

Supplementary table S1: Bacterial species composition and relative abundance present in urine samples collected from individual male *Crinia signifera* (n=14). Each row represents a species of bacteria identified to the finest scale that was able to be identified according to the SILVA rRNA database by the Australian Genome Research Facility. Unassigned species are species that were not able to be identified to taxonomic order. Total absolute bacterial abundance is the sum of all absolute abundance raw reads counts for each species within each urine sample; data for each species is the relative abundance of each species within the sample, displayed as a percentage (total number of reads assigned to a species divided by the total number of reads in the sample * 100).

ORDER	FAMILY	SPECIES	Frog ID													
			CS3 ^a	CS9 ^a	CS13 ^a	CS16 ^a	CS19 ^a	CS23 ^a	CS29 ^a	CS31 ^a	CS1 ^b	CS7 ^b	CS8 ^b	CS20 ^b	CS22 ^b	CS26 ^b
Total count of unique bacteria species present:			57	29	71	20	8	7	62	34	58	52	52	16	46	15
Total absolute bacterial abundance (sum of raw read counts):			98622	43540	101343	12637	6506	9451	228574	91122	102646	163300	104759	33123	167601	45769
Bacillales	Alicyclobacillaceae	<i>Tumebacillus sp.</i>	1.709							0.461		0.963				1.042
		<i>Tumebacillus sp.</i>														0.411
	Paenibacillaceae	<i>Brevibacillus sp.</i>	0.189													
Bacteroidales	Bacteroidaceae	<i>Bacteroides sp.</i>	2.030	0.285	0.221				8.769	6.537	0.420	1.823	4.363		13.977	
	Marinifilaceae	<i>Odoribacter sp.</i>			0.059				2.889		1.720	0.294			0.109	
	Paludibacteraceae	<i>Paludibacter sp.</i>			0.456											
	Rikenellaceae	<i>Alistipes sp.</i>									0.161					
		<i>Alistipes sp.</i>	0.353	11.33	12.29				1.387	13.426	0.009	0.57	2.22	1.461	4.649	
		<i>Rikenella sp.</i>	0.244	0.064	1				1.862		0.34	2.699			0.183	
		<i>Rikenella sp.</i>							0.036							
		<i>Rikenella sp.</i>			0.376											
			2.698	2.079	5.282				1.253	3.042	0.203	0.626	0.692		1.245	
	Tannerellaceae	<i>Macellibacteroides sp.</i>			0.025					0.762	0.509	0.235	0.641			
		<i>Parabacteroides sp.</i>	5.504		1.402		0.938		5.536	1.992	0.161	0.622			3.502	

			2.705	0.140	0.101				0.038	0.967	1.360		4.040		0.245	0.221
			0.558		0.078				0.095	3.743	0.041				1.335	
Betaproteo- bacteriales	Burkholderiaceae	<i>Aquabacterium sp.</i>									0.096					
		<i>Burkholderia- Caballeronia- Paraburkholderia sp.</i>	0.026	2.591	0.030	3.909	62.143	4.306	0.273	0.11	0.066	1.25	0.289	5.422	0.307	
		<i>Curvibacter gracilis</i>			0.019											
		<i>Lautropia sp.</i>												0.338		
		<i>Massilia sp.</i>					24.424								0.148	
		<i>Pelomonas sp.</i>														
		<i>Ralstonia sp.</i>											0.038			
			0.033								0.318	0.039	0.107			
	Chromobacteriaceae	<i>Crenobacter sp.</i>			0.100								0.159			
			0.251											0.007		
Brachyspirales	Brachyspiraceae	<i>Brachyspira sp.</i>									0.163					
Brevinematales	Brevinemataceae	<i>Brevinema sp.</i>												0.856		
Chitinophagale s	Chitinophagaceae	<i>Filimonas aurantiibacter</i>					0.338									
					2.181				8.077	5.186		5.851	7.149			
Chloroplast						0.016										
Clostridiales	Clostridiales vadinBB60 group		1.069		0.022		0.215	4.751	0.056			0.031	0.053	0.217		
	Family XIII		1.375	1.835	0.103				0.701	0.415	1.316	0.544	0.530		0.189	

