

Table S4. Major functions differentially represented between *A. wheeleri* and *Nasutitermes* spp. metagenomes

Function ID	Function description	Estimated gene copies ^a			<i>A. wheeleri</i> vs. laboratory <i>N. corniger</i>			<i>Amitermes</i> vs. Costa Rican <i>Nasutitermes</i> sp.		
		Ami ^b	Lab Nas ^b	CR Nas ^b	Z-LOR ^c	p-value	Significant ^d	Z-LOR ^c	p-value	Significant ^d
Glycoside hydrolases in plant cell wall degradation										
pfam02449	Glyco_hydro_42: Oligosaccharide degrading	41	57	41	-4.6687	3E-06	Yes	-5.02625	5E-07	Yes
pfam08532	Glyco_hydro_42M: Oligosaccharide degrading	22	35	29	-4.00926	6.1E-05	Yes	-4.90337	9.4E-07	Yes
pfam00933	Glyco_hydro_3: Oligosaccharide degrading	268	205	120	-3.86579	0.00011	Yes	-2.79182	0.00524	Yes
pfam03512	Glyco_hydro_52: Oligosaccharide degrading	0	22	4	-3.6359	0.00028	Yes	-2.23273	0.02557	No
pfam00232	Glyco_hydro_1: Oligosaccharide degrading	70	62	30	-2.89659	0.00377	Yes	-1.2038	0.22867	No
pfam10566	Glyco_hydro_97: Oligosaccharide degrading	7	14	1	-2.85069	0.00436	Yes	0.78198	0.43422	No
pfam02837	Glyco_hydro_2_N: Oligosaccharide degrading	142	48	70	2.74517	0.00605	Yes	-2.75784	0.00582	Yes
pfam01055	Glyco_hydro_31: Oligosaccharide degrading	167	52	40	3.40358	0.00067	Yes	1.81374	0.06972	No
pfam07745	Glyco_hydro_53: Hemicellulase	17	64	26	-7.15545	8.3E-13	Yes	-4.92124	8.6E-07	Yes
pfam01270	Glyco_hydro_8: Hemicellulase	37	80	32	-7.03073	2.1E-12	Yes	-3.99692	6.4E-05	Yes
pfam00331	Glyco_hydro_10: Hemicellulase	225	208	119	-5.6994	1.2E-08	Yes	-4.17515	3E-05	Yes
pfam02156	Glyco_hydro_26: Hemicellulase	34	58	24	-5.37367	7.7E-08	Yes	-2.85709	0.00428	Yes
pfam00457	Glyco_hydro_11: Hemicellulase	110	94	23	-3.3417	0.00083	Yes	1.9851	0.04713	No
pfam00150	Cellulase, GH5: Cellulase	258	341	167	-10.9823	4.6E-28	Yes	-6.80117	1E-11	Yes
pfam02015	Glyco_hydro_45: Cellulase	20	71	7	-7.48051	7.4E-14	Yes	-0.13691	0.8911	No
pfam00759	Glyco_hydro_9: Cellulase	104	138	51	-7.00507	2.5E-12	Yes	-2.32518	0.02006	No
pfam05592	Bac_rhamnosid: Debranching	48	8	9	3.05183	0.00227	Yes	1.55292	0.12044	No
COG3534	Alpha-L-arabinofuranosidase: Debranching	217	57	42	4.79881	1.6E-06	Yes	1.65457	0.09801	No
Cohesin and dockerin										
pfam09603	Fib_succ_major, corresponding to TIGR02145	255	2420	687	-43.9205	0	Yes	-28.7156	2E-181	Yes
pfam00404	Dockerin_1	29	0	0	2.69491	0.00704	Yes	2.2195	0.02645	No
pfam00963	Cohesin	30	0	0	2.72976	0.00634	Yes	2.25409	0.02419	No
Nitrogen fixation										
COG2710	Nitrogenase molybdenum-iron protein, alpha and beta chains	227	295	121	-10.0305	1.1E-23	Yes	-6.52729	6.7E-11	Yes
COG0347	Nitrogen regulatory protein PII	89	90	47	-4.24258	2.2E-05	Yes	-4.02142	5.8E-05	Yes
COG1348	Nitrogenase subunit NifH (ATPase)	61	55	17	-2.79347	0.00521	Yes	-0.31277	0.75445	No
Sum of all COGs involved^e		578	574	243	-10.5756	3.9E-26	Yes	-6.72356	1.8E-11	Yes
Peptidoglycan degradation (by COGs)										
COG5632	N-acetylmuramoyl-L-alanine amidase	53	9	4	3.19057	0.00142	Yes	2.35414	0.01857	No
COG0860	N-acetylmuramoyl-L-alanine amidase	212	72	27	3.35195	0.0008	Yes	3.41394	0.00064	Yes

