

Table S1. Sequences of metatranscriptome cDNA reads with top matches against nitrogen fixation related mRNAs of eubacteria (reads 1-33) or archaea (reads 34-50). The reads are numbered consecutively, followed by the actual sequences and the IDs of top matches in blastX and blastN-searches against genbank, including the positions within the respective matching protein or DNA sequences.

No.	Sequence	Top hit blastX	from to blastX hit	Top hit blastN	from to blastN hit
1	> c1 HWI-ST1172:64:D1FDDACXX:8:1201:16124:50639_2:N:0:CTCACG TGGGCACATCTTCTCCTATGGTTTCACTCAGGCAGGTTGTAGCTATGCTATGAGTTCGGGATGTACTGCTTATTATG TTTTCAACGGCGAGTTTAA	putative Nitrogenase molybdenum-iron protein beta chain [delta proteobacteriu	80-112	Chlorobium limicola DSM 245, complete genome	751818-751911
2	> c1 HWI-ST1172:64:D1FDDACXX:8:1202:18787:93508_1:N:0:ATCACG GCCCGGAGAAAGCGCTCCTTATGTCCAGGTATATGAAGCGCATCTTATGGCCCGTGTATCAGGTGAAGGGCGTAG GCAATAGGGGACAAAACCACC	protein NifE [Desulfobacterium autotrophicum HRM2]	47-79	Dehalococcoides ethenogenes 195, complete genome	1055736-1055836
3	> c1 HWI-ST1172:64:D1FDDACXX:8:1203:13160:84401_1:N:0:ATCACG TTCAAATGCAAACTCTCGGACAGAAAATACGACTGTGTAAATGAAAGCAGACGGGTGTAACAGCCGAGTTCTGATTCGG AGACAGGGCATGCCCTATCTT	nitrogenase cofactor biosynthesis protein NifB [delta proteobacterium NaphS2]	31-63	Clostridium sp. BNL1100, complete genome	2950235-2950175
4	> c1 HWI-ST1172:64:D1FDDACXX:8:1206:19713:16690_1:N:0:ATCGCG GTTTACGGTTTCAAGGTTGTTCCACCTATATCAGAAAGATATCTGATCAGCAATTTTAATGAACCTGTAGATATTGCAT GCTCAAATTTTACTGAAGAAA	putative Nitrogenase molybdenum-iron protein beta chain [delta proteobacteriu	38 - 70	Desulfobacterium autotrophicum HRM2, complete genome	1112554-1112648
5	> c1 HWI-ST1172:64:D1FDDACXX:8:1208:7458:38650_1:N:0:ATCACG CTCAAACCTGAAGATAGACCTCTTTTGGGAGATGTATCATTCGCTGTAACCTGCCAGGGATATTTTCTTCATCGTT GTGGTCACAGAAATCAAAATCCC	nitrogenase MoFe cofactor biosynthesis protein NifE [Dehalococcoides ethenog	403-434	Spirochaeta smaragdinae DSM 11293, complete genome	3217549-3217627
6	> c1 HWI-ST1172:64:D1FDDACXX:8:1303:9743:72998_1:N:0:CTCACG TAAGGATCTCGACATGCCCTCCGGCGCTTAGGAAATGATCTTAAACCAGGGGATCCGATATTTTTCTCCAATCATCTCCG CCACATAGTTGATTGACCTGT	nitrogenase molybdenum-iron protein subunit alpha [Treponema primitia ZAS-2	277-309	Treponema azotonutricium ZAS-9, complete genome	2964943-2965025
7	> c1 HWI-ST1172:64:D1FDDACXX:8:1308:11447:49253_1:N:0:ATCACG GATGTTGATTTCTGTTGCAAACTGTAACTGAAGAAAAGGGGATCCGGTCTTCCGGTTCATTCTGAAGGATCAAGGG AACTAAAAGGACGGATACAA	nitrogenase MoFe cofactor biosynthesis protein NifE [Chlorobium phaeobactero	136-168	Chlorobium phaeobacteroides DSM 266, complete genome	840912-840812
