

Supplementary Table 2. *N. helminthoeca*-specific proteins compared to *N. sennetsu* and *N. risticii* ¹

Locus_ID	Protein Name	AA#	Main Role	Sub Role	Top Hits Species (Class, E-value) ²
NHE_RS00250	aspartate kinase domain protein	397	Amino acid biosynthesis	Aspartate family	<i>Bacillus muralis</i> (Bacilli, 3e ⁻⁵⁵)
NHE_RS02825	succinyl-diaminopimelate desuccinylase	371	Amino acid biosynthesis	Aspartate family	<i>Wolbachia</i> sp. of <i>Drosophila simulans</i> (α -Proteobacteria, 1e ⁻⁹⁴)
NHE_RS03445	dihydrodipicolinate reductase, family protein	151	Amino acid biosynthesis	Aspartate family	<i>Campylobacter ureolyticus</i> (ϵ -Proteobacteria, 2e ⁻²⁰)
NHE_RS03415	magnesium chelatase, subunit Chll family protein	1049	Biosynthesis of cofactors and prosthetic groups	Chlorophyll and bacteriochlorophyll	
NHE_RS00710	UDP-N-acetylglucosamine diphosphorylase (glucosamine-1-phosphate N-acetyltransferase)	432	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Paracoccus tibetensis</i> (α -Proteobacteria, 4e ⁻¹²²)
NHE_RS03095	phosphoglucosamine mutase	439	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Magnetospirillum marisnigri</i> (α -Proteobacteria, 2e ⁻¹⁴³)
NHE_RS01455	penicillin binding transpeptidase domain protein	528	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Ca. Neoehrlichia lotoris</i> (α -Proteobacteria, 2e ⁻¹²⁶)
NHE_RS03220	rod shape-determining MreC family protein	256	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	
NHE_RS02450	D-alanyl-D-alanine carboxypeptidase family protein	399	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Wolbachia</i> sp. of <i>Cimex lectularius</i> (α -Proteobacteria, e ⁻¹¹⁴)
NHE_RS02495	D-ala D-ala ligase family protein	313	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Wolbachia</i> sp. of <i>Cimex lectularius</i> (α -Proteobacteria, 5e ⁻⁶⁰)
NHE_RS03375	UDP-N-acetylmuramate--alanine ligase	424	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Thermodesulfobivrio</i> sp. N1 (Nitrospirales, 2e ⁻⁷⁹)
NHE_RS04135	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	418	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Ca. Pelagibacter</i> sp. IMCC9063 (α -Proteobacteria, 3e ⁻¹⁰⁹)
NHE_RS02795	phospho-N-acetylmuramoyl-pentapeptide-transferase	324	Cell envelope	Biosynthesis and degradation of murein	<i>Bacillus bataviensis</i> (Bacilli, 4e ⁻⁶⁸)

¹ *N. helminthoeca*-specific proteins were identified by comparison with *N. sennetsu* and *N. risticii* protein databases using BLASTP algorithm with E-value < 1e⁻¹⁰.

² *N. helminthoeca*-specific proteins were blasted against NCBI protein database NR excluding *Neorickettsia* spp. with E-value < 1e⁻¹⁰. The species, class, and E-value of the top matches to the *N. helminthoeca* proteins were listed. Blank fields, no matches were identified based on the search criteria.