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		Ami ^b	Lab Nas ^b	CR Nas ^b	Z-LOR ^c	p-value	Significant ^d	Z-LOR ^c	p-value	Significant ^d
COG1686	D-alanyl-D-alanine carboxypeptidase	209	66	30	3.75365	0.00017	Yes	2.96017	0.00307	Yes
COG2173	D-alanyl-D-alanine dipeptidase	61	5	1	4.03868	5.4E-05	Yes	2.72541	0.00642	Yes
Sum of all COGs involved		665	201	84	7.05765	1.7E-12	Yes	5.9588	2.5E-09	Yes

Peptidoglycan degradation (by pfams)

pfam02016	Peptidase_S66: Muramoyl-tetrapeptide carboxypeptidase	57	1	0	3.38727	0.00071	Yes	2.90792	0.00364	Yes
pfam01520	Amidase_3: N-acetylmuramoyl-L-alanine amidase	206	68	27	3.44737	0.00057	Yes	4.50693	6.6E-06	Yes
pfam00768	Peptidase_S11: D-alanyl-D-alanine carboxypeptidase	178	53	26	3.74023	0.00018	Yes	3.87718	0.00011	Yes
pfam01471	PG_binding_1: Putative peptidoglycan binding domain	85	1	8	3.79432	0.00015	Yes	3.38939	0.0007	Yes
pfam01510	Amidase_2: N-acetylmuramoyl-L-alanine amidase	91	18	9	3.85416	0.00012	Yes	3.4453	0.00057	Yes
pfam01427	Peptidase_M15: D-alanyl-D-alanine dipeptidase	57	5	1	3.87498	0.00011	Yes	2.90792	0.00364	Yes
Sum of all pfams involved^e		723	165	78	8.09736	5.6E-16	Yes	8.09736	5.6E-16	Yes

Amino acid transport

COG3842	ABC-type spermidine/putrescine transport, ATPase components	191	161	69	-4.22695	2.4E-05	Yes	-2.45921	0.01392	No
COG4166	ABC-type oligopeptide transport, periplasmic component	145	128	40	-4.10925	4E-05	Yes	-0.4233	0.67208	No
COG1176	ABC-type spermidine/putrescine transport, permease component I	78	72	33	-3.32226	0.00089	Yes	-2.42376	0.01536	No
COG0601	ABC-type dipeptide/oligopeptide/nickel transport, permease components	251	176	63	-2.72669	0.0064	Yes	0.13412	0.89331	No
COG4608	ABC-type oligopeptide transport, ATPase component	131	99	28	-2.57501	0.01002	Yes	0.86268	0.38831	No
COG1173	ABC-type dipeptide/oligopeptide/nickel transport, permease components	212	146	86	-2.32485	0.02008	No	-3.60919	0.00031	Yes
COG1115	Na ⁺ /alanine symporter	129	28	17	4.34046	1.4E-05	Yes	2.57083	0.01015	No
COG0834	ABC-type amino acid transport/signal transduction, periplasmic component	507	145	85	6.68402	2.3E-11	Yes	3.6078	0.00031	Yes

Amino acid and amine oxidation

COG1012	NAD-dependent aldehyde dehydrogenases	95	132	55	-7.07674	1.5E-12	Yes	-4.8225	1.4E-06	Yes
COG3546	Mn-containing catalase	31	0	0	2.76694	0.00566	Yes	2.03804	0.04155	No
COG0753	Catalase	39	0	0	3.00257	0.00268	Yes	2.27132	0.02313	No
COG0665	Glycine/D-amino acid oxidases (deaminating)	76	3	4	4.43312	9.3E-06	Yes	3.08233	0.00205	Yes
pfam07833	Cu_amine_oxidN1, copper amine oxidase	167	6	5	6.49891	8.1E-11	Yes	5.28619	1.2E-07	Yes
COG2414	Aldehyde:ferredoxin oxidoreductase	198	17	15	7.25153	4.1E-13	Yes	4.54519	5.5E-06	Yes

