

Supplementary Materials Table S1. Catalogue of bacterial genera from splenic tissue in all rodents sampled. Table includes only genera deemed positive in at least one animal. OTU = operational taxonomic unit ; NC = negative controls ; Bold genera include OTUs deemed potentially pathogenic ; % reads in positive animals = Nb reads - NCs - Nb reads in animals not meeting criteria for positive infection (specified in the main text).

Phylum	Class	(sub-)Order	Family	Genus	Minimum Bootstrap	Biology	Nb of OTUs	Total Nb Reads (incl. NCs)	% reads in NC	Nb Positive Infections	% Reads in Positive Animals	
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	<i>unclassified Acidobacteriaceae</i>	100	Common soil microbes, known contaminant of molecular biology reagents.	1	53	0	1	38 %	
		Pseudonocardiales	Pseudonocardaceae	<i>Pseudonocardia</i>	79		1	344	0	1	14 %	
Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	<i>Bifidobacterium</i>	100	Long thought to be fungi, most are soil or aquatic microbes. Some can cause opportunistic infections in humans, such as <i>Corynebacterium</i> , <i>Dietzia</i> and <i>Williamsia</i> species. <i>Mycobacteria</i> in the sub-order Corynebacteriales are pathogens that cause tuberculosis and leprosy in humans and other mammals, and one species of <i>Rhodococcus</i> is an important pathogen of young horses. However, many of these have also been recognized as common contaminants of molecular biology equipment and reagents (indicated here with an asterisk *).	2	649	0	5	28 %	
			Corynebacteriaceae	<b><i>Corynebacterium</i></b> *	100		1	1853	0	3	32 %	
		Corynebacteriales	Dietziaceae	<b><i>Dietzia</i></b> *	100		1	2553	0	9	98 %	
			Nocardiaceae	<i>Rhodococcus</i> *	100		1	240	0	2	47 %	
			<b><i>Williamsia</i></b>	100	1		274	0	2	54 %		
		Micrococcales	Brevibacteriaceae	<i>Brevibacterium</i> *	100		1	1251	0	6	33 %	
			Dermabacteraceae	<i>Brachybacterium</i> *	100		1	4787	0	9	94 %	
			Microbacteriaceae	<i>Microbacterium</i> *	80		1	392	6.12 %	1	8 %	
			Micrococcaceae	<i>Kocuria</i>	63		1	632	0	4	22 %	
		Coriobacteria	Propionibacteriales	Nocardoidaceae	<i>Marmoricola</i>		91	1	329	0	1	5 %
				Coriobacteriaceae	<i>Adlercreutzia</i>		100	1	139	0	2	36 %
			Coriobacteriales	<i>Enterorhabdus</i>	100		1	127	0	1	10 %	
				<i>unclassified Coriobacteriaceae</i>	100		3	878	0	8	60 %	
				<i>unclassified Coriobacteriaceae</i>	100		3	878	0	8	60 %	
Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	<i>Bacteroides</i>	100	Most are normal flora or environmental microbes, rarely associated with opportunistic infections (e.g., <i>Prevotella</i> species can cause infection from animal bites). The Flavobacteriaceae family includes a number of important fish pathogens, some respiratory pathogens of birds, and more recently discovered isolates from human sewage and clinical specimens (such as <i>Elizabethkingia meningoseptica</i> ). One rodent respiratory pathogen has been recently described ( <i>Filobacterium rodentium</i> gen. nov., sp. nov.) but was not found here.	5	581	0	7	70 %	
			<i>unclassified Bacteroidales</i>	98	110		33495	0	283	68 %		
			Homeothermaceae	<i>Candidatus Homeothermaceae</i>	100		1	153	0	1	30 %	
		Porphyromonadaceae	Odoribacter	100	5		999	0	5	94 %		
			Prevotellaceae	<i>Prevotella</i>	100		6	2967	0	11	77 %	
		Rikenellaceae	<i>Alistipes</i>	100	4		885	< 1 %	6	60 %		