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Ruminococcaceae	<i>Anaerotruncus sp.</i>			0.01				0.062		0.387	0.083	0.096		0.273	
	<i>Anaerotruncus sp.</i>	0.114		1.428						0.403	1.034	0.498		0.040	
	<i>Candidatus Soleaferrea [Anaerotruncus] sp.</i>									0.048					
	<i>Candidatus Soleaferrea sp.</i>									0.396					
	<i>Caproiciproducens sp.</i>			0.912							0.239				
	<i>GCA-900066225 Ruminococcaceae sp.</i>	0.366	0.163	0.319	0.522			1.091		1.042		0.596		1.316	
	<i>GCA-900066225 sp.</i>	0.930								2.021	1.958	0.371			
	<i>[Harryflintia] Provencibacterium massiliense</i>							0.053							
	<i>Hydrogenoanaeroba cterium sp.</i>	1.351		0.014				0.471		2.512					
	<i>Hydrogenoanaeroba cterium sp.</i>			0.110											
	<i>Negativibacillus sp.</i>	0.097									1.076				
	<i>Pygmaibacter massiliensis</i>	3.442						0.338		3.449		0.973		0.032	
	<i>Ruminiclostridium 5 sp.</i>			0.233							0.415	0.249			
	<i>Ruminiclostridium 5 sp.</i>											1.061		0.351	

<i>Ruminiclostridium 9 bacterium enrichment culture clone M244</i>	0.482													
<i>Ruminiclostridium 9 sp.</i>	1.645	2.876	2.821			62.036	1.986	3.341	0.737	0.922	2.654	12.14	1.715	13.529
<i>Ruminococcaceae NK4A214 group sp.</i>	1.000													
<i>Ruminococcaceae UCG-004 sp.</i>							1.283		0.292				0.055	
<i>Ruminococcaceae UCG-005 sp.</i>									0.012					
<i>[Ruminococcaceae UCG-008] Intestinibacillus massiliensis</i>	0.259		2.391				0.3	0.128	0.972		0.283			
<i>Ruminococcaceae UCG-009 sp.</i>	1.121		0.167						0.422	0.04	0.346			
<i>Ruminococcaceae UCG-009 sp.</i>		2.285	0.86				0.127		0.03	0.108			0.634	
<i>Ruminococcaceae UCG-014 sp.</i>									0.002				0.145	
<i>Ruminococcus 1 sp.</i>	0.039									0.326	0.046			
<i>[Eubacterium] coprostanoligenes group sp.</i>	1.770													
	0.038													
	8.778	7.811	9.694	0.04			3.921	9.183	12.55	5.75	11.21	5.941	3.505	

			0.813					0.477	0.002	0.021		0.028			
Corio-bacteriales	Coriobacteriales	<i>Raoultibacter sp.</i>												0.098	
	Incertae Sedis	Eggerthellaceae	0.341												
Coryne-bacteriales	Corynebacteriaceae	<i>Corynebacterium 1 sp.</i>									0.524				
	Dietziaceae	<i>Dietzia sp.</i>	0.971												
	Nocardiaceae	<i>Rhodococcus hoagii</i>													
Deferri-bacteriales	Deferribacteraceae	<i>Mucispirillum sp. 69</i>						0.007							
		<i>Mucispirillum bacterium 'Lincoln Park 3'</i>			0.574			0.171			0.716	0.095			
		<i>Mucispirillum sp.</i>	0.108		15.276			1.512							
		<i>Mucispirillum sp.</i>			0.225			0.073				0.022			
					2.169			0.922		0.009		20.593			
Deinococcales	Deinococcaceae	<i>Deinococcus yunweiensis</i>										0.123			
		<i>Deinococcus sp.</i>				1.037									
	Trueperaceae	<i>Truepera sp.</i>													
Desulfo-bacteriales	Desulfobacteraceae									0.081					
Desulfovi-brionales	Desulfovibrionaceae	<i>Bilophila sp.</i>						0.657							
		<i>Desulfovibrio sp.</i>	8.327		0.08	2.509		5.141			0.01	21.7			
					0.399			0.07							
			8.513	19.07	7.738	33.49		0.825	20.975	5.737	5.031	10.715	1.281	19.683	

Entero- bacteriales	Enterobacteriaceae	<i>Citrobacter sp.</i>		0.073						0.003						
		<i>Enterobacter sp.</i>							0.046							
		<i>Hafnia- Obesumbacterium sp.</i>		0.292	4.453					1.787		4.154	0.403	5.018	1.980	
		<i>Morganella sp.</i>							0.211						0.169	
		<i>Proteus sp.</i>													0.440	
		<i>Serratia sp.</i>			0.113											
				5.175	10.161	0.578			0.346	3.485	0.641	7.069	1.216	41.41	4.008	21.659
											0.044					
Erysipelo- trichales	Erysipelotrichaceae	<i>Coprobacillus sp.</i>									0.044					
		<i>Dielma fastidiosa</i>								0.458						
		<i>Dielma sp.</i>	1.592	3.484	0.864				0.917	3.547	1.842	0.031	0.844		1.372	
		<i>[Erysipelatoclostridiu m] Beduini massiliensis</i>			0.053	0.443			0.101		0.567	0.697	0.047		0.026	
		<i>Erysipelatoclostridiu m sp.</i>			0.101				1.608		0.23		0.284		0.039	
		<i>Faecalitalea [Eubacterium] dolichum</i>	0.051		0.566				0.154		0.105					
		<i>Holdemania sp.</i>			0.016				0.004	0.89	0.006		0.019		0.056	0.741
			0.059	0.427	0.827	0.055			1.237	4.398	3.727	0.201	0.397	20.080	2.665	
Flavo- bacteriales	Flavobacteriaceae	<i>Flavobacterium Cytophaga sp. SA1</i>									0.508					
Frankiales	Geodermatophilaceae	<i>Blastococcus sp.</i>			0.032								0.066			

