
OTU_19_Candidatus_Planktoluna_sp.	0.006	<0.001	0.001						
OTU_20_Betaproteobacteriales				0.012		<0.001			
OTU_22_Polynucleobacter_sp.	<0.001		<0.001						

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OTU_24_Empedobacter_sp.	<0.001	<0.001	0.001					
OTU_26_Flavobacterium_sp.			0.015					
OTU_27_Polynucleobacter_sp.		<0.001	<0.001		0.009			
OTU_28_Acinetobacter_sp.	<0.001	<0.001				<0.001		<0.001
OTU_29_Acinetobacter_sp.						<0.001		0.022
OTU_31_Betaproteobacteriales					<0.001			
OTU_34_Burkholderia-Caballeronia-Paraburkholderia_sp.	<0.001	<0.001						
OTU_35_Burkholderiaceae			0.019					
OTU_37_Pseudorhodobacter_sp.	0.011					<0.001		<0.001
OTU_38_Acinetobacter_sp.	<0.001							
OTU_39_Polynucleobacter_sp.		<0.001	<0.001					
OTU_40_Staphylococcus_sp.				<0.001				
OTU_41_Aurantimicrobium_sp.	<0.001	<0.001		0.008	0.010		0.034	
OTU_42_Rhodoferax_sp.	0.005	<0.001						
OTU_43_Shinella_sp.					0.026	<0.001	0.045	
OTU_45_Burkholderiaceae	<0.001	<0.001	0.018					
OTU_46_Acinetobacter_sp.		0.018						<0.001
OTU_47_Gemella_sp.				0.009	0.038			
OTU_48_Streptococcus_sp.	0.040							
OTU_50_Candidatus_Bacilloplasma_sp.	0.017			0.002				
OTU_52_Acinetobacter_sp.						<0.001		<0.001
OTU_53_Aeromonas_sp.	0.047							
OTU_54_Betaproteobacteriales				0.050	0.024			
OTU_56_Streptococcus_sp.	<0.001					0.034		
OTU_57_Limnohabitans_sp.		0.003						
OTU_59_Burkholderiaceae		<0.001	<0.001					
OTU_60_GKS98_freshwater_group_sp.			0.003					
OTU_61_Cutibacterium_sp.			0.029					
OTU_62_Pedobacter_sp.						<0.001	0.034	
OTU_63_Pseudomonas_sp.		0.007						
OTU_65_Prevotella_sp.	0.005		0.046			0.022	0.045	
OTU_66_Bradyrhizobium_sp.	<0.001							
OTU_67_Aurantimicrobium_sp.		0.033		0.010		<0.001		<0.001
OTU_69_Prevotella_7_sp.	<0.001		0.006			0.002	0.007	

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OTU_70_Sphingomonas_sp.	<0.001									
OTU_72_Limnohabitans_sp.	0.004		0.018							
OTU_74_Rothia_sp.	0.005							0.009		
OTU_75_Haemophilus_sp.	<0.001							0.020		<0.001
OTU_76_Gemmobacter_sp.	0.038							0.004	0.027	
OTU_77_Burkholderiaceae			0.042							
OTU_78_Cutibacterium_sp.						0.023				
OTU_79_Neisseria_sp.	0.038					0.003				
OTU_83_Gemmobacter_sp.	<0.001							<0.001		<0.001
OTU_87_Flavobacterium_sp.	0.015					0.019				
OTU_88_Legionella_sp.						0.029				
OTU_90_Veillonella_sp.	<0.001		0.007					0.004	0.044	
OTU_91_Streptococcus_sp.						0.036				
OTU_92_Paenibacillus_sp.		0.014								
OTU_100_Shinella_sp.	<0.001					<0.001				
OTU_102_Shinella_sp.						<0.001		0.032		

Table S7. Significant results of the statistical analysis on the effect of genotype, microbiome treatment, parasite community treatment and their interactions on body size, survival and alpha-diversity variables (OTU richness, Shannon entropy'). Obtained P-values were adjusted for multiple comparisons through the control of the false discovery rate (FDR). Significant data ($p < 0.05$) is indicated in bold. Highly significant data ($p < 0.001$) are underlined. Raw and adjusted (adjusted for multiple comparisons through the control of the false discovery rate (FDR)) p-values are given for the results on *Daphnia* gut microbial communities.