Ammonia transport and assimilation

COG0004	Ammonia permease	129	117	27	-4.11561	3.9E-05	Yes	0.94786	0.3432	No
COG0069	Glutamate synthase domain 2	172	127	57	-2.73268	0.00628	Yes	-1.69523	0.09003	No
COG0174	Glutamine synthetase	241	10	4	7.93291	2.1E-15	Yes	5.42699	5.7E-08	Yes

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		Ami ^b	Lab Nas ^b	CR Nas ^b	Z-LOR ^c	p-value	Significant ^d	Z-LOR ^c	p-value	Significant ^d
Urease										
COG0804	Urea amidohydrolase (urease) alpha subunit	12	40	26	-5.55089	2.8E-08	Yes	-6.12284	9.2E-10	Yes
COG2371	Urease accessory protein UreE	0	9	11	-2.67544	0.00746	Yes	-3.60133	0.00032	Yes
COG0830	Urease accessory protein UreF	3	9	16	-2.5823	0.00981	Yes	-4.82805	1.4E-06	Yes
COG0831	Urea amidohydrolase (urease) gamma subunit	1	8	8	-2.54782	0.01084	Yes	-3.24606	0.00117	Yes
	Sum of all COGs involved	45	83	93	-6.70647	2E-11	Yes	-11.6002	4.1E-31	Yes
Amino acid biosynthesis										
Arginine biosynthesis										
COG0002	Acetylglutamate semialdehyde dehydrogenase	87	99	26	-5.11931	3.1E-07	Yes	-0.69639	0.48619	No
COG1364	N-acetylglutamate synthase (N-acetylornithine aminotransferase)	138	111	30	-3.17893	0.00148	Yes	0.80754	0.41936	No
COG0137	Argininosuccinate synthase	143	111	42	-2.92257	0.00347	Yes	-0.78799	0.4307	No
Histidine biosynthesis										
COG0040	ATP phosphoribosyltransferase	111	90	34	-2.9136	0.00357	Yes	-0.91986	0.35765	No
COG0131	Imidazoleglycerol-phosphate dehydratase	73	62	38	-2.66143	0.00778	Yes	-3.55282	0.00038	Yes
COG0139	Phosphoribosyl-AMP cyclohydrolase	30	31	24	-2.56037	0.01046	Yes	-4.16415	3.1E-05	Yes
COG1387	Histidinol phosphatase and related hydrolases of the PHP family	139	43	57	3.1549	0.00161	Yes	-3.00199	0.00268	Yes
Isoleucine biosynthesis										
COG0059	Ketol-acid reductoisomerase	85	105	32	-5.71894	1.1E-08	Yes	-1.86399	0.06232	No
COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase	128	133	85	-5.34206	9.2E-08	Yes	-6.82119	9E-12	Yes
COG0028	Thiamine pyrophosphate-requiring enzymes	314	220	113	-3.04042	0.00236	Yes	-3.11458	0.00184	Yes
COG1171	Threonine dehydratase	65	15	14	2.94487	0.00323	Yes	0.5835	0.55956	No
	Sum of all COGs involved	805	604	288	-6.36242	2E-10	Yes	-5.1355	2.8E-07	Yes
Leucine biosynthesis										
COG0059	Ketol-acid reductoisomerase	85	105	32	-5.71894	1.1E-08	Yes	-1.86399	0.06232	No
COG0473	Isocitrate/isopropylmalate dehydrogenase	111	121	67	-5.39748	6.8E-08	Yes	-5.55151	2.8E-08	Yes
COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase	128	133	85	-5.34206	9.2E-08	Yes	-6.82119	9E-12	Yes
COG0066	3-isopropylmalate dehydratase small subunit	30	52	36	-5.11662	3.1E-07	Yes	-6.25371	4E-10	Yes
COG0028	Thiamine pyrophosphate-requiring enzymes	314	220	113	-3.04042	0.00236	Yes	-3.11458	0.00184	Yes
COG0065	3-isopropylmalate dehydratase large subunit	144	107	45	-2.55431	0.01064	Yes	-1.17309	0.24076	No
	Sum of all COGs involved	1440	1120	535	-9.5164	1.8E-21	Yes	-7.72287	1.1E-14	Yes