8	> c1 HWI-ST1172:64:D1FDDACXX:8:1314:1952:14240_1:N:0:ATTACG GTTCAAACCTCAATACGGTTTTTCTGTTATCTCCGCCCTTTGAACCATGTTGTCCCGGGAACAAAATGAATCATGTGG GATCCAAAGCTGGTCGGCAAAAC	Nitrogenase iron protein [uncultured Desulfobacterium sp.]	187-219	Desulfotomaculum carboxydivorans CO-1-SRB, complete genome	1251590-1251493
9	> c1 HWI-ST1172:64:D1FDDACXX:8:2114:13216:59122_1:N:0:ATCACG TCAACAGATCCTGTGCCGACAGCATGGATAAGGATTCACAGCGCCCTGTATCCATCTTTTTTAGTTCCCTTGAAGCC TTCAGATGAACAGGAAAGAAC	nitrogenase MoFe cofactor biosynthesis protein NifE [Prosthecochloris aestuarii	152-183	Prosthecochloris aestuarii DSM 271, complete genome	1776253-1776159
10	> c1 HWI-ST1172:64:D1FDDACXX:8:2114:13216:59122_2:N:0:ATCACG CTCGGGCCGGAACTGCACAGGATGAGTTTTTCAACCGATCTCAGGGAGAGAGATATTATCTTCGGGGCCGAGAAAAAAT TGTACGCTTCACTGTGCGCAGC	nitrogenase MoFe cofactor biosynthesis protein NifE [Desulfovibrio africanus str	77-109	Desulfovibrio magneticus RS-1 DNA, complete genome	1950009-1949932
11	> c1 HWI-ST1172:64:D1FDDACXX:8:2209:8097:20415_1:N:0:ATCACG CATACAAACTGGGGATTGGATTCTGTGACCACAACCATGAAAGAAAATATCCCTGGCAGGTTGCAGCGGAATGATCATT CTCGCAAAAGAGGCTTATCTT	nitrogenase MoFe cofactor biosynthesis protein NifE [Spirochaeta smaragdinae I	405-437	Spirochaeta smaragdinae DSM 11293, complete genome	3217643-3217549
12	> c1 HWI-ST1172:64:D1FDDACXX:8:2210:17672:39029_1:N:0:ATCACG ATGTGTTTCTCGCGTTCCAGGGTGGTTTTGTACCCATTTGCCGACGCCCTTCACTCATACAGGGCCCATAGGATGGC CTTATATACCTGGACATAA	nitrogenase MoFe cofactor biosynthesis protein NifE [delta proteobacterium Naj	40-72	Desulfobacterium autotrophicum HRM2, complete genome	1111143-1111241
13	> c1 HWI-ST1172:64:D1FDDACXX:8:2212:11497:68723_1:N:0:ATCACG AAACAAGTGGCGCATAACTATAATTTCCACGCTCAGCGGCAACTCAAGCGTTGATTTTTTGCAAAATCCACACAGCAG ACTTAAATCTGATTATGTGCC	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph	255-286	Spirochaeta smaragdinae DSM 11293, complete genome	3221175-3221081
14	> c1 HWI-ST1172:64:D1FDDACXX:8:2214:19404:9694_1:N:0:ATCGCG ATAGGACATGTACTGTCTCGGAGTCAAGAACAGCGCTTGTACACCCGGCTGTCTTTCATTTACACATTCGTATTTTCTGT CGAAGTATTTGCAATGAATAT	nitrogenase cofactor biosynthesis protein NifB [delta proteobacterium NaphS2]	30-62	Clostridium sp. BNL1100, complete genome	2950175-2950240
15	> c1 HWI-ST1172:64:D1FDDACXX:8:2216:16216:81037_2:N:0:ATCACG TCTCGGGCAGATCATCACCAGGAAATGTTCAGAGAGATGGGATGACACCTTTTGGCAGGTTACGAGTTCCGGCACAG GGATGATTACGAAGGGAGGCT	nitrogenase molybdenum-iron protein subunit alpha [Pelodictyon phaeoclathrat	355-387	Chlorobaculum parvum NCIB 8327, complete genome	1772879-1772973
