

Supplementary Figures and Tables

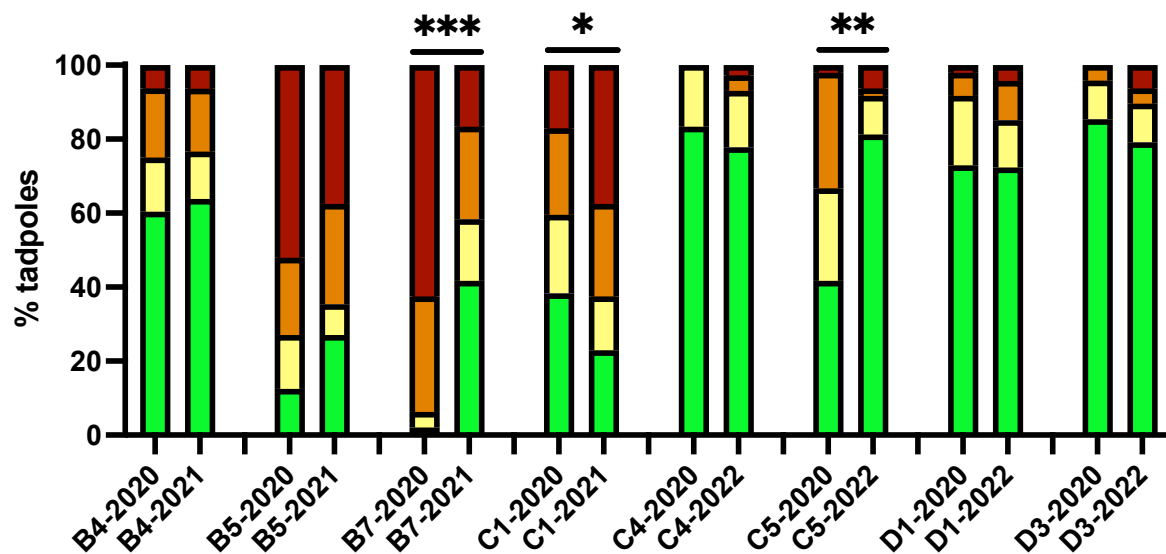


Figure S1. Reproducibility of regeneration in sibships from the same female frog.

A second spawning was obtained from 8 of the 12 females in the study. Regeneration assays were used to test for reproducibility of the regenerative outcomes from subsequent spawnings (top bar graph). For five of the eight frogs, regenerative outcomes were not significantly different between spawnings. B7, C1 and C5 females however yielded significantly different results, suggesting some impact from the environment had altered the two outcomes. N=48 for all cohorts except N=47 for B4 2021, C1 2020 and D1 2022, N=44 for C4 2020 and N=72 for C4 2022). Four frogs did not produce enough eggs for analysis. Ordinal χ^2 was used to indicate significant differences in regeneration within each sibship, adjusted p values * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, non-significant comparisons are not shown. Raw counts and analysis can be found in Table S29.