			<i>Rikenella</i>	100	1		65	0	1	65 %		
		<i>unclassified Bacteroidales</i>	<i>unclassified Bacteroidales</i>	94	4		997	0	9	73 %		
			<i>unclassified Bacteroidales</i>	100	1		264	0	1	31 %		
		Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Chryseobacterium</i>		100	1	438	0	2	36 %
				<i>Cloacibacterium</i>	100		1	2760	0	2	2 %	
				<i>Flavobacterium</i>	100		1	673	0	3	46 %	
				<i>unclassified Flavobacteriaceae</i>	100		3	668	0	4	86 %	
		Sphingobacteria	Sphingobacteriales	Chitinophagaceae	<i>Sediminibacterium</i>		100	1	10426	7.6 %	1	4 %
				Sphingobacteriaceae	<i>Pedobacter</i> *		92	2	531	0	2	75 %
				<i>Sphingobacterium</i>	100		1	80	0	1	20 %	
				<i>unclassified Sphingobacteriaceae</i>	69		1	341	0	2	27 %	
		<i>unclassified Bacteroidetes</i>	100	3	1074		0	9	73 %			
		Cyanobacteria	Melainabacteria	Gastranaerophilales	<i>unclassified Gastranaerophilales</i>		100	Most likely natural gut flora.	1	202	0	3
Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Geobacillus</i>	99	While most Firmicutes species are abundant in normal flora or environmental samples, a number are associated with important diseases and opportunistic infections in animals and humans (nasopharyngeal diseases from <i>Streptococcus</i> spp. infections; among the <i>Bacillales</i> : anthrax from infection by <i>Bacillus anthracis</i> , and Listeriosis disease of the central nervous system from <i>Listeria</i> species; <i>Clostridium</i> species infections are probably the most abundant, with clinical relevancy for cases of tetanus, botulism and food poisoning, gangrene, and for diarrhea in patients following antibiotic therapy.	1	306	0	1	13 %	
			Listeriaceae	<i>Brochothrix</i>	100		1	379	0	1	10 %	
			<i>unclassified Bacillales</i>	<i>unclassified Bacillales</i>	90		3	1651	0	4	30 %	
		Lactobacillales	Carnobacteriaceae	<i>Trichococcus</i>	59		1	53	0	1	43 %	
			Enterococcaceae	<i>Enterococcus</i>	59		1	355	0	2	29 %	
			Lactobacillaceae	<i>Lactobacillus</i>	96		5	7645	0	30	76 %	
			<i>unclassified Lactobacillaceae</i>	75	1		265	0	2	20 %		
		Leuconostocaceae	<i>Leuconostoc</i>	100	1		862	0	2	57 %		
		Streptococcaceae	<i>Lactococcus</i>	100	1		5499	0	3	12 %		
		Clostridia	Clostridiales	Anaerococcus	<b><i>Streptococcus</i></b>		98	5	2604	0	16	72 %
				<i>Anaerococcus</i>	100		1	147	0	1	86 %	
				<i>Candidatus Arthromitus</i>	100		1	98	0	1	93 %	
				<i>Clostridium sensu stricto 12</i>	97		1	59	0	1	56 %	
				<i>Incertae sedis</i>	100		1	68	0	2	62 %	
				<i>unclassified Defluviitaleaceae</i>	100		1	189	0	1	38 %	
				Defluviitaleaceae	<i>Defluviitaleaceae</i>		82	5	1676	0	19	64 %
				Lachnospiraceae	<i>Acetatifactor</i>		100	1	87	0	1	23 %
				<i>Anaerostipes</i>	51		19	10445	0	81	64 %	
				<i>Blautia</i>	69		1	64	0	1	28 %	
				<i>Dorea</i>	70		1	68	0	1	28 %	
		<i>Incertae sedis</i>	66	6	1381		0	12	62 %			
<i>Roseburia</i>	66	6	1381	0	12	62 %						

Phylum	Class	(sub-)Order	Family	Genus	Minimum Bootstrap	Biology	Nb of OTUs	Total Nb Reads (incl. NCs)	% reads in NC	Nb Positive Infections	% Reads in Positive Animals				
Firmicutes (cont.)				<i>unclassified Lachnospiraceae</i>	52		72	23886	0	189	68 %				
			Peptostreptococcaceae	<i>Incertae sedis</i>	100		1	161	0	1	52 %				
			Ruminococcaceae	<i>Anaerotruncus</i>	77		1	98	0	2	40 %				
				<i>Faecalibacterium</i>	100		1	356	0	2	93 %				