	DF	Body size	Survival	OTU richness		Shannon entropy'		Microbial community composition		
		p-value	p-value	p-value	Adjusted p-value	p-value	Adjusted p-value	R ²	p-value	Adjusted p-value
Genotype	2	0.857	<u><0.001</u>	<u><0.001</u>	<u><0.001</u>	<u><0.001</u>	<u><0.001</u>	0.075	0.002	0.014

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Microbiome treatment	2	0.034		0.279	0.348	0.843	0.859	0.030	0.296	0.414
Parasite treatment	2	0.334	0.002	0.298	0.348	0.216	0.379	0.029	0.266	0.414
Genotype x Microbiome treatment	4	0.240		0.0043	0.015	0.001	0.004	0.066	0.146	0.414
Genotype x Parasite treatment	4	0.086	0.003	0.4831	0.483	0.690	0.859	0.048	0.539	0.539
Microbiome treatment x Parasite treatment	4	0.079		0.2080	0.348	0.020	0.047	0.053	0.430	0.502
Genotype x Microbiome treatment x Parasite treatment	8	0.478		0.2461	0.348	0.859	0.859	0.122	0.197	0.414

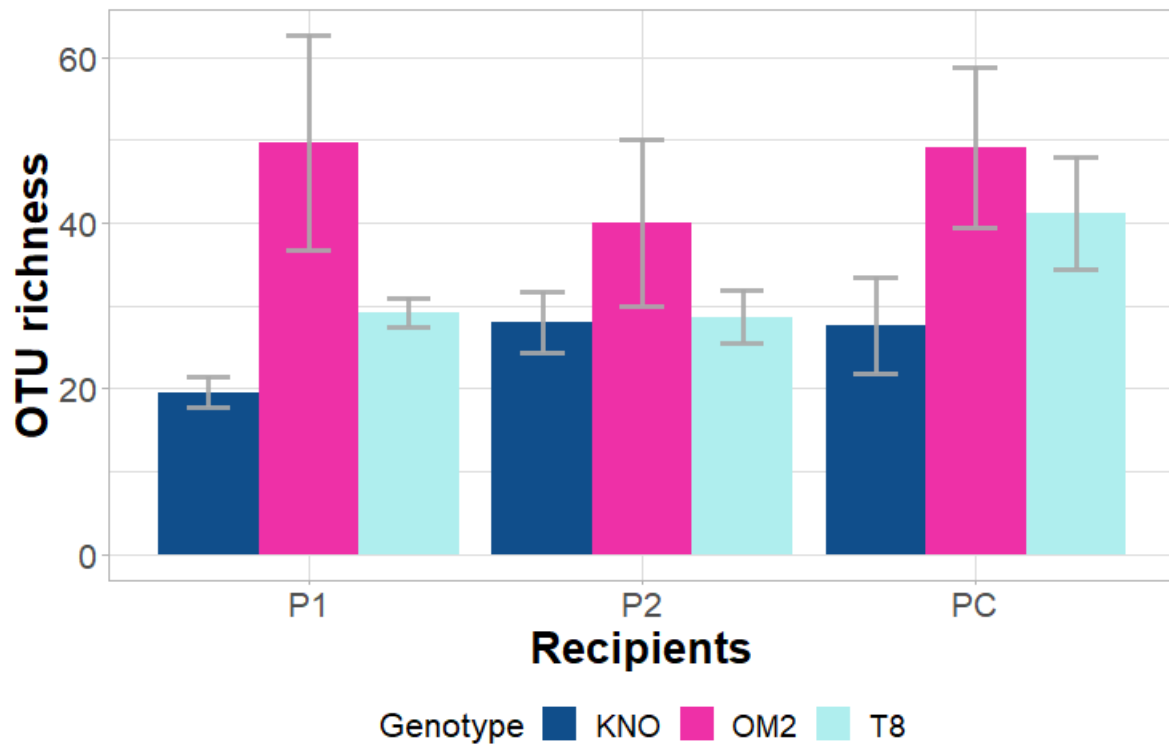


Figure S1. Effect of the genotype x parasite interaction on OTU richness. Colours indicate the different genotypes. Error bars indicate standard error.