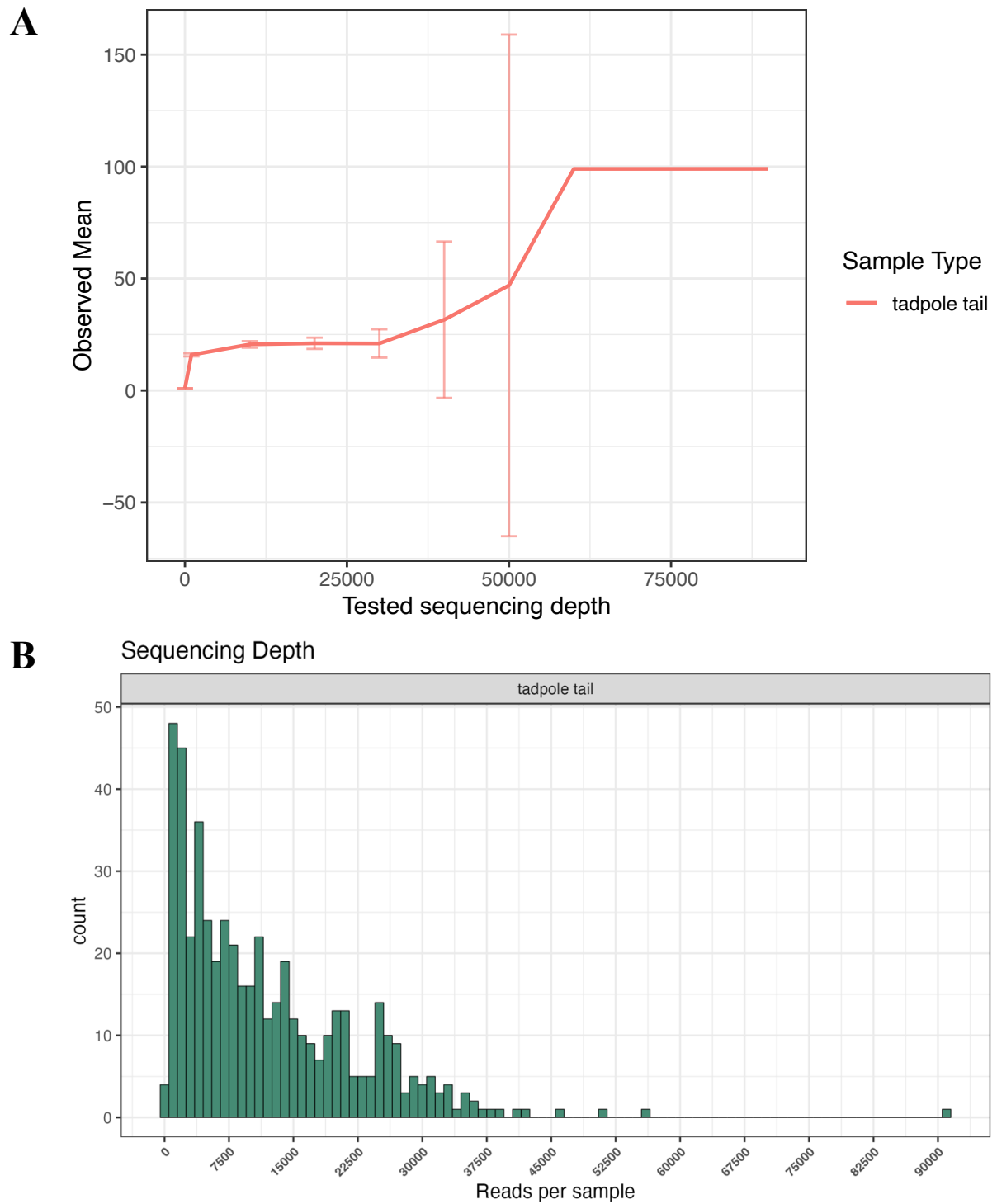


Figure S2. A. Rarefaction curve for 16S rRNA sequenced tadpole tail samples. B. Read count histogram.

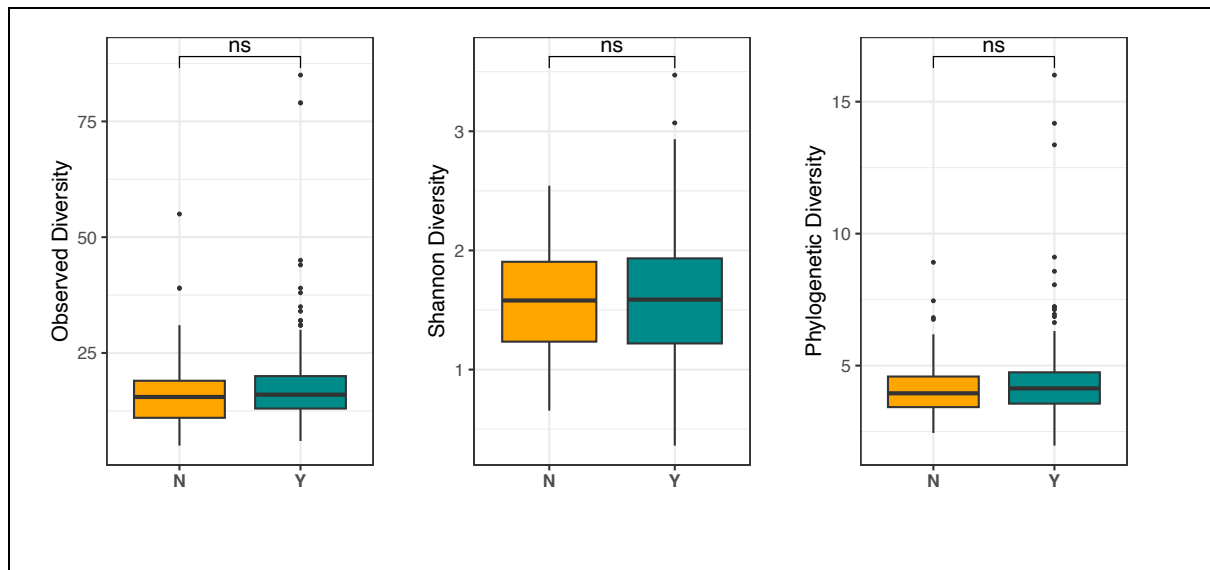
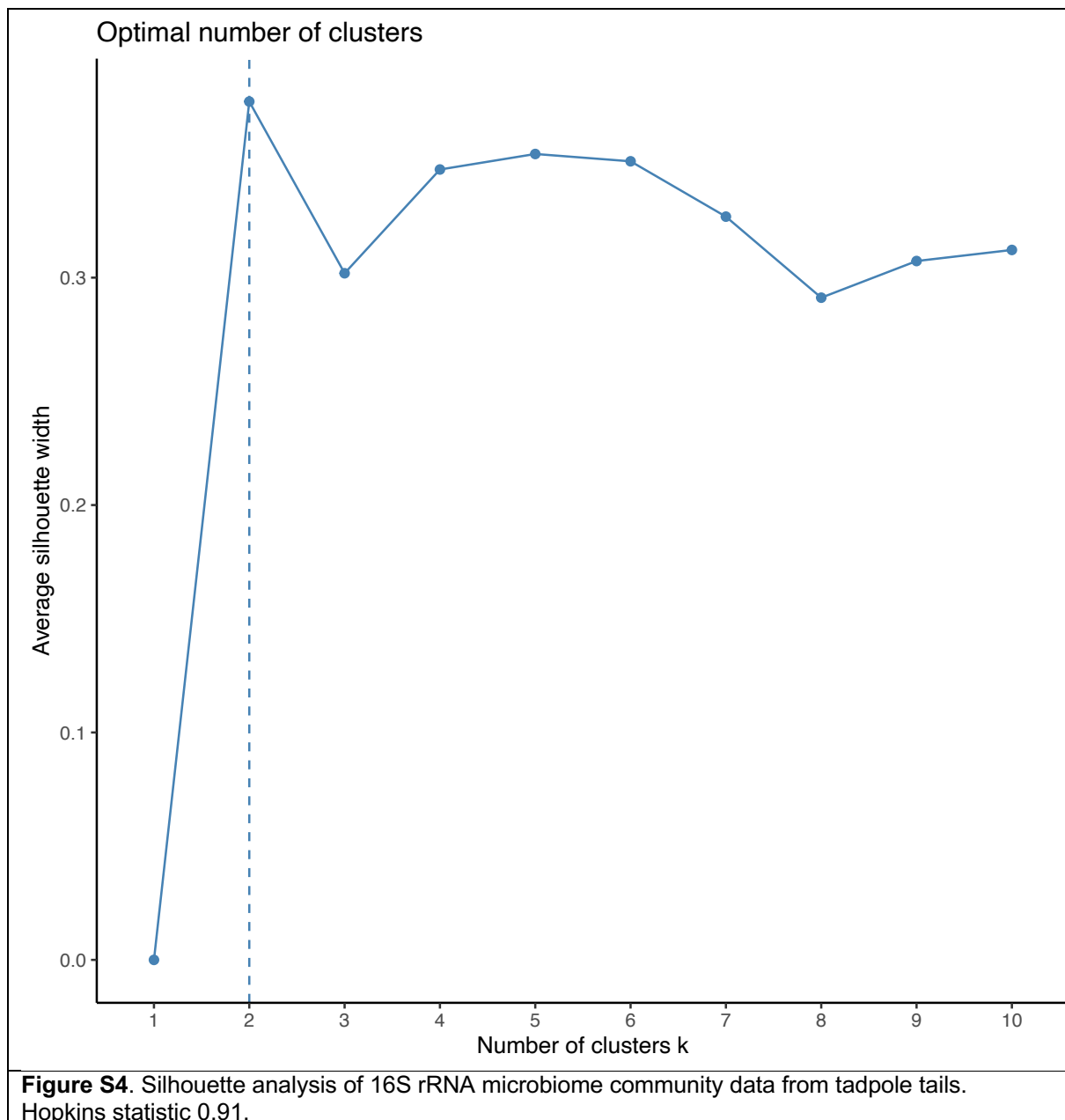