				sacculus and peptidoglycan	
NHE_RS02980	D-alanyl-D-alanine carboxypeptidase family protein	284	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Crenothrix polyspora</i> (γ -Proteobacteria, 8e ⁶⁸)
NHE_RS00945	UDP-N-acetylmuramoylalanine--D-glutamate ligase	468	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Robiginitomaculum antarcticum</i> (α -Proteobacteria, 3e ⁵⁷)
NHE_RS00380	undecaprenyldiphospho-muramoylpentapeptide β -N-acetyl-glucosaminyl-transferase	338	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Caedibacter varicaedens</i> (α -Proteobacteria, 3e ⁵⁷)
NHE_RS03115	penicillin binding transpeptidase domain protein	566	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Anaplasma marginale</i> (α -Proteobacteria, 2e ¹⁰⁸)
NHE_RS03175	diaminopimelate epimerase DapF	266	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Prochlorococcus marinus</i> (Synechococcales, 9e ³⁰)
NHE_RS03990	D-alanine aminotransferase	310	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	<i>Ralstonia solanacearum</i> (β -Proteobacteria, 1e ⁵⁸)
NHE_RS01430	putative membrane protein	164	Cell envelope	Other	
NHE_RS04200	rare lipoA family protein	226	Cell envelope	Other	<i>Wolbachia pipientis</i> (α -Proteobacteria, 1e ⁴³)
NHE_RS01810	cell division protein FtsW	369	Cellular processes	Cell division	<i>Caedibacter varicaedens</i> (α -Proteobacteria, 4e ⁹¹)
NHE_RS02385	rod shape-determining protein RodA	377	Cellular processes	Cell division	Rhodospirillaceae bacterium BRH_c57 (α -Proteobacteria, 4e ⁷⁷)
NHE_RS02100	hydroxyacylglutathione hydrolase	247	Cellular processes	Detoxification	<i>Vibrio halioticoli</i> (γ -Proteobacteria, 2e ⁶⁷)
NHE_RS00090	carbonic anhydrase family protein	213	Central intermediary metabolism	Other	<i>Desulfovibrio vulgaris</i> (δ -Proteobacteria, 1e ⁶²)
NHE_RS01115	ribosomal protein L29	63	Protein synthesis	Ribosomal proteins: synthesis and modification	
NHE_RS03975	ribosomal L36 family protein	44	Protein synthesis	Ribosomal proteins: synthesis and modification	
NHE_RS03330	putative Mg chelatase-like domain protein	116	Transport and binding proteins	Unknown substrate	
NHE_RS03535	tol-Pal system beta propeller repeat protein TolB	426	Transport and binding proteins	Other	<i>Thalassospira profundimaris</i> (α -Proteobacteria, 1e ¹²⁶)
NHE_RS02060	hexapeptide transferase family protein	611	Transport and binding proteins	Unknown substrate	

NHE_RS03955	biopolymer transport ExbD/TolR family protein	136	Transport and binding proteins	Cations and iron carrying compounds	<i>Xanthobacter</i> sp. 126 (α -Proteobacteria, $2e^{-29}$)
NHE_RS03960	motA/TolQ/ExbB proton channel family protein	218	Transport and binding proteins	Cations and iron carrying compounds	<i>Rickettsia prowazekii</i> (α -Proteobacteria, $1e^{-42}$)
NHE_RS02515	BON domain protein	535	Unknown function	General	
NHE_RS01320	quinolinate synthetase A family protein	236	Unknown function	Enzymes of unknown specificity	
NHE_RS04220	bacterial SH3 domain protein	148	Unknown function	General	<i>Wolbachia</i> sp. of <i>Cimex lectularius</i> (α -Proteobacteria, $5e^{-20}$)
NHE_RS01565	bacterial transferase hexapeptide family protein	280	Unknown function	Enzymes of unknown specificity	<i>Ehrlichia chaffeensis</i> (α -Proteobacteria, $7e^{-113}$)
NHE_RS02225	inhibitor of apoptosis-promoting Bax1 family protein	321	Unclassified		
NHE_RS00600	ccmB family protein	203	Unclassified		
NHE_RS00220	conserved hypothetical protein	841	Hypothetical proteins	Conserved	<i>Klebsormidium flaccidum</i> (Streptophyta, $8e^{-35}$)
NHE_RS00330	hypothetical protein	123	Unknown function	General	
NHE_RS01050	hypothetical protein	259	Hypothetical proteins	General	
NHE_RS03510	hypothetical protein	407	Hypothetical proteins	General	
NHE_RS00300	hypothetical protein	67	Hypothetical proteins	General	
NHE_RS00555	hypothetical protein	224	Hypothetical proteins	General	
NHE_RS03875	hypothetical protein	84	Hypothetical proteins	General	
NHE_RS00420	hypothetical protein	257	Hypothetical proteins	General	
NHE_RS02660	hypothetical protein	401	Hypothetical proteins	General	
NHE_RS02195	hypothetical protein	59	Hypothetical proteins	General	
NHE_RS00350	hypothetical protein	208	Hypothetical proteins	General	
NHE_RS01395	hypothetical protein	60	Hypothetical proteins	General	
NHE_RS03520	hypothetical protein	403	Hypothetical proteins	General	
NHE_RS00320	hypothetical protein	272	Hypothetical proteins	General	
NHE_RS03885	hypothetical protein	70	Hypothetical proteins	General	
NHE_RS02765	hypothetical protein	133	Hypothetical proteins	General	
NHE_RS00425	hypothetical protein	286	Hypothetical proteins	General	
NHE_RS00665	hypothetical protein	292	Hypothetical proteins	General	
NHE_RS02365	hypothetical protein	434	Hypothetical proteins	General	