16	> c1 HWI-ST1172:64:D1FDDACXX:8:2303:15514:26630_1:N:0:ATCACG ATGGTCCCATCGGCTGTGGTTTCTATAGCTGGCTTACCOCAGGAAACCAGACCGATCCTTCCACGACCCCGGATGGCCAT CATTTCTGAACACTACTGTTTT	Nitrogenase molybdenum-iron protein alpha chain [uncultured Desulfobacteriu	99-131	Desulfatibacillum alkenivorans AK-01, complete genome	2006482-2006384
17	> c1 HWI-ST1172:64:D1FDDACXX:8:2306:19562:46993_1:N:0:CTCACG ATCTCCAGAGAGGGCTTGTGCTATGGGGCTGCAAGGTTGTGTGATGGGGCCGACAGAGACATAATCAACCTGACACA TGTTCCCATCGGCTGTGGTTT	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph	70-102	Chlorobium phaeovibrioides DSM 265, complete genome	1502885-1502985
18	> c1 HWI-ST1172:64:D1FDDACXX:8:2309:9871:35025_1:N:0:ATCACG CAAGGGTGTGTGATGGGGCCGACAGAGACATAATCAACCTGACACATGGTCCCATCGGCTGTGGTTTCTATAGCTGGC TTACCCGGGAAACAGACTG	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph	81-113	Chlorobium phaeovibrioides DSM 265, complete genome	1502917-1503015
19	> c1 HWI-ST1172:64:D1FDDACXX:8:1112:19397:45582_1:N:0:ATCGCG TATCCAGGAGGCTTACGATATATTTCAAGCCAAAGATGATTTCCGATTCGCCACCTGTCCCTGTGGCCCTATTCGGAGAG ATGCCATGCGGTCAACAGG	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph	150-182	Desulfovibrio desulfuricans ND132, complete genome	1436104-1436006
20	> c1 HWI-ST1172:64:D1FDDACXX:8:1115:16099:37352_1:N:0:ATCACG TGCGTTTGGAGAAGCAAAAAGCTTATTATGTTTTTACGACGTTTTGGCGCAGCTGGTTCGCGCGGGTTTCCCATGC CGATGAGAGAGGGTAAGGCAA	nitrogenase (EC 1.18.6.1) iron protein NifH - Halodule wrightii rhot zhosphere t	69-101	Uncultured microorganism clone BCa2c_nif3d NifH (nifH) gene, partial cds	82-2
21	> c1 HWI-ST1172:64:D1FDDACXX:8:1209:13980:50794_1:N:0:ATCACG CCCAGGTGATACCCGCAACCCGATGGGGCCATGACCAGGTGACGGGCATCAGTATGGGGTATAGAGGACAACCCGTGAG CCGCAAAAACGACAGCCCTC	Nitrogenase MoFe cofactor biosynthesis protein NifE, partial [uncultured bacteri	38-70	Desulfovibrio salexigenes DSM 2638, complete genome	481864-481964
22	> c1 HWI-ST1172:64:D1FDDACXX:8:1303:14763:60218_1:N:0:CTCACG GGACAGGTGGCAATACGAAATCATCTTTGGCTGAATATATCTGAAGCTTACTGAATCGCGCTCTTAATTTTTTTTC	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph	137-168	Desulfovibrio salexigenes DSM 2638, complete genome	3217643-3217549

23	ACCGCCAAAAATAATCTCTAT > cl HWI-ST1172:64:D1FDDACXX:8:1310:10182:13459_1:N:0:ATTACG GGGGCTGGCAATAGGGTACAAAACAACCCCTGGAAACCGCAAAAAACATGCTCTCTGACTCAGCGAACCGCGGAGACT TTGTATTGGAGTAAAAATA	nitrogenase MoFe cofactor biosynthesis protein NifE [Chloroherpeton thalassium Desulfovibrio salexigenis DSM 2638, complete genome Sequence ID: ref YP_001995941.1	27-57	Sequence ID: gb CP001649.1	486881-486978