Figure S3. Alpha diversity of the microbial communities found on tadpole tail skin is not distinct between regenerating (Y=PB, PG, FR) and non-regenerating (N=NR) groups. Statistical analyses can be found in Table S9.



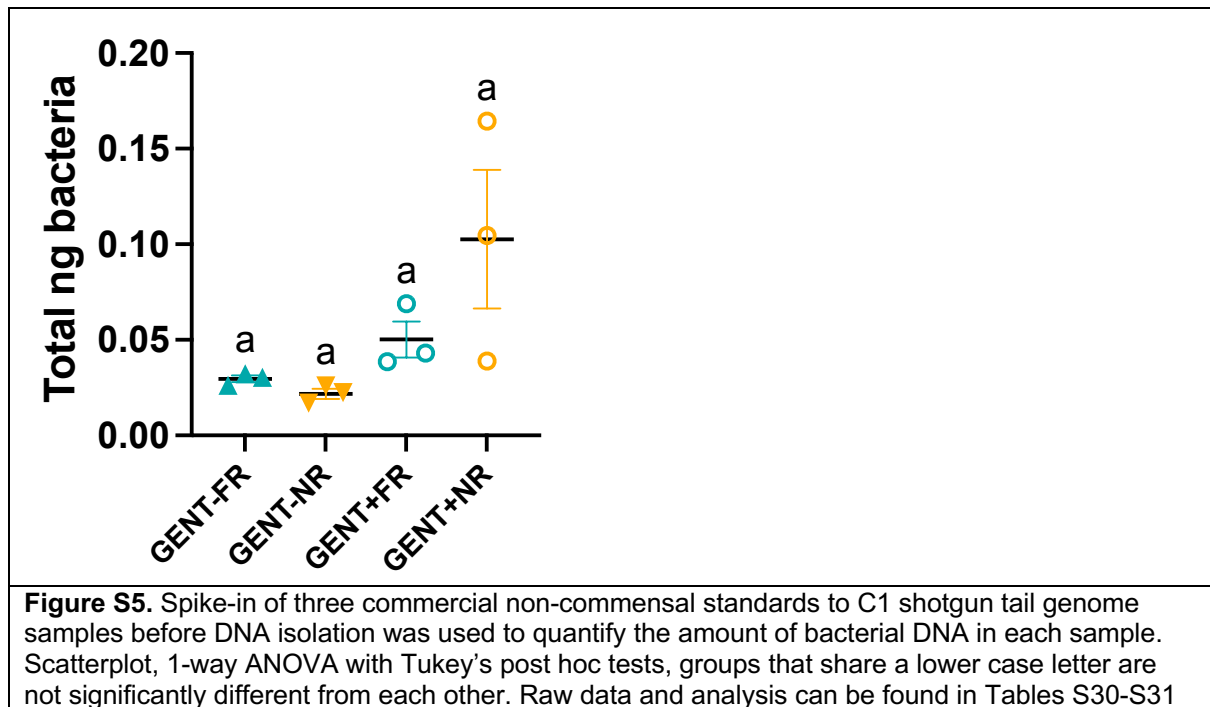


Table S1: Tlr2 CRISPR/Cas9 knockdown regeneration category counts

Treatment		Regeneration counts				Sample size (N)	% any regeneration
		NR	PB	PG	FR		
Left sibship	Controls Cas9	3	2	1	25	31	90.3
	<i>tlr2</i> sgRNA rnk29	17	3	1	1	22	22.7
	<i>tlr2</i> sgRNA rnk30	13	5	4	4	26	50.0
Right sibship	Controls Cas9	12	0	0	24	36	66.7
	<i>tlr2</i> sgRNA rnk29	33	5	1	1	40	17.5
	<i>tlr2</i> sgRNA rnk30	16	4	1	9	30	46.7

Table S2: Tlr2 CRISPR/Cas9 knockdown regeneration asymptotic generalised Pearson Chi-squared test, data ordered logistically.