NHE_RS00355	hypothetical protein	118	Hypothetical proteins	General	
NHE_RS01500	hypothetical protein	287	Hypothetical proteins	General	
NHE_RS03525	hypothetical protein	601	Hypothetical proteins	General	
NHE_RS00325	hypothetical protein	201	Hypothetical proteins	General	
NHE_RS03925	hypothetical protein	99	Hypothetical proteins	General	
NHE_RS03130	hypothetical protein	60	Hypothetical proteins	General	
NHE_RS00430	hypothetical protein	91	Hypothetical proteins	General	
NHE_RS00725	hypothetical protein	138	Hypothetical proteins	General	
NHE_RS00360	hypothetical protein	98	Hypothetical proteins	General	
NHE_RS02570	hypothetical protein	711	Hypothetical proteins	General	
NHE_RS03950	hypothetical protein	285	Hypothetical proteins	General	Ca. Neoehrlichia lotoris (α -Proteobacteria, 1e ⁻³¹)
NHE_RS01550	hypothetical protein	93	Hypothetical proteins	General	
NHE_RS03860	hypothetical protein	126	Hypothetical proteins	General	
NHE_RS00335	hypothetical protein	92	Hypothetical proteins	General	
NHE_RS00435	hypothetical protein	111	Hypothetical proteins	General	
NHE_RS00755	hypothetical protein	74	Hypothetical proteins	General	
NHE_RS00365	hypothetical protein	260	Hypothetical proteins	General	
NHE_RS02575	hypothetical protein	561	Hypothetical proteins	General	
NHE_RS04070	hypothetical protein	441	Hypothetical proteins	General	
NHE_RS01935	hypothetical protein	182	Hypothetical proteins	General	
NHE_RS03865	hypothetical protein	70	Hypothetical proteins	General	
NHE_RS00340	hypothetical protein	247	Hypothetical proteins	General	
NHE_RS00865	hypothetical protein	141	Hypothetical proteins	General	
NHE_RS03180	hypothetical protein	103	Hypothetical proteins	General	
NHE_RS00540	hypothetical protein	373	Hypothetical proteins	General	
NHE_RS00415	hypothetical protein	277	Hypothetical proteins	General	
NHE_RS02580	hypothetical protein	699	Hypothetical proteins	General	
NHE_RS04100	hypothetical protein	101	Hypothetical proteins	General	
NHE_RS02145	hypothetical protein	93	Hypothetical proteins	General	
NHE_RS00345	hypothetical protein	201	Hypothetical proteins	General	

NHE_RS00440	hypothetical protein	163	Unknown function	General
NHE_RS00445	hypothetical protein	152	Unknown function	General