				<i>Incertae sedis</i>	57		5	1892	0	21	61 %				
				<i>Intestinimonas</i>	79		3	618	0	6	25 %				
				<i>Oscillibacter</i>	83		4	2081	< 0.1 %	19	55 %				
				<i>Ruminococcus</i>	89		11	3779	< 1 %	34	70 %				
				<i>unclassified Ruminococcaceae</i>	59		24	16720	0	116	74 %				
				<i>unclassified Clostridiales</i>	72		13	2560	0	32	57 %				
			vadinBB60	<i>Clostridiales</i>	100		2	9590	0	32	82 %				
				<i>vadinBB60</i> genus	100		2	956	0	8	72 %				
				<i>unclassified Clostridiales</i>	100		2	956	0	8	72 %				
			unclassified Clostridia	<i>unclassified Clostridia</i>	100		1	516	0	2	27 %				
		Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Allobaculum</i>	99		2	911	0	6	90 %			
		Erysipelotrichales		<i>Catenibacterium</i>	100		1	256	0	1	96 %				
	Negativicutes	Selenomonadales	Acidaminococcaceae	<i>Phascolarctobacterium</i>	100		1	157	0	2	83 %				
		Selenomonadales	Veillonellaceae	<i>Veillonella</i>	100		1	268	0	1	24 %				
	unclassified Firmicutes			<i>unclassified Firmicutes</i>	100		1	53	0	1	49 %				
Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	<b>Fusobacterium</b>	100	Fusobacterium species are associated with a range of gastro-intestinal diseases and skin ulcerations, but it is not clear to what degree this association is opportunistic.	1	108	0	2	94 %				
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Brevundimonas</i>	100	Many <i>Proteobacteria</i> are important animal pathogens, including those with sustained zoonotic transmission to humans.	1	275	0	1	28 %				
					Rhizobiales	Bartonellaceae	<b>Bartonella</b>	100	<i>Bartonella</i> species are thought to have undergone a recent expansion and now commonly infect rodent species around the world. Many of these species are implicated in causing zoonotic human infections.	1	6327077	0.01	245	99%	
						Methylbacteriaceae	<i>Methylbacterium*</i>	100		2	7113	1.8 %	4	7 %	
						Phyllobacteriaceae	<i>Phyllobacterium</i>	70	The remaining <i>Rhizobiales</i> and <i>Rhodobacteriales</i> are important soil microbes.	1	120	0	1	39 %	
						Rhizobiaceae	<i>Rhizobium</i>	100		1	968	1.96 %	1	40 %	
					Rhodobacteriales	Rhodobacteraceae	<i>Paracoccus</i>	89		1	1229	1.46 %	1	3 %	
						Rickettsiales	Anaplasmataceae	<b>Candidatus Neoehrlichia</b>	100	Causes anaplasmosis in humans and domestic animals, carried by a diverse array of rodents as well as <i>Ixodes</i> tick vectors. 100% sequence identity to <i>Candidatus N. mukarensis</i> .	1	18358	0	8	99 %
							Rickettsiaceae	<b>Orientia</b>	100	The only species in this order, <i>Orientia tsutsugamushi</i> , causes scrub typhus in humans and is transmitted by chiggers.	1	876	0	8	91 %
								<b>Rickettsia</b>	100	Closest sequence identities (98%) were to the spotted fever group of <i>Rickettsia</i> species, responsible for a number of important vector-transmitted human and animal diseases.	1	57226	0	8	99 %
						Sphingomonadales	Sphingomonadaceae	<i>Novosphingobium</i>	95	The Sphingomonads have been implicated in nosocomial infections, but are widely distributed in nature with a diverse array of biological characteristics. However, in our dataset, positive results appeared more likely to be contaminants.	1	235	0	1	8 %
								<i>Sphingobium</i>	100		1	574	0	2	34 %
								<i>Sphingomonas</i>	100		1	593	0	1	31 %
					Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Lautropia</i>	100	Though some <i>Burkholderiaceae</i> are well-known pathogens (e.g., whooping cough agent <i>Bordetella pertussis</i> ), this is not expected for any of the <i>Burkholderiales</i> found in our study.	1	58	0	1	71 %
								<i>Ralstonia*</i>	97		1	1624	0	2	4 %
							Comamonadaceae	<i>unclassified Comamonadaceae</i>	100		1	3407	< 1 %	7	17 %
			Oxalobacteraceae	<i>Duganella</i>	65		1	266	0	2	39 %				
	Hydrogenophilales	Hydrogenophilaceae	Hydrogenophilus	<i>unclassified Neisseriaceae</i>	100	Among the remaining Betaproteobacteria, the only recognized pathogenic species are a few of many in the genus <i>Neisseria</i> . One infection carrying the bulk of reads shared 98% sequence identity to bacteria found in healthy human nasal passages.	1	2617	2.98 %	1	6 %				
		Neisseriales	Neisseriaceae	<b>Neisseriaceae</b>	97		2	928	0	2	95 %				
		Rhodocyclales	Rhodocyclaceae	<i>Dechloromonas</i>	94		1	302	0	1	95 %				
		unclassified Betaproteobacteria		<i>unclassified Betaproteobacteria</i>	100		1	143	1.4 %	1	8 %				

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Proteobacteria (continued)	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio	74	<i>Deltaproteobacteria</i> live in extreme environments, and only one pathogenic species is currently known ( <i>Lawsonia intercellularis</i> in horses).	8	1690	0	22	78 %	
				<i>unclassified</i>	61		5	962	0	10	72 %	
				<i>unclassified</i>	100		1	52	0	1	100 %	
	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Arcobacter	Arcobacter	100	Very little is known about the Arcobacter species, but their potential for pathogenicity in animals has been recently described (Houf & Stephan 2007). We noted 100% sequence homology to <i>Arcobacter cryaerophilus</i> , which has been associated with disease in humans and laboratory rats.	1	403	0	2	85 %
					Helicobacter	100		5	47394	0	56	93 %
	Gammaproteobacteria	Alteromonadales	Pseudoalteromonadales	Pseudoalteromonadales	Pseudoalteromonas	100	Marine bacteria.	1	116	0	1	32 %
					Shewanella	100		1	78	0	1	23 %
		Enterobacteriales	Enterobacteriaceae	Escherichia-Shigella	Escherichia-Shigella	91	1	979	3.17 %	2	29 %	
					Providencia	96	1	600	0	1	88 %	
		Yersinia	Yersinia	85	1	7414	0	14	85 %			
			<i>unclassified</i>	93	1	964	0	3	50 %			
		Legionellales	Coxiellaceae	Rickettsiella	76	1	592	0	3	45 %		
		Oceanospirillales	Oceanospirillaceae	Marinospirillum	100	1	263	0	1	97 %		
		Pasteurellales	Pasteurellaceae	<i>unclassified</i>	81	2	1951	0	5	54 %		
		Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter	97	Among the <i>Pseudomonadales</i> , the <i>Pseudomonas</i> (nosocomial superbug) and <i>Psychrobacter</i> (endocarditis-causing) species have the largest implications for pathogenicity. However, along with <i>Acinetobacter</i> , disease is mostly limited to opportunistic infection.	4	11290	2.3 %	14	32 %
	Alkanindiges				100	1		184	0	1	9 %	
	Enhydrobacter				100	1		8497	1.06 %	1	7 %	
	Psychrobacter				100	3		1033	< 0.1 %	5	62 %	
	<i>unclassified</i>				100	2		18473	1.72 %	20	56 %	
	Vibrionales	Vibrionaceae	Vibrio	Vibrio	96	1	182	0	2	64 %		
				<i>unclassified</i>	100	1	63	0	1	76 %		
	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	100	1	1123	0	2	14 %			
	<i>unclassified</i>	<i>unclassified</i>	<i>unclassified</i>	100	1	63	0	1	76 %			