Group	Chi-squared	Comparison	p.value	p.adjust	significance
Left sibship	chi-squared = 31.033, df = 2, p-value = 0.0000001825	control : sgRNArnk29	2.28E-08	6.84E-08	****
		control: sgRNArnk30	0.00000549	0.00000824	****
		sgRNArnk29: sgRNArnk30	0.0438	0.0438	*
Right sibship	chi-squared = 67.464, df = 2, p-value = 0.00000000000000222	control : sgRNArnk29	3.69E-08	0.000000111	****
		control: sgRNArnk30	0.0118	0.0118	*
		sgRNArnk29: sgRNArnk30	0.00104	0.00156	**

Table S3: CRISPR/Cas9 editing of Tlr2 from randomly chosen embryos

Tadpoles	Guide RNA_sample	Editing %		
		Total	mean	SEM
Left sibship	<i>tlr2</i> sgRNA rnk29_1	28.6		
	<i>tlr2</i> sgRNA rnk29_2	53.6		
	<i>tlr2</i> sgRNA rnk29_3	49.1	43.8	7.69
Right sibship	<i>tlr2</i> sgRNA rnk29_1	47.3		
	<i>tlr2</i> sgRNA rnk29_2	50.1		
	<i>tlr2</i> sgRNA rnk29_3	52.5	50.0	1.50
Left sibship	<i>tlr2</i> sgRNA rnk30_1	6.3		
	<i>tlr2</i> sgRNA rnk30_2	12		
	<i>tlr2</i> sgRNA rnk30_3	11.5	9.9	1.82
Right sibship	<i>tlr2</i> sgRNA rnk29_1	12.5		
	<i>tlr2</i> sgRNA rnk29_2	20.9		
	<i>tlr2</i> sgRNA rnk29_3	24.1	19.2	2.01

Table S4: Peptidoglycan and Lipopolysaccharide treatments, category counts

Treatment		Regeneration counts				Sample size (N)	% any regeneration
		NR	PB	PG	FR		
Native MMR	none	7	5	5	6	23	69.6
	PG	7	8	6	2	23	69.6
	LPS	8	9	1	4	22	63.6
	PG and LPS	3	5	4	11	23	87.0
Gentamicin	none	14	6	3	2	25	44.0
50 ug/ml	PG	7	9	3	5	24	70.8
MMR	LPS	8	7	3	8	26	69.2
	PG and LPS	4	5	1	10	20	80.0

Table S5: Peptidoglycan and Lipopolysaccharide treatments regeneration asymptotic generalised Pearson Chi-squared test, data ordered logistically.

Group	Chi-squared	Comparison	p.value	p.adjust	significance
Control MMR	chi-squared = 9.8291, df = 3, p-value = 0.02008	none : PG	0.338	0.406	ns
		none : LPS	0.251	0.376	ns
		none : PG and LPS	0.102	0.204	ns
		PG : LPS	0.777	0.777	ns
		PG : PG and LPS	0.00824	0.0247	*
		LPS : PG and LPS	0.00691	0.0247	*
Gentamicin 50 ug/ml In MMR	chi-squared = 10.453, df = 3, p-value = 0.01508	none : PG	0.08	0.146	ns
		none : LPS	0.0293	0.0879	ns
		none : PG and LPS	0.00215	0.0129	*
		PG : LPS	0.598	0.598	ns
		PG : PG and LPS	0.0976	0.146	ns
		LPS : PG and LPS	0.248	0.298	ns

Table S6 Regeneration category counts for samples used in 16S rRNA amplicon sequencing, by mother and culture plate and pairwise comparisons of plate replicates.

Female-plate replicate	Regeneration counts				Sample size (N)	% any regeneration	Asymptotic Linear-by-Linear Association Test		
	FR	PG	PB	NR			Z	p-value	significance
B4-1	10	2	7	2	21	90.5	2.1056	0.0352	*
B4-2	14	5	2	0	21	100.0			
B5-1	2	2	8	9	21	57.1	-0.4799	0.6313	ns
B5-2	1	5	2	13	21	38.1			
B7-1	1	1	8	11	21	47.6	-1.1043	0.2695	ns
B7-2	0	1	6	14	21	33.3			
B9-1	20	1	0	0	21	100.0	-1.1854	0.2359	ns
B9-2	18	2	1	0	21	100.0			
C1-1	10	4	2	4	20	69.6	-1.3862	0.1657	ns
C1-2	4	6	8	3	21	75.0			
C3-1	18	1	1	1	21	83.3	-1.5344	0.1249	ns
C3-2	14	1	3	3	21	75.0			
C4-1	16	5	0	0	21	87.5	0.7859	0.4319	ns
C4-2	18	3	0	0	21	87.5			
C5-1	11	5	5	0	21	87.5	-1.3404	0.1801	ns
C5-2	8	4	8	1	21	83.3			
D1-1	18	2	0	1	21	83.3	-1.2820	0.1998	ns
D1-2	13	5	3	0	21	87.5			
D2-1	18	2	1	0	21	87.5	-0.5420	0.5879	ns
D2-2	17	2	2	0	21	87.5			
D3-1	18	2	1	0	21	87.5	0.3573	0.7209	ns
D3-2	18	3	0	0	21	87.5			
D4-1	13	3	4	1	21	83.3	0.5136	0.6075	ns
D4-2	15	1	5	0	21	87.5			

Table S7: Top five Genera for each female tank

Tank housing (mother)	Genus	Phylum	Mean_abundance
Tank B B4, B5, B7, B9	Rhizobium Genera	Proteobacteria	749.23
	Chryseobacterium	Bacteroidota	385.07
	Delftia	Proteobacteria	67.14
	Lachnospir. NK4A136	Firmicutes	66.60
	Fluviicola	Bacteroidota	52.86
Tank C C1, C3, C4, C5	Aeromonas	Proteobacteria	575.04
	Rhizobium Genera	Proteobacteria	258.20
	Fluviicola	Bacteroidota	221.07
	Chryseobacterium	Bacteroidota	161.75
	Acinetobacter	Proteobacteria	129.04
Tank D D1, D2, D3, D4	Rhizobium Genera	Proteobacteria	759.12
	Lactiplantibacillus	Firmicutes	254.74
	Chryseobacterium	Bacteroidota	235.67
	Lachnospir. NK4A136	Firmicutes	67.16
	Pseudomonas	Proteobacteria	30.94