24	> cl HWI-ST1172:64:D1FDDACXX:8:2201:20152:62271_1:N:0:ATCAGC AAGCGGGACCATAGTCAATAGACACATAAGCCAGTACGAACTGAAAGGCTGTGAAACCTACAAACCGCGAGTATTCT GCGCGGCATAAAAGAAAAAT	nitrogenase molybdenum-iron protein subunit alpha [Syntrophobacter fumaroxi Syntrophobacter fumaroxidans MPOB, complete genome Sequence ID: ref YP_845145.1	456-487	Sequence ID: gb CP000478.1	481909-481984
25	> cl HWI-ST1172:64:D1FDDACXX:8:2212:8973:2829_1:N:0:ATCAGC AATTTGGCAGAACCCTGCCTGCCTCGTAATCATCCCTGTGGCGCAACTCGTAACCTGCGCAAAAAGTTATCATCCCAT TCCCTGAACATTTCTGGTAA	nitrogenase molybdenum-iron protein alpha chain [Desulfocapsa sulfexigenis DS1 Desulfovibrio magneticus RS-1 DNA, complete genome Sequence ID: ref YP_007466574.1	365-397	Sequence ID: dbj AP010904.1	1252242-1252147
26	> cl HWI-ST1172:64:D1FDDACXX:8:2305:14913:68840_1:N:0:ATCAGC CTGTTTACCATCCGGTCGATTTCCGTGTAATAAATTAATGGCACCCCTGTAAGCTGCCGCGTTATCATAACT GTGGAGCTGTTTCATTGGGAT	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph Desulfatibacillum alkenivorans AK-01, complete genome Sequence ID: ref ZP_07199529.1	501-533	Sequence ID: gb CP001322.1	2318740-2318834
27	> cl HWI-ST1172:64:D1FDDACXX:8:1210:17881:63905_1:N:0:ATTACG TCACAGCCGGCACCAAGGAGGACTATGAGAACTGGCCGAGATTACGACCCGGCCACCATCATTTGTGATGACTCAAA TCCTCTGGAACTGACCTCCTT	nitrogenase MoFe cofactor biosynthesis protein NifE [Desulfurivibrio alkaliphilus Desulfobulbus propionicus DSM 2032, complete genome Sequence ID: ref YP_003691755.1	359-391	Sequence ID: gb CP002364.1	2005173-2005273
28	> cl HWI-ST1172:64:D1FDDACXX:8:2210:12394:33725_1:N:0:ATTACG CTGTCTGACTACTTTCAAATTTGGCAGAACCCTGCCTCCCTCGTAATCATCCCTGTGGCGGAACTCGTAACCTGCGCA AAAGTTGTCAATCCCATCTC	nitrogenase molybdenum-iron protein alpha chain [Chlorobaculum parvum NCIE Desulfocapsa sulfexigenis DSM 10523, complete genome Sequence ID: ref YP_001999218.1	366-398	Sequence ID: gb CP003985.1	3117364-3117264
29	> cl HWI-ST1172:64:D1FDDACXX:8:1201:16124:50639_1:N:0:CTCAGC GTCCACCATATACAAGATATCTGATCAGCCATTTAATGAACCTGTAGATATTTGCATGCTCAAATTTACTGAAGAA ACAGCCGTATTCGGAGGAGGC	putative Nitrogenase molybdenum-iron protein beta chain [delta proteobacterium Desulfobacterium autotrophicum HRM2, complete genome Sequence ID: ref ZP_07199543.1	45-77	Sequence ID: gb CP001087.1	389846-389850