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Methionine biosynthesis										
COG1410	Methionine synthase I, cobalamin-binding domain	177	197	71	-7.05189	1.8E-12	Yes	-3.2044	0.00135	Yes
COG0626	Cystathionine beta-lyases/cystathionine gamma-synthases	94	118	32	-6.15222	7.6E-10	Yes	-1.39706	0.16239	No
COG0620	Methionine synthase II (cobalamin-independent)	0	5	9	-2.03784	0.04157	No	-3.37804	0.00073	Yes
	Sum of all COGs involved	1420	969	340	-5.94634	2.7E-09	Yes	0.82445	0.40968	No
Phenylalanine/tyrosine biosynthesis										
COG0169	Shikimate 5-dehydrogenase	86	84	51	-3.90799	9.3E-05	Yes	-4.75912	1.9E-06	Yes
COG0077	Prephenate dehydratase	76	67	53	-2.96541	0.00302	Yes	-5.6059	2.1E-08	Yes
COG0710	3-dehydroquinate dehydratase	41	42	22	-2.94728	0.00321	Yes	-2.80375	0.00505	Yes
	Sum of all COGs involved	1029	706	456	-5.17658	2.3E-07	Yes	-10.0865	6.3E-24	Yes
Tryptophan biosynthesis										
COG0512	Anthranilate/para-aminobenzoate synthases component II	55	68	32	-4.60552	4.1E-06	Yes	-3.69697	0.00022	Yes
COG0547	Anthranilate phosphoribosyltransferase	120	117	27	-4.6009	4.2E-06	Yes	0.60214	0.54708	No
COG0159	Tryptophan synthase alpha chain	75	83	55	-4.54696	5.4E-06	Yes	-5.93449	2.9E-09	Yes
COG0147	Anthranilate/para-aminobenzoate synthases component I	93	92	41	-4.16359	3.1E-05	Yes	-2.90469	0.00368	Yes
COG0169	Shikimate 5-dehydrogenase	86	84	51	-3.90799	9.3E-05	Yes	-4.75912	1.9E-06	Yes
COG0135	Phosphoribosylanthranilate isomerase	43	46	39	-3.25483	0.00113	Yes	-5.72517	1E-08	Yes
COG0134	Indole-3-glycerol phosphate synthase	85	75	29	-3.14243	0.00168	Yes	-1.33981	0.18031	No
COG0710	3-dehydroquinate dehydratase	41	42	22	-2.94728	0.00321	Yes	-2.80375	0.00505	Yes
COG0133	Tryptophan synthase beta chain	134	100	53	-2.49968	0.01243	No	-2.68705	0.00721	Yes
	Sum of all COGs involved	1440	1145	583	-10.1353	3.9E-24	Yes	-9.72277	2.4E-22	Yes
Valine biosynthesis										
COG0059	Ketol-acid reductoisomerase	85	105	32	-5.71894	1.1E-08	Yes	-1.86399	0.06232	No
COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase	128	133	85	-5.34206	9.2E-08	Yes	-6.82119	9E-12	Yes
COG0436	Aspartate/tyrosine/aromatic aminotransferase	520	350	153	-3.28706	0.00101	Yes	-1.52434	0.12742	No
COG0028	Thiamine pyrophosphate-requiring enzymes	314	220	113	-3.04042	0.00236	Yes	-3.11458	0.00184	Yes
	Sum of all COGs involved	1260	939	427	-7.79551	6.4E-15	Yes	-5.33275	9.7E-08	Yes
Vitamin biosynthesis										
Thiamine biosynthesis										
COG1060	Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes	110	162	50	-8.17842	2.9E-16	Yes	-3.372	0.00075	Yes
COG0422	Thiamine biosynthesis protein ThiC	40	47	9	-3.64565	0.00027	Yes	0.34759	0.72815	No
COG0352	Thiamine monophosphate synthase	37	43	33	-3.44837	0.00056	Yes	-5.21717	1.8E-07	Yes