Table S8 Top five genera found in each regeneration category

Regeneration category	Genus	Phylum	Mean_abundance
FR	Rhizobium Genera	Proteobacteria	582.98
	Chryseobacterium	Bacteroidota	254.53
	Aeromonas	Proteobacteria	218.99
	Lactiplantibacillus	Firmicutes	111.63
	Fluviicola	Bacteroidota	83.24
PG	Rhizobium Genera	Proteobacteria	573.45
	Aeromonas	Proteobacteria	253.23
	Chryseobacterium	Bacteroidota	203.58
	Fluviicola	Bacteroidota	122.87
	Lactiplantibacillus	Firmicutes	105.42
PB	Rhizobium Genera	Proteobacteria	518.03
	Aeromonas	Proteobacteria	297.03
	Chryseobacterium	Bacteroidota	229.92
	Fluviicola	Bacteroidota	157.49
	Lachnospir. NK4A136	Firmicutes	75.54
NR	Rhizobium Genera	Proteobacteria	579.75
	Chryseobacterium	Bacteroidota	339.59
	Aeromonas	Proteobacteria	167.29
	Fluviicola	Bacteroidota	126.13
	Delftia	Proteobacteria	121.95

Table S9 Alpha diversity measures: Regenerators (PB, PG, FR categories) vs non-regenerators (NR) (Figures 3C and S4)

	Observed	Shannon	Phylogenetic Diversity
Shapiro-Wilk normality test W	0.727	0.992	0.75
Shapiro-Wilk normality test p-val	p<0.00001	p=0.013	p<0.00001
Normal?	No	No	No
Wilcoxon rank sum test with continuity correction W	9284	10470	9475
Wilcoxon rank sum test with continuity correction p-val	0.110	0.799	0.168
Significant difference?	No	No	No

Table S10 NMDA PERMANOVA-Weighted UniFrac any regeneration vs. NR

	Df	SumOfSqs	R2	F	Pr(>F)	% effect
RegenYN	1	0.366	0.006	5.617	0.001	0.6
FemCode	11	22.179	0.352	30.973	0.001	35.2
FemCode:TadpolePlate	12	9.576	0.152	12.259	0.001	15.2
Residual	474	30.856	0.490	NA	NA	49.0
Total	498	62.977	1.000	NA	NA	100.0

Table S11 NMDA PERMANOVA-Weighted UniFrac by mother tank (B, C or D)

	Df	SumOfSqs	R2	F	Pr(>F)	% effect
RegenYN	1	0.366	0.006	4.395	0.001	0.6
Tank	2	11.551	0.183	69.424	0.001	18.3
Tank:FemCode	9	10.628	0.169	14.194	0.001	16.9
Residual	486	40.432	0.642	NA	NA	64.2
Total	498	62.977	1	NA	NA	100.0

Table S12 Random Forest analysis. Top 20 most important taxa for classifying tadpoles into regenerator or non-regenerator categories.

Genus	p_value	statistic	significance	Mean	SD	Min	Max	RegenYN
Delftia	0.0001	16132	***	0.0072	0.0030	0.0032	0.0168	N
Aeromonas	0.5524	11887	ns	0.0030	0.0008	0.0016	0.0048	Y
Rhizobium Genera	0.9394	12374	ns	0.0019	0.0005	0.0009	0.0029	Y
Fluviicola	0.3922	13232	ns	0.0019	0.0007	0.0006	0.0034	N
Chryseobacterium	0.0189	14782	*	0.0016	0.0007	0.0004	0.0029	N
Bosea	0.0060	9742	**	0.0014	0.0006	0.0003	0.0027	Y
Staphylococcus	0.1956	13504	ns	0.0008	0.0005	0.0002	0.0019	Y
Lactiplantibacillus	0.0000	8944	***	0.0008	0.0005	0.0001	0.0018	Y
Undibacterium	0.4725	12943	ns	0.0008	0.0004	0.0002	0.0016	Y
Klebsiella	0.0011	14763	**	0.0008	0.0005	0.0000	0.0021	N
Lactobacillus	0.2365	13289	ns	0.0008	0.0003	0.0003	0.0014	N
Lachnospir. NK4A136	0.7951	12249	ns	0.0005	0.0002	0.0001	0.0009	N
Ralstonia	0.1097	10864	ns	0.0005	0.0007	-0.0008	0.0019	Y
Vogesella	0.1302	11265	ns	0.0004	0.0003	0.0000	0.0012	Y
Flavobacterium	0.3260	13364	ns	0.0004	0.0004	-0.0004	0.0010	Y
Lachnospiraceae UCG-001	0.2929	13045	ns	0.0004	0.0003	-0.0001	0.0010	N
Acinetobacter	0.0641	10835	ns	0.0004	0.0005	-0.0003	0.0017	Y
Mycobacterium	0.0071	13335	**	0.0004	0.0003	-0.0001	0.0010	N
Oscillibacter	0.1613	13121	ns	0.0003	0.0003	-0.0001	0.0011	N
Pedobacter	0.8375	12310	ns	0.0003	0.0003	-0.0003	0.0011	Y

Table S13 Differential Abundance analyses with tadpole mother identity (sibship) added as a fixed effect for two comparisons.

Comparison	Genus	ANCOMBC2			MaAsLin2		
		p val	q val	Higher in:	p val	q val	Higher in:
Regenerating Vs. Non-Regenerating, N=503 samples	<i>Fluviicola</i>	ns	ns	-	0.066	0.198	Regeneration
	<i>Variovorax</i>	ns	ns	-	0.040	0.139	Regeneration
	<i>Herbaspirillum</i>	ns	ns	-	0.065	0.194	Regeneration
	<i>Streptococcus</i>	ns	ns	-	0.096	0.243	Non-regeneration
	<i>Klebsiella</i>	0.004	0.221	Non-regeneration	0.002	0.010	Non-regeneration
FR vs. NR N=353 samples	<i>Shinella</i>	ns	ns	-	0.040	0.164	FR

* cut-off FDR q<0.25

Table S14 Lactiplantibacillus Differential Abundance (no regeneration vs. full regeneration).