30	> cl HWI-ST1172:64:D1FDDACXX:8:1203:6694:59780_1:N:0:ATCAGC TATAGTTATGCGCCACTTGTTTAATACTCTCTCTATTTCAAAGGAGTCTCCGCCATATATATACTCTCCAAGGATTGA CCCTGTAATCACCCTCCTTAA	nitrogenase molybdenum-iron protein subunit alpha [Syntrophobacter fumaroxi Uncultured Desulfobacterium sp. genomic DNA, clone contig00524 Sequence ID: ref YP_845145.1	223-255	Sequence ID: emb FR695864.1	112572-112669
31	> cl HWI-ST1172:64:D1FDDACXX:8:1205:4224:16940_1:N:0:ATCAGC FTGACCTGTGGCACATAATCAGATTTAAGTCTGCTGTGGGAGTTTCAAATAATCGACGCTCGAATTGCCCTGAAAC GTGGAAATTTATAGTTATGCC	nitrogenase molybdenum-iron protein alpha chain [delta proteobacterium Naph Desulfatibacillum alkenivorans AK-01, complete genome Sequence ID: ref ZP_07199529.1	257-289	Sequence ID: gb CP001322.1	133288-133380
32	> cl HWI-ST1172:64:D1FDDACXX:8:2203:17575:34637_1:N:0:ATCACA TTGAGCATGCAATATCTACAGGTTTCATTAATAAGCTGATCAGATATCTCTGATATAGGTGGAACAACCTTTGTGAAC GTGAAGCAGTGAATCGACT	putative Nitrogenase molybdenum-iron protein beta chain [delta proteobacterium Desulfatibacillum alkenivorans AK-01, complete genome Sequence ID: ref ZP_07199543.1	34-65	Sequence ID: gb CP001322.1	2005910-2005979
33	> cl HWI-ST1172:64:D1FDDACXX:8:2215:13443:71762_1:N:0:ATTACG GTAATAATACCCCTGCCGCGCACCCACCCCGGCTCAGGCCCTCTGATTCAGTACATAAAGTGCCCGGAAACCTGT TTTGGGAGATCGGAAGAGCAC	nitrogenase iron protein [delta proteobacterium NaphS2] Uncultured microorganism clone ERB_1_H10 NifH (nifH) gene, partial cds Sequence ID: ref ZP_07199542.1	73-100	Sequence ID: gb GQ452703.1	2001983-2002076
34	> cl HWI-ST1172:64:D1FDDACXX:8:1103:17995:9909_1:N:0:ATCAGC CCCAGCCTGGCAAAACCCCTGCAGATATTATGGCCGCATACAGTGGCATGTATTCTCCGGAAGTGAGCACATATGTATC ATTACCAGCCCTTGGCGGAT	nitrogenase subunit NifH (ATPase) [Methanomethylovarans hollandica DSM 159 Methanobolus psychrophilus R15, complete genome Sequence ID: ref ZP_07199542.1	134-166	Sequence ID: gb GQ452703.1	275-189 954084-954177
35	> cl HWI-ST1172:64:D1FDDACXX:8:1105:10473:15278_1:N:0:ATCACA GACTGTGACCTGATCATATATGACGTGCCAGGGGATATTGTGTGGCGGGGTTGCAGCACCGTCCGCAAGGGGCTGGT GAATGATACATATGTGCTGAC	nitrogenase subunit NifH (ATPase) [Methanomethylovarans hollandica DSM 159 Methanohalophilus mahii DSM 5219, complete genome Sequence ID: ref ZP_07199542.1	117-149	Sequence ID: gb GQ452703.1	1416501-1416595
36	> cl HWI-ST1172:64:D1FDDACXX:8:1113:5135:77070_1:N:0:ATCAGC ACCCTTGACGATATTATTTGGCCGCATACAGTGGCATGTATTCTCCGAGCGTGAGCACATATGTATCATTCACCAGCCCT TGCGGATCGGGGCTGCAAAAC	nitrogenase subunit NifH (ATPase) [Methanomethylovarans hollandica DSM 159 Methanohalophilus mahii DSM 5219, complete genome Sequence ID: ref ZP_07199542.1	134-166	Sequence ID: gb GQ452703.1	1416643-1416546