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COG0476	Dinucleotide-utilizing enzymes in molybdopterin/thiamine biosynthesis	97	72	49	-2.08872	0.03673	No	-3.88391	0.0001	Yes
COG0351	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	47	39	29	-2.01451	0.04396	No	-3.72964	0.00019	Yes
Sum of all COGs involved		523	488	240	-8.90767	5.2E-19	Yes	-7.71726	1.2E-14	Yes

Biotin

COG0502	Biotin synthase and related enzymes	53	63	44	-4.2699	2E-05	Yes	-5.77369	7.8E-09	Yes
COG0161	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	22	28	5	-3.03302	0.00242	Yes	0.23854	0.81146	No
COG0156	7-keto-8-aminopelargonate synthetase and related enzymes	96	27	16	2.96429	0.00303	Yes	1.58653	0.11262	No
Sum of all COGs involved		280	186	100	-2.32779	0.01992	Yes	-3.0082	0.00263	Yes

Cobalamin biosynthesis

COG0310	ABC-type Co2+ transport system, permease component	7	40	6	-5.77504	7.7E-09	Yes	-2.17365	0.02973	No
COG1429	Cobalamin biosynthesis protein CobN and related Mg-chelataes	13	25	10	-3.73424	0.00019	Yes	-2.61781	0.00885	No

Inorganic phosphate metabolism

COG1785	Alkaline phosphatase	40	54	18	-4.42507	9.6E-06	Yes	-1.9906	0.04653	No
COG1283	Na+/phosphate symporter	163	122	43	-2.78402	0.00537	Yes	-0.18018	0.85701	No
COG0855	Polyphosphate kinase	191	139	76	-2.73772	0.00619	Yes	-3.25971	0.00112	Yes

Sugar transporter

COG4213	ABC-type xylose transport, periplasmic component	91	113	26	-5.96143	2.5E-09	Yes	-0.49776	0.61866	No
COG0395	ABC-type sugar transport, permease component	783	357	190	2.5488	0.01081	Yes	0.65247	0.5141	No
COG3090	TRAP-type C4-dicarboxylate transport, small permease component	35	6	9	2.58176	0.00983	Yes	-0.0142	0.98867	No
COG1653	ABC-type sugar transport, periplasmic component	729	327	197	2.69079	0.00713	Yes	-0.68551	0.49302	No
COG4211	ABC-type glucose/galactose transport, permease component	46	9	0	2.76721	0.00565	Yes	2.439	0.01473	No
COG2211	Na+/melibiose symporter and related transporters	204	68	47	3.39866	0.00068	Yes	0.64641	0.51802	No
COG1129	ABC-type sugar transport, ATPase component	578	232	64	3.73491	0.00019	Yes	6.36224	2E-10	Yes
COG1175	ABC-type sugar transport, permease components	525	205	101	3.85909	0.00011	Yes	2.62438	0.00868	No
COG0738	Fucose permease	104	8	13	5.29397	1.2E-07	Yes	2.43445	0.01491	No
COG1172	Ribose/xylose/arabinose/galactoside ABC transport, permease components	249	57	34	5.80172	6.6E-09	Yes	3.43462	0.00059	Yes
Sum of all COGs involved		4651	2034	919	7.51814	5.6E-14	Yes	6.76013	1.4E-11	Yes

Glycolysis

COG0205	6-phosphofructokinase	323	271	100	-5.43506	5.5E-08	Yes	-1.66977	0.09497	No
COG0837	Glucokinase	6	15	6	-3.18651	0.00144	Yes	-2.36158	0.0182	No
COG0696	Phosphoglyceromutase	216	154	36	-2.6995	0.00694	Yes	2.38035	0.0173	No

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COG3635	Predicted phosphoglycerate mutase, AP superfamily	97	7	10	5.12615	3E-07	Yes	2.73646	0.00621	Yes