Shapiro-Wilk test	NR	FR
W	0.144	0.4098
P value	<0.0001	<0.0001
Passed normality test (alpha=0.05)?	No	No
P value summary	****	****
Descriptive stats	NR	FR
Number of values	56	259
Minimum	0	0
Maximum	0.04971	0.92
Range	0.04971	0.92
Mean	0.00104	0.06379
Std. Deviation	0.00665	0.17890
Std. Error of Mean	0.00089	0.01112
Mann Whitney test	NR vs. FR	
P value	<0.0001	
Exact or approximate P value?	Exact	
P value summary	****	
Significantly different (P < 0.05)?	Yes	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	6426 , 43345	
Mann-Whitney U	4830	

Table S15 Pseudomonas Differential Abundance (no regeneration vs. full regeneration).

Shapiro-Wilk test	NR	FR
W	0.4028	0.63
P value	<0.0001	<0.0001
Passed normality test (alpha=0.05)?	No	No
P value summary	****	****
Descriptive stats	NR	FR
Number of values	56	259
Minimum	0	0
Maximum	0.188	0.2183
Range	0.188	0.2183
Mean	0.01035	0.01611
Std. Deviation	0.02841	0.02714
Std. Error of Mean	0.00380	0.00169
Mann Whitney test	NR vs. FR	
P value		0.0058
Exact or approximate P value?		Exact
P value summary		**
Significantly different (P < 0.05)?		Yes
One- or two-tailed P value?		Two-tailed
Sum of ranks in column A,B		7195 , 42575
Mann-Whitney U		5599

Table S16 Sphingobium Differential Abundance (no regeneration vs. full regeneration).

Shapiro-Wilk test	NR	FR
W	0.2784	0.5511
P value	<0.0001	<0.0001
Passed normality test (alpha=0.05)?	No	No
P value summary	****	****
Descriptive stats	NR	FR
Number of values	56	259
Minimum	0	0
Maximum	0.048	0.06
Range	0.048	0.06
Mean	0.0021	0.0054
Std. Deviation	0.0085	0.0113
Std. Error of Mean	0.0011	0.0007
Mann Whitney test	NR vs. FR	
P value	0.0013	
Exact or approximate P value?	Exact	
P value summary	**	
Significantly different (P < 0.05)?	Yes	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	7258 , 42512	
Mann-Whitney U	5662	

Table S17 Cupriavidus Differential Abundance (no regeneration vs. full regeneration)

Shapiro-Wilk test	NR	FR
W	0.1439	0.2486
P value	<0.0001	<0.0001
Passed normality test (alpha=0.05)?	No	No
P value summary	****	****
Descriptive stats	NR	FR
Number of values	56	259
Minimum	0	0
Maximum	0.00685	0.07943
Range	0.00685	0.07943
Mean	0.00014	0.00193
Std. Deviation	0.00093	0.00823
Std. Error of Mean	0.00012	0.00051
Mann Whitney test	NR vs FR	
P value	0.0129	
Exact or approximate P value?	Exact	
P value summary	*	
Significantly different (P < 0.05)?	Yes	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	7950 , 41821	
Mann-Whitney U	6354	

Table S18 Klebsiella Differential Abundance (no regeneration vs. full regeneration)

Shapiro-Wilk test	NR	FR
W	0.4619	0.2982
P value	<0.0001	<0.0001
Passed normality test (alpha=0.05)?	No	No
P value summary	****	****
Descriptive stats	NR	FR
Number of values	56	259
Minimum	0	0
Maximum	0.07657	0.1006
Range	0.07657	0.1006
Mean	0.00545	0.00285
Std. Deviation	0.01338	0.01054
Std. Error of Mean	0.00179	0.00065
Mann Whitney test	NR vs FR	
P value	0.0012	
Exact or approximate P value?	Exact	
P value summary	**	
Significantly different (P < 0.05)?	Yes	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	10316, 39454	
Mann-Whitney U	5784	

Table S19 Delftia Differential Abundance (no regeneration vs. full regeneration)

Shapiro-Wilk test	NR	FR
W	0.7795	0.5448
P value	<0.0001	<0.0001
Passed normality test (alpha=0.05)?	No	No
P value summary	****	****
Descriptive stats	NR	FR
Number of values	56	259
Minimum	0	0
Maximum	0.3017	0.1949
Range	0.3017	0.1949
Mean	0.06968	0.01882
Std. Deviation	0.0873	0.0382
Std. Error of Mean	0.01167	0.002373
Mann Whitney test	NR vs FR	
P value	<0.0001	
Exact or approximate P value?	Exact	
P value summary	****	
Significantly different (P < 0.05)?	Yes	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	11721, 38049	
Mann-Whitney U	4379	

Table S20 LAL assay results for tails (Endotoxin Units/mL) (Figure 6A)

Reg_Y Gent_N	Reg_N Gent_N	Reg_Y Gent_Y	Reg_N Gent_Y
3.226	2.989	-0.098	0.126
2.785	1.580	-0.246	0.052
2.79	1.884	-0.224	-0.282
0.731	1.962	0.021	0.003
0.65	2.574	-0.038	-0.052
1.337	0.643	-0.074	-0.029
0.155	0.22	0.337	0.450
0.083	1.171	0.428	0.096
0.671	0.113	0.236	0.389

Table S21 Statistical comparison of LAL assay results for tails by 1-way ANOVA (Figure 6A)