37	> cl HWI-ST1172:64:D1FDDACXX:8:1202:12813:56617_1:N:0:ATTACG GAGACGCCAAAGTACGACCTGTGTGTGGGGCGACCCGATGGACCCGGCTGCTACTGTACGCCAAACACCTGCTCCG TGGCATCATGGATCGGATCAC	nitrogenase iron protein [Methanosarcina mazei Go1] Methanobolus psychrophilus R15, complete genome Sequence ID: ref ZP_07199542.1	93-125	Sequence ID: gb GQ452703.1	2769733-2769647
38	> cl HWI-ST1172:64:D1FDDACXX:8:1303:12775:13410_1:N:0:ATCAGC TATCATTCACCAGCCCTTGGCGGATCGGTGTCGAAACCCGCGCACACAATATCCCTGGCAGCTCATATATGATCAGG TCACAGTCCCTGATGACAGT	Mo-nitrogenase iron protein subunit NifH [Methanohalophilus mahii DSM 5219] Methanohalophilus mahii DSM 5219, complete genome Sequence ID: ref YP_003542556.1	116-146	Sequence ID: gb GQ452703.1	1416580-1416501
39	> cl HWI-ST1172:64:D1FDDACXX:8:1303:14625:35142_1:N:0:ATCACA ATGTGCTCACTTCCGGAGAATACATGCCACTGTATGGCGCAATAATATCTGCAAGGGTTTGGCAGGCTGGGCAACCC TTAAACGGTGTGATCTGCCAAC	Nitrogenase subunit NifH, type 1 [Methanosarcina mazei Tuc01] Methanobolus psychrophilus R15, complete genome Sequence ID: ref ZP_07199542.1	149-181	Sequence ID: gb GQ452703.1	954144-954084
40	> cl HWI-ST1172:64:D1FDDACXX:8:2103:13393:53822_1:N:0:ATCCCG AAAACCCCTGCAGATATTATTTGGCCGCATACAGTGGCATGTATTCTCCGGAAGTGAGCACATATGTATCATTCACCAGCC CCTTGGCGGATCGGGGCTGCAA	nitrogenase subunit NifH (ATPase) [Methanomethylovarans hollandica DSM 159 Methanohalophilus mahii DSM 5219, complete genome Sequence ID: ref ZP_07199542.1	136-167	Sequence ID: gb GQ452703.1	1416643-1416552
41	> cl HWI-ST1172:64:D1FDDACXX:8:2110:9073:85238_2:N:0:ATCAGC AATACTCCGCTTAGCGGTGTGATATGCAATGCCCGCAATGTCAGCCGTGAAGAAGAGATCGTTAGCAAAATTTGGCGAGGA GATAGGGAGCGAACTGATATC	nitrogenase [Methanosalsum zhiinae DSM 4017] Methanomethylovarans hollandica DSM 15978, complete genome Sequence ID: ref ZP_07199542.1	171-203	Sequence ID: gb GQ452703.1	540698-540610
42	> cl HWI-ST1172:64:D1FDDACXX:8:2215:2022:42394_1:N:0:CTCAGC GAGCAGTGTGATGGACGAATCCGCTTTCGGGTCGACGCTATGATGGTGACACTATATCCCTCATCTGCACATGCCGAG CCACATTTGGACGCTGTAATC	dinitrogenase reductase-like protein [uncultured archaeon] Uncultured microorganism clone E504-90 putative nitrogenase reductase (nifH) gene, partial cds Sequence ID: ref ZP_07199542.1	1 to 33	Sequence ID: gb GQ452703.1	122-25
43	> cl HWI-ST1172:64:D1FDDACXX:8:2115:11360:38121_1:N:0:ATCAGC TTCAAATGATCAAATGTTTCGTCATTTGGCAAGAGGCTCCCAAGGCTCCGATTTTATGAATGGGTGCT CCTTAATGACATCCCTTACTT	radical SAM domain-containing protein [Methanohalobium evestigatum Z-7303] Methanosarcina mazei strain Goe1, complete genome Sequence ID: ref YP_003726787.1	83-114	Sequence ID: gb GQ452703.1	906592-906518