Pentose phosphate pathway

COG0021	Transketolase	104	163	61	-8.54722	1.3E-17	Yes	-5.14751	2.6E-07	Yes
COG0120	Ribose 5-phosphate isomerase	27	46	32	-4.76749	1.9E-06	Yes	-5.86838	4.4E-09	Yes
COG0362	6-phosphogluconate dehydrogenase	85	81	27	-3.70193	0.00021	Yes	-0.98074	0.32672	No
COG0363	6-phosphogluconolactonase/Glucosamine-6-P isomerase/deaminase	82	23	13	2.74817	0.00599	Yes	1.60259	0.10902	No
COG0698	Ribose 5-phosphate isomerase RpiB	79	13	9	3.94842	7.9E-05	Yes	2.2993	0.02149	No
Sum of all COGs involved		648	449	207	-4.27707	1.9E-05	Yes	-2.99373	0.00276	Yes

Hydrogenase

COG4624	Iron only hydrogenase large subunit, C-terminal domain	341	225	163	-2.41317	0.01581	No	-6.57231	5E-11	Yes
pfam02906	Fe_hyd_lg_C	364	245	217	-2.79211	0.00524	Yes	-6.91755	4.6E-12	Yes
COG3261	Ni,Fe-hydrogenase III large subunit	39	5	1	3.01321	0.00258	Yes	2.27132	0.02313	No

Pyruvate decarboxylation

COG0280	Phosphotransacetylase	103	93	26	-3.64155	0.00027	Yes	0.06017	0.95202	No
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Homoacetogenesis

COG1456	CO dehydrogenase/acetyl-CoA synthase gamma subunit (corrinoid Fe-S protein)	49	70	39	-5.25996	1.4E-07	Yes	-5.29079	1.2E-07	Yes
COG1152	CO dehydrogenase/acetyl-CoA synthase alpha subunit	12	26	8	-4.00056	6.3E-05	Yes	-2.09887	0.03583	No
COG1151	6Fe-6S prismatic cluster-containing protein	46	53	42	-3.79454	0.00015	Yes	-5.96318	2.5E-09	Yes
COG2069	CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe-S protein)	19	25	11	-2.94847	0.00319	Yes	-2.15624	0.03107	No
COG1614	CO dehydrogenase/acetyl-CoA synthase beta subunit	33	33	34	-2.53041	0.01139	No	-5.70236	1.2E-08	Yes
COG0243	Anaerobic dehydrogenases, typically selenocysteine-containing	75	7	5	4.42522	9.6E-06	Yes	2.91156	0.0036	Yes
COG1882	Pyruvate-formate lyase	207	33	30	6.47531	9.5E-11	Yes	2.90913	0.00362	Yes

Cell motility

Chemotaxis

COG0840	Methyl-accepting chemotaxis protein	825	1878	565	-34.7592	1E-264	Yes	-18.0801	4.6E-73	Yes
COG1352	Methylase of chemotaxis methyl-accepting proteins	183	143	40	-3.3725	0.00074	Yes	0.90086	0.36766	No
COG1776	Chemotaxis protein CheC, inhibitor of MCP methylation	110	29	16	3.40341	0.00067	Yes	2.11008	0.03485	No
Sum of all COGs involved		2055	2578	847	-29.1401	1E-186	Yes	-12.1467	6E-34	Yes