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Proteobacteria (continued)	unclassified Proteobacteria			<i>unclassified Proteobacteria</i>	100	Unknown	4	970	0	7	68 %	
Spirochaetae	Spirochaetes	Spirochaetales	Brevinemataceae	<b>Brevinema</b>	100	96% sequence identity to <i>Brevinema andersonii</i> , an infectious spirochaete of the short-tailed shrew and white footed mouse in North America.	1	5603	0	3	100 %	
			Leptospiraceae	<b>Leptospira</b>	100	100% sequence identity to human pathogenic <i>Leptospira borgpetersenii</i> and <i>L. interrogans</i> ; rodents are considered the primary reservoir species	1	257	0	2	95 %	
			Spirochaetaeae	<b>Borrelia</b>	100	Borrelia1: 100% sequence identity to <i>Borrelia miyamotoi</i> in humans and <i>Ixodes</i> ticks, zoonotic fever that may relapse (co-infects with but is not Lyme disease agent <i>B. burgdorferi</i> ); Borrelia2: 96% sequence identity to <i>Borrelia</i> sp. <i>Nov</i> in <i>Peromyscus leucopus</i> ; Borrelia3: positive in two animals beyond positive control reads	3	703	< 1 %	5	90 %	
				<b>Treponema</b>	99	<i>Treponema</i> species are pathogenic in humans (e.g., syphilis), but many occur in natural gut flora such as the rumen of cows. The closest sequence identity (92%) of our samples is to these non-pathogenic species, and they were found only in animals with several gut microbiota (probable contaminated dissection).	2	985	0	7	77 %	
Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<b>Anaeroplasma</b>	100	Rumen microbes.	1	137	0	1	22 %	
			Entomoplasmatales	Spiroplasmataceae	<b>Spiroplasma</b>	100	95% species identity with pathogenic <i>Spiroplasma</i> species isolated from <i>Ixodes</i> ticks, 94% identity with samples pulled from ticks on dogs ( <i>Spiroplasma eriocheiris</i> ); The pathogenicity of these species is disputed, with questions revolving around its role in transmissible spongiform encephalopathies in humans and animals. 1 animal very infected (BR10049 >2000 reads per sample), second animal low copy numbers (BR10114 <15 copies per sample)	1	4738	0	2	100 %
			Mycoplasmatales	Mycoplasmataceae	<b>Mycoplasma</b>	100	<i>Mycoplasma</i> species are pathogenic in both humans and animals, implicated in respiratory and pelvic infections. Some OTUs were overlapping, and more detail is provided in the text.	11	1786662	2.56 %	204	99%
				<i>unclassified Mycoplasma species</i>	100		1	39767	0	10	100%	
Verrucomicrobia	Spartobacteria	Chthoniobacterales	unclassified Chthoniobacterales	<i>unclassified Chthoniobacterales</i>	100		1	786	0	2	11 %	
	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<b>Luteolibacter</b>	98	Not pathogenic	1	147	0	1	24 %	
<i>entirely unclassified Bacteria</i>					100	Unknown	25	4390	< 1 %	37	65 %	
Eukaryote												
Apicomplexa	Conoidasida	Eucoccidiorida	Sarcocystidae	<i>unclassified Sarcocystidae</i>	100	Protazoan intracellular organisms in the family Sarcocystidae cause a variety of diseases in animals and humans, such as Toxoplasmosis ( <i>Toxoplasma gondii</i> 90-96% similarity) and reproductive failure ( <i>Neospora caninum</i> 92-97% similarity). 98% sequence similarity to <i>Sarcocystis muris</i> , a coccidian parasite closely related to <i>Toxoplasma</i> and <i>Neurospora</i> , first found in mice.	3	13581	0	15	95 %	

\* Indicates taxa found to be frequent contaminants of molecular biology reagents and consumables