Tukey's multiple comparisons test	Mean Diff.	Summary	P Adj.
Reg_Y Gent_N vs. Reg_N Gent_N	-0.07867	ns	0.9968
Reg_Y Gent_N vs. Reg_Y Gent_Y	1.343	**	0.0069
Reg_Y Gent_N vs. Reg_N Gent_Y	1.297	**	0.0095
Reg_N Gent_N vs. Reg_Y Gent_Y	1.422	**	0.0040
Reg_N Gent_N vs. Reg_N Gent_Y	1.376	**	0.0055
Reg_Y Gent_Y vs. Reg_N Gent_Y	-0.04567	ns	0.9994

Table S22 LAL assay results for tadpole media (Endotoxin Units/mL) (Figure 6B)

Media	Sibship1		Sibship2	
	Gent_Y	Gent_N	Gent_Y	Gent_N
0.039	0.698	8.909	1.125	8.28
0.055	1.019	8.541	0.657	8.719

Table S22 Statistical comparison of LAL assay results by ANOVA (Figure 6B)

Holm-Sídák's multiple comparisons test	Mean Diff.	Summary	P Adj.
Sibship 1 Gent_Y vs. Sibship1 Gent_N	-7.867	****	<0.0001
Sibship 1 Gent_Y vs. Sibship2 Gent_Y	-0.033	ns	0.9147
Sibship 1 Gent_Y vs. Sibship2 Gent_N	-7.641	****	<0.0001
Sibship1 Gent_N vs. Sibship2 Gent_Y	7.834	****	<0.0001
Sibship1 Gent_N vs. Sibship2 Gent_N	0.226	ns	0.7225
Sibship2 Gent_Y vs. Sibship2 Gent_N	-7.609	****	<0.0001

Table S24 Shotgun whole genome normalised bacterial reads (for Figure 6C)

Row.names	total_assigned	Bacteria_nospike	Regen?	Gent?	Proportion bacterial	% bacterial
trim_B5_3_1_S5	45931261	105390	N	N	0.00229	0.22945
trim_B5_3_2_S4*	37033091	323099	N	N	0.00872	0.87246
trim_B5_3_7_S3	36384582	85867	Y	N	0.00236	0.23600
trim_B5_3_8_S10	40934212	44567	Y	N	0.00109	0.10887
trim_D1_4_25_S9	40001883	33947	Y	N	0.00085	0.08486
trim_D1_4_26_S7	41273491	49189	Y	N	0.00119	0.11918
trim_D1_4_31_S2	45560679	25742	N	N	0.00057	0.05650
trim_D1_4_45_S6	46796129	31100	N	N	0.00066	0.06646
trim_D1_G1_39_S8	52404117	12071	N	Y	0.00023	0.02303
trim_D1_G2_25_S1	42693469	25028	N	Y	0.00059	0.05862
trim_D1_G2_31_S12	34446662	34389	Y	Y	0.00100	0.09983
trim_D1_G2_35_S11	43390731	18301	Y	Y	0.00042	0.04218
trim_XenSpike_10C1_10_G7_S10	112845693	36932	Y	Y	0.00033	0.03273
trim_XenSpike_11C1_11_H7_S11	189201328	165847	Y	Y	0.00088	0.08766
trim_XenSpike_12C1_12_A6_S12	130195965	42515	N	Y	0.00033	0.03265
trim_XenSpike_1C1_1_F8_S1	129453835	69219	N	N	0.00053	0.05347
trim_XenSpike_2C1_2_G8_S2	95368123	76359	Y	N	0.00080	0.08007
trim_XenSpike_3C1_3_H8_S3	123677773	74134	Y	N	0.00060	0.05994
trim_XenSpike_4C1_4_A7_S4	103976851	42654	N	N	0.00041	0.04102
trim_XenSpike_5C1_5_B7_S5	96076610	99372	Y	N	0.00103	0.10343
trim_XenSpike_6C1_6_C7_S6	91545097	46608	N	N	0.00051	0.05091
trim_XenSpike_7C1_7_D7_S7	97517274	63826	N	Y	0.00065	0.06545
trim_XenSpike_8C1_8_E7_S8	49819742	107849	N	Y	0.00216	0.21648
trim_XenSpike_9C1_9_F7_S9	128305599	131744	Y	Y	0.00103	0.10268

* Outlier removed from analysis.

Table S25: Statistical analysis of normalised shotgun bacterial read counts Full Regeneration (FR) vs. No Regeneration (NR), For Figure 6C.

Descriptive statistics	NR	FR
Number of values	12	11
Minimum	0.0230	0.0327
Maximum	0.236	0.2295
Range	0.213	0.1967
Mean	0.0991	0.0784
Std. Deviation	0.0661	0.0555
Std. Error of Mean	0.0191	0.0167
Shapiro-Wilk test	NR	FR
W	0.8596	0.73
P value	0.0483	0.0011
Passed normality test (alpha=0.05)?	No	No
P value summary	*	**
Mann Whitney test	NR vs FR	
P value	0.2316	
Exact or approximate P value?	Exact	
P value summary	ns	
Significantly different (P < 0.05)?	No	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	176, 100	
Mann-Whitney U	45	

Table S26: Statistical analysis of normalised shotgun bacterial read counts Gentamicin raised vs. naturally raised For Figure 6D.