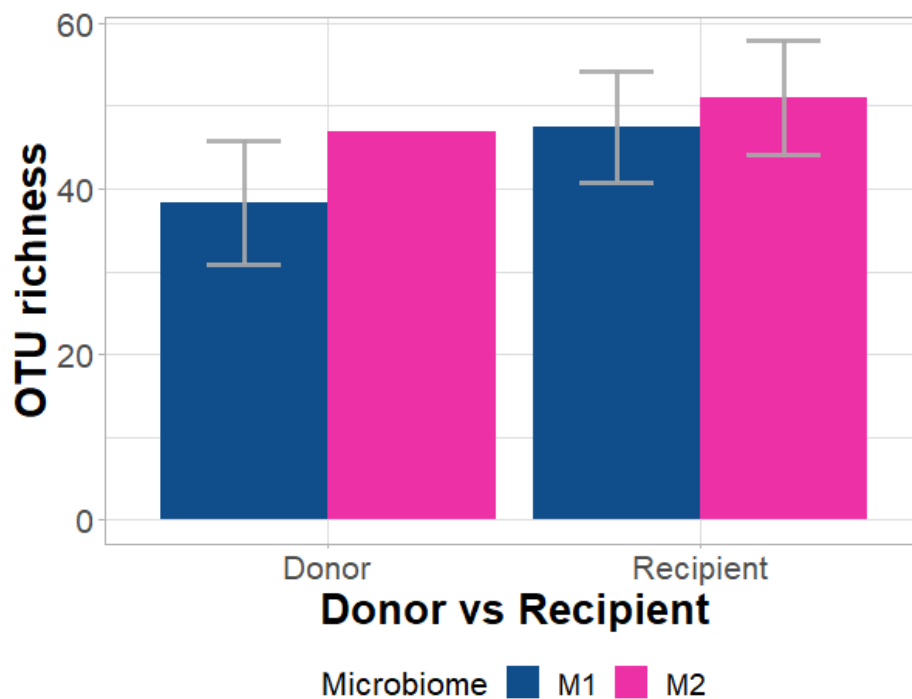


Figure S2: Effect of microbiome (M1 and M2) for donor and recipient samples on OTU richness. Error bars indicate standard error. Colours indicate the different microbiome treatments. OTU richness in the M1 inoculum (mean=38.333, sd=13.051) was, on average, lower compared with the M2 inoculum

(OTU

richness=47.000).,

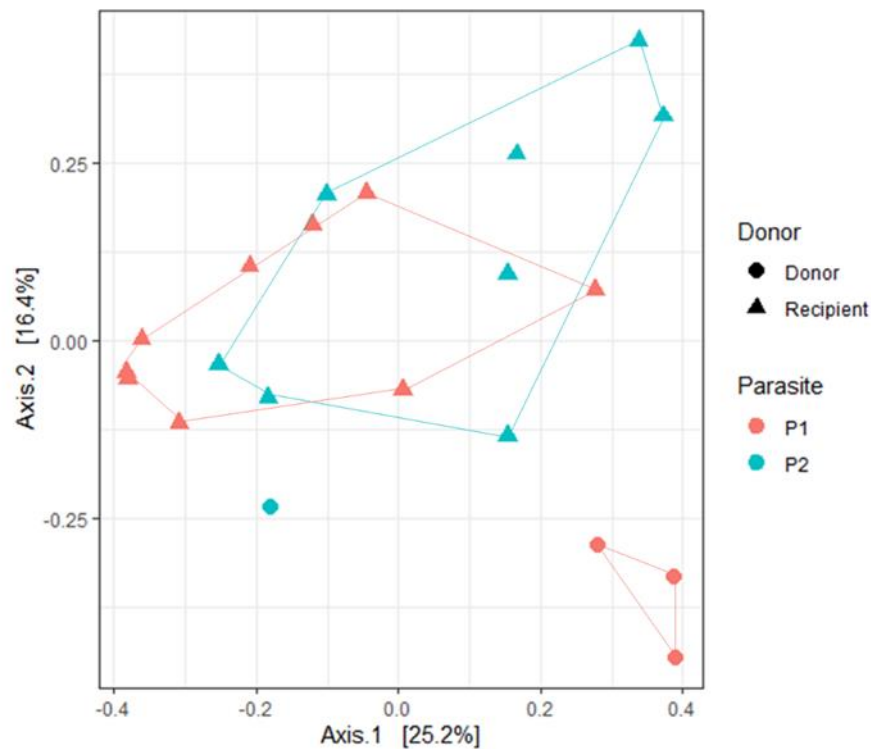


Figure S3: PCA of the gut microbial communities of recipients using weighted UniFrac distance for the donors (P1 and P2) and matching recipients (M1 x P1, M2 x P2) using weighted UniFrac distance for donor/recipient type and parasite treatment. Analyses on donor (P1 and P2) and matching recipient (M1 x P1, M2 x P2) bacterial communities, showed a significant difference in structure for P1 ($p=0.005$; $R^2=0.147$), but not for P2 ($p=0.783$; $R^2=0.330$). Bray-Curtis ordinations revealed that both P1 and P2, showed complete segregation between donors and recipients (Figure 7b), indicating that the donors and recipients for both the P1 and P2 treatment were differently structured (Figure 7b), however non-significant for P2.