Flagellum structure and biogenesis

COG1344	Flagellin and related hook-associated proteins	617	533	225	-8.07159	6.9E-16	Yes	-4.5605	5.1E-06	Yes
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Function ID	Function description	Estimated gene copies ^a			<i>A. wheeleri</i> vs. laboratory <i>N. corniger</i>			<i>Amitermes</i> vs. Costa Rican <i>Nasutitermes</i> sp.		
		Ami ^b	Lab Nas ^b	CR Nas ^b	Z-LOR ^c	p-value	Significant ^d	Z-LOR ^c	p-value	Significant ^d
COG1987	Flagellar biosynthesis pathway, component FliQ	41	52	17	-4.12089	3.8E-05	Yes	-1.67477	0.09398	No
COG1580	Flagellar basal body-associated protein	28	41	23	-4.0967	4.2E-05	Yes	-4.14634	3.4E-05	Yes
COG3144	Flagellar hook-length control protein	31	41	14	-3.79215	0.00015	Yes	-1.76564	0.07746	No
COG1419	Flagellar GTP-binding protein	87	81	33	-3.57222	0.00035	Yes	-1.92771	0.05389	No
COG1749	Flagellar hook protein FlgE	167	135	46	-3.5454	0.00039	Yes	-0.44503	0.6563	No
COG1536	Flagellar motor switch protein	218	168	125	-3.53148	0.00041	Yes	-7.19951	6E-13	Yes
COG1157	Flagellar biosynthesis/type III secretory pathway ATPase	162	130	62	-3.42239	0.00062	Yes	-2.69938	0.00695	Yes
COG1886	Flagellar motor switch/type III secretory pathway protein	53	54	39	-3.31863	0.0009	Yes	-5.00956	5.5E-07	Yes
COG1766	Flagellar biosynthesis/type III secretory pathway lipoprotein	174	131	35	-2.93211	0.00337	Yes	1.29749	0.19446	No
COG1317	Flagellar biosynthesis/type III secretory pathway protein	73	57	40	-2.12466	0.03362	No	-3.87353	0.00011	Yes
COG1868	Flagellar motor switch protein	151	106	71	-2.124	0.03367	No	-4.23255	2.3E-05	Yes
COG1815	Flagellar basal body protein	74	57	34	-2.05377	0.04	No	-2.8276	0.00469	Yes
COG1334	Uncharacterized flagellar protein FlaG	25	24	24	-2.03694	0.04166	No	-4.62859	3.7E-06	Yes
COG1843	Flagellar hook capping protein	163	57	58	2.78105	0.00542	Yes	-2.15998	0.03077	No
Sum of all COGs involved		4011	2803	1401	-11.1036	1.2E-28	Yes	-10.6674	1.4E-26	Yes

Pilus

COG3063	Tfp pilus assembly protein PilF	217	207	148	-5.92919	3E-09	Yes	-9.20561	3.4E-20	Yes
COG4972	Tfp pilus assembly protein, ATPase PilM	31	38	6	-3.41528	0.00064	Yes	0.62513	0.53188	No
COG3166	Tfp pilus assembly protein PilN	2	11	1	-3.02806	0.00246	Yes	-0.54729	0.58418	No
COG3188	P pilus assembly protein, porin PapC	11	18	13	-2.91453	0.00356	Yes	-3.73605	0.00019	Yes
COG2805	Tfp pilus assembly protein, pilus retraction ATPase PilT	139	45	24	2.94472	0.00323	Yes	1.77837	0.07534	No
COG2804	Type II secretory pathway, ATPase Pule/Tfp pilus assembly pathway	226	80	45	3.19613	0.00139	Yes	1.53491	0.1248	No
Sum of all COGs involved		719	445	245	-2.4794	0.01316	Yes	-4.10584	4E-05	Yes

Defense

COG4096	Type I site-specific restriction-modification system, R (restriction) subunit	86	119	25	-6.69779	2.1E-11	Yes	-0.56326	0.57326	No
COG4452	Inner membrane protein involved in colicin E2 resistance	47	76	18	-5.94765	2.7E-09	Yes	-1.45642	0.14528	No
COG0841	Cation/multidrug efflux pump	840	580	206	-4.68651	2.8E-06	Yes	0.5424	0.58754	No
COG0286	Type I restriction-modification system methyltransferase subunit	477	216	81	2.06695	0.03874	No	3.41188	0.00065	Yes
COG4823	Abortive infection bacteriophage resistance protein	88	24	6	2.93771	0.00331	Yes	3.13399	0.00172	Yes
COG2720	Uncharacterized vancomycin resistance protein	45	2	0	3.44673	0.00057	Yes	2.41668	0.01566	No
COG1619	Uncharacterized proteins, homologs of microcin C7 resistance protein MccF	62	1	0	3.47656	0.00051	Yes	2.7419	0.00611	Yes
COG0732	Restriction endonuclease S subunits	178	50	42	4.04285	5.3E-05	Yes	0.47052	0.63799	No
COG1403	Restriction endonuclease	75	9	10	4.24516	2.2E-05	Yes	1.93544	0.05294	No
COG1136	ABC-type antimicrobial peptide transport system, ATPase component	662	223	108	6.01582	1.8E-09	Yes	4.33898	1.4E-05	Yes