		<i>Blastococcus sp.</i>				0.063										
			0.111													
Fuso- bacteriales	Fusobacteriaceae	<i>Fusobacterium sp.</i>										0.042				
Lacto- bacillales	Aerococcaceae	<i>Aerococcus sp.</i>										0.438				
	Enterococcaceae	<i>Enterococcus sp.</i>	0.083						0.066		2.790	0.129				
			0.003													
	Streptococcaceae	<i>Lactococcus garvieae subsp. garvieae</i>							0.492							
		<i>Streptococcus sp.</i>				13.563								2.56		
Micrococcales	Brevibacteriaceae	<i>Brevibacterium sp.</i>										0.492				
	Cellulomonadaceae	<i>Cellulomonas sp.</i>					11.820									
	Dermabacteraceae	<i>Brachybacterium sp.</i>	0.006													
	Dermacoccaceae	<i>Dermacoccus sp.</i>									0.516					
	Micrococcaceae	<i>Micrococcus sp.</i>						7.248								
Mycoplasmatales	Mycoplasmataceae	<i>Mycoplasma muris</i>										0.002				
Opitutales	Opitutaceae			0.457	0.04							0.107			0.761	
	Puniceicoccaceae												0.008			
Propioni- bacteriales	Nocardioidaceae	<i>Nocardioides sp.</i>				8.602										
	Propionibacteriaceae	<i>Cutibacterium sp.</i>	1.428	5.025		7.85								1.875		
Pseudo- monadales	Moraxellaceae	<i>Enhydrobacter sp.</i>										0.276				
	Pseudomonadaceae	<i>Pseudomonas sp.</i>			0.006								0.103	0.063		

Rhizobiales	Beijerinckiaceae	<i>Bosea sp.</i>														0.035
		<i>Methylobacterium sp.</i>							0.001							
	Rhizobiaceae	<i>Aureimonas sp.</i>				3.229										
		<i>Mesorhizobium sp.</i>			0.006	9.749				0.721			0.013	0.166		
	Xanthobacteraceae	<i>Bradyrhizobium sp.</i>														3.706
Rhodo-bacterales	Rhodobacteraceae	<i>Paracoccus sp.</i>			0.038											
Rickettsiales	Mitochondria	<i>alpha proteobacterium sp.</i>	0.082	1.417	0.087			14.051	0.297	1.213				2.790		
					0.063						0.009					
		<i>alpha proteobacterium sp.</i>	0.811		1.669			6.782	0.518	0.065	0.73	28.69	0.147		0.126	41.720
Sacchari-monadales					0.009											
Seleno-monadales	Veillonellaceae	<i>Anaerosinus sp.</i>	0.678		0.249						1.416					
Sphingo-bacterales	env.OPS 17	<i>eubacterium env.OPS 17 sp.</i>							0.007							
Spingo-monadales	Sphingomonadaceae	<i>Sphingomonas sp.</i>			0.021							0.005	0.01		0.529	
											0.006					
Spirochaetales	Spirochaetaceae	<i>Treponema 2 sp.</i>							0.059							
Synergistales	Synergistaceae	<i>Cloacibacillus sp.</i>			0.861				2.246							
Thermales	Thermaceae	<i>Thermus sp.</i>												0.359		
Thermo-microbiales	JG30-KF-CM45	<i>Thermomicrobium sp.</i>								0.063						

			0.039												
Verruco- microbiales	Akkermansiaceae	<i>Akkermansia sp.</i>	19.365							22.3					
Xantho- monadales	Xanthomonadaceae	<i>Stenotrophomonas sp.</i>				0.34					0.231				
Unassigned					0.028										
			5.706	19.639							2.999	0.530		0.757	
			0.038	4.568					1.039						
									0.001						
							0.092			0.002		0.002		0.002	
						0.024	0.031								0.013

^a denotes urine samples collected at a single time point and frozen immediately at -80°C until sample processing (microbiome extraction and profiling); ^b denotes urine samples collected at two time-points, 2-hours apart that were pooled and then frozen at -80°C until sample processing (microbiome extraction and profiling). Each urine sample was collected from an individual male *Crinia signifera* (samples that were pooled, were only pooled within and not across individual males).