Descriptive statistics	MMR	GENT
Number of values	13	10
Minimum	0.0410	0.0230
Maximum	0.2360	0.2165
Range	0.1950	0.1934
Mean	0.0992	0.0761
Std. Deviation	0.0639	0.0570
Std. Error of Mean	0.0177	0.0180
Test for normal distribution		
Shapiro-Wilk test	MMR	GENT
W	0.7713	0.8132
P value	0.0032	0.0209
Passed normality test (alpha=0.05)?	No	No
P value summary	**	*
Number of values	13	10
Mann Whitney test	MMR vs GENT	
P value	0.2316	
Exact or approximate P value?	Exact	
P value summary	ns	
Significantly different (P < 0.05)?	No	
One- or two-tailed P value?	Two-tailed	
Sum of ranks in column A,B	176, 100	
Mann-Whitney U	45	

Table S27 Tail regeneration category counts, vancomycin and gentamycin treatments (Figure 8)

Tadpole sibship #	Treatment-plate	NR	PB	PG	FR	Sample size N
1	MMR-1	4	3	1	22	30
	MMR-2	5	3	1	17	26
	MMR-3	2	3	4	23	32
	GENT-1	8	5	0	5	18
	GENT-2	7	6	5	0	18
	GENT-3	12	4	1	3	20
	VANC-1	18	3	3	4	28
	VANC-2	18	6	3	2	29
	VANC-3	20	3	2	4	29
2	MMR-1	8	3	1	15	27
	MMR-2	16	3	0	4	23
	MMR-3	9	8	1	7	25
	GENT-1	21	2	2	2	27
	GENT-2	14	3	7	3	27
	GENT-3	18	1	2	7	28
	VANC-1	19	3	4	4	30
	VANC-2	21	4	0	5	30
	VANC-3	18	4	3	4	29
3	MMR-1	5	2	1	20	28
	MMR-2	2	0	2	24	28
	MMR-3	3	3	3	20	29
	MMR-4	1	0	4	20	25
	GENT-1	14	3	8	8	33
	GENT-2	12	8	3	2	25
	GENT-3	4	5	14	9	32
	GENT-4	6	3	6	13	28
	VANCO-1	12	3	6	15	36
	VANCO-2	7	3	3	16	29
	VANCO-3	8	1	3	19	31
	VANCO-4	2	6	2	20	30
4	MMR-1	17	4	1	8	30
	MMR-2	10	8	2	10	30
	MMR-3	12	7	3	10	32
	MMR-4	11	3	2	11	27
	GENT-1	20	4	3	1	28
	GENT-2	22	3	5	2	32
	GENT-3	23	1	4	3	31
	GENT-4	22	4	4	2	32
	VANCO-1	24	4	3	1	32
	VANCO-2	22	3	2	8	35
	VANCO-3	10	6	5	8	29
	VANCO-4	15	6	6	5	32

Table S28 Effect of raising tadpoles in antibiotics on regeneration asymptotic generalised Pearson Chi-squared test, data ordered logistically (Figure 8)

Sibship #	Comparison	p.value	p.adjust	Significance
1	Gentamicin vs. vancomycin	0.197	0.197	ns
	MMR vs. gentamicin	6.33E-11	9.50E-11	****
	MMR vs. vancomycin	4.44E-16	1.33E-15	****
2	Gentamicin vs. vancomycin	0.723	0.723	ns
	MMR vs. gentamicin	0.0134	0.0201	*
	MMR vs. vancomycin	0.00417	0.0125	*
3	Gentamicin vs. vancomycin	0.00206	0.00206	**
	MMR vs. gentamicin	0.000521	0.000782	***
	MMR vs. vancomycin	1.50E-10	4.50E-10	****
4	Gentamicin vs. vancomycin	0.00806	0.0121	*
	MMR vs. gentamicin	0.00000114	0.00000342	****
	MMR vs. vancomycin	0.0147	0.0147	*

Table S29 Regeneration category counts of tadpoles derived from consecutive spawns from the same female frog. Asymptotic Linear-by-Linear Association Test (Figure S1)

Comparison (female_year)	p.value	significance
B4_2020 vs. B4_2021	0.808	ns
B5_2020 vs. B5_2021	0.114	ns
B7_2020 vs. B7_2021	7.06E-09	****
C1_2020 vs. C1_2022	0.0173	*
C4_2020 vs. C4_2022	0.161	ns
C5_2020 vs. C5_2022	0.00104	**
D1_2020 vs. D1_2022	0.559	ns
D3_2020 vs. D3_2022	0.182	ns

Table S30 Figure S5

Sample	Regeneration	Gentamicin	total_ng
trim_XenSpike_10C1_10_G7_S10	Y	Y	0.03859159
trim_XenSpike_11C1_11_H7_S11	Y	Y	0.04316589
trim_XenSpike_12C1_12_A6_S12	N	Y	0.10452818
trim_XenSpike_1C1_1_F8_S1	N	N	0.02240141
trim_XenSpike_2C1_2_G8_S2	Y	N	0.03036359
trim_XenSpike_3C1_3_H8_S3	Y	N	0.03226991
trim_XenSpike_4C1_4_A7_S4	N	N	0.0258809
trim_XenSpike_5C1_5_B7_S5	Y	N	0.0262268
trim_XenSpike_6C1_6_C7_S6	N	N	0.01695871
trim_XenSpike_7C1_7_D7_S7	N	Y	0.16444212
trim_XenSpike_8C1_8_E7_S8	N	Y	0.03898403
trim_XenSpike_9C1_9_F7_S9	Y	Y	0.06889198

Table S31 Figure S5 1 way ANOVA

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Summary	Adjusted P Value
GENT_N REG_N vs. GENT_N REG_Y	-0.007873	-0.09294 to 0.07720	ns	0.9903
GENT_N REG_N vs. GENT_Y REG_N	-0.0809	-0.1660 to 0.004166	ns	0.0624
GENT_N REG_N vs. GENT_Y REG_Y	-0.02847	-0.1135 to 0.05660	ns	0.715
GENT_N REG_Y vs. GENT_Y REG_N	-0.07303	-0.1581 to 0.01204	ns	0.0948
GENT-REG_Y vs. GENT_Y REG_Y	-0.0206	-0.1057 to 0.06447	ns	0.8635
GENT+REG_N v s. GENT_Y REG_Y	0.05243	-0.03264 to 0.1375	ns	0.2731

Table S32 Read count summary, 503 samples 16S rRNA from tails

SampleType	Samples	Min	Median	Mean	Max	SD	Total
tadpole tail	503	82	9093	11868.9662	91228	10525.9963	5970090