Function ID	Function description	Estimated gene copies ^a			A. wheeleri vs. laboratory N. corniger			Amitermes vs. Costa Rican Nasutitermes sp.		
		Ami ^b	Lab Nas ^b	CR Nas ^b	Z-LOR ^c	p-value	Significant ^d	Z-LOR ^c	p-value	Significant ^d
COG1131	ABC-type multidrug transport system, ATPase component	740	238	107	6.87338	6.3E-12	Yes	5.52279	3.3E-08	Yes
COG2274	ABC-type bacteriocin/lantibiotic exporters	590	147	57	8.32696	8.3E-17	Yes	7.02703	2.1E-12	Yes
Sum of all COGs involved		6768	3186	1247	5.86928	4.4E-09	Yes	10.2527	1.2E-24	Yes

Sporulation

pfam05036	SPOR : Sporulation related domain	124	95	61	-2.64127	0.00826	Yes	-2.56194	0.01041	No
pfam09546	Spore_III_AE : Stage III sporulation protein AE (spore_III_AE)	27	2	1	2.69688	0.007	Yes	2.14659	0.03183	No
pfam06686	SpolIAC : Stage III sporulation protein AC/AD protein family	30	1	2	2.72976	0.00634	Yes	2.18841	0.02864	No
pfam08769	SpoOA_C : Sporulation initiation factor SpoOA C terminal	35	0	0	2.88809	0.00388	Yes	2.41132	0.01589	No
pfam03862	SpoVA : SpoVA protein	34	3	2	2.99099	0.00278	Yes	2.36854	0.01786	No
pfam07451	SpoVAD : Stage V sporulation protein AD (SpoVAD)	44	1	0	3.12265	0.00179	Yes	2.64452	0.00818	Yes
pfam07454	SpolIP : Stage II sporulation protein P (SpolIP)	45	0	0	3.14565	0.00166	Yes	2.66741	0.00764	Yes
pfam02650	HTH_WhiA : Sporulation Regulator WhiA C terminal domain	52	0	0	3.29351	0.00099	Yes	2.81456	0.00488	Yes
pfam09547	Spore_IV_A : Stage IV sporulation protein A (spore_IV_A)	57	0	0	3.38727	0.00071	Yes	2.90792	0.00364	Yes
pfam05580	SpoIVB peptidase S55: SpoIVB peptidase S55	51	2	0	3.62416	0.00029	Yes	2.7948	0.00519	Yes
pfam01943	Polysacc_synt: Spore formation	121	20	6	4.86321	1.2E-06	Yes	4.52949	5.9E-06	Yes
Sum of all pfams involved		1395	458	262	6.26254	3.8E-10	Yes	6.26254	3.8E-10	Yes

Germination

pfam03418	Peptidase_A25 : Germination protease	30	0	0	2.72976	0.00634	Yes	2.25409	0.02419	No
pfam03323	GerA : Bacillus/Clostridium GerA spore germination protein	78	1	1	3.70692	0.00021	Yes	3.22645	0.00125	Yes
Sum of all pfams involved		202	31	20	5.52594	3.3E-08	Yes	5.52594	3.3E-08	Yes

^aEstimated gene copy is the number of genes weighted by their individual read depth, which reflects population abundance.

^bAmi = *A. wheeleri*; Lab Nas = Laboratory *N. corniger*; CR Nas = Costa Rican *Nasutitermes* sp.

^cZ-LOR is the calculated as the natural logarithm of odds ratio (LOR) divided by the standard error of LOR. P-value is calculated from Z-LOR.

^dStatistical significance was determined after adjusting for multiple hypothesis test, with a false discovery rate cutoff of 0.05.

^eFunctions involved in this pathway were added up, although only the individual function with a statistical differences was shown.

^fColor indication: = function statistically overrepresented in *A. wheeleri* in both comparisons; = function statistically overrepresented in *A. wheeleri* in only one comparison, and the overrepresentation is supported by the other comparison (Z-LOR > 2); = function statistically overrepresented in *A. wheeleri* in only one comparison, and the overrepresentation is neither supported nor against by the other comparison (abs(Z-LOR) < 2); = function statistically underrepresented in *A. wheeleri* in both comparisons; = function statistically underrepresented in *A. wheeleri* in only one comparison, and the underrepresentation is supported by the other comparison (Z-LOR < -2); = function statistically underrepresented in *A. wheeleri* in only one comparison, and the underrepresentation is neither supported nor against by the other comparison; = function with statistical differences but conflicting between the two comparisons.