44	> cl HWI-ST1172:64:D1FDDACXX:8:1102:10301:73615_1:N:0:ATCAGC GTGGAAATCTTCTGACGATCTTGTAGGCGACGATTTATGCCCTGCTGCACAGCCGATACCTGGCTCGGGACACCCGAC	putative nitrogenase reductase, partial [uncultured microorganism] Uncultured microorganism clone E505-12 putative nitrogenase reductase (nifH) gene, partial cds Sequence ID: gb ADX43181.1	70-102	Sequence ID: gb GQ452703.1	

<p>45</p> <p>TTC AACACACCTGACACCTTT</p> <p>>1c1 HWI-ST1172:64:D1FDDACXX:8:1304:3277:40580_1:N:0:ATCAGC</p> <p>CATAACTGTGGGGATGCGATGCCCCCAAGCAGTGTGATGGACGAATCGCTCTTCGGGTGCGAGCCTATGATGGTGACAC</p> <p>TATATCCCTCATCTGCACATG</p>	<p>putative nitrogenase reductase, partial [uncultured microorganism]</p> <p>Sequence ID: gb ADX43560.1 </p> <p>18-50</p>	<p>305-208</p> <p>Uncultured microorganism clone E504-87 putative nitrogenase reductase (nifH) gene, partial cds</p> <p>Sequence ID: gb HQ224300.1 </p> <p>150-50</p>
<p>46</p> <p>>1c1 HWI-ST1172:64:D1FDDACXX:8:1312:6240:73415_1:N:0:ATCAGC</p> <p>AAATGTGTGGAAGTAGGTGGACCCGAGCCGGGAATAGGATGCCGAGCAGCGGGATCATTGTGGCTATCCAGAAACTTAA</p> <p>GAAGATATCAAAGGTACAGGA</p>	<p>dinitrogenase reductase-like protein [uncultured archaeon]</p> <p>Sequence ID: dbj BAF96825.1 </p> <p>65-97</p>	<p>Uncultured archaeon nifH gene for dinitrogenase reductase-like protein, partial cds, clone: K8MV-C22nifH_05</p> <p>Sequence ID: dbj AB362397.1 </p> <p>194-294</p>
<p>47</p> <p>>1c1 HWI-ST1172:64:D1FDDACXX:8:2114:4888:96964_1:N:0:ATCAGC</p> <p>GAGATCACTGAAAAGGATGTGGTATTTGAGGGTTACAAAGGTGCAGGTGTGAAGTGGTGGTCCCGAGCCAGGTAT</p> <p>CGGCTGTGCGGGCAGGGCAG</p>	<p>dinitrogenase reductase-like protein [uncultured archaeon]</p> <p>Sequence ID: dbj BAF96825.1 </p> <p>50-82</p>	<p>Uncultured archaeon nifH gene for dinitrogenase reductase-like protein, partial cds, clone: K8MV-C22nifH_05</p> <p>Sequence ID: dbj AB362397.1 </p> <p>149-240</p>
<p>48</p> <p>>1c1 HWI-ST1172:64:D1FDDACXX:8:2114:5543:63174_1:N:0:ATCAGC</p> <p>TCACCACATCATAGTTCTTAACAAGGCGATCCATGATACCACGAAGCAGGTGTTTGCATAGCAGTAACATCCCGRACCT</p> <p>TCGGGACGCCCATCACAAGC</p>	<p>Nitrogenase iron protein [Methanosarcina mazei Go1]</p> <p>Sequence ID: gb AAM31782.1 </p> <p>100-132</p>	<p>Methanococcoides burtonii DSM 6242, complete genome</p> <p>Sequence ID: gb CP000300.1 </p> <p>906726-906630</p>
<p>49</p> <p>>1c1 HWI-ST1172:64:D1FDDACXX:8:2207:20907:70380_1:N:0:ATCAGC</p> <p>GGTCCGGTGAAGGATGTCATACATCTGTTACACGCGCCCATCGGCTGTGCTTACTACACATGGGGCGGGGACGCGAGGCA</p> <p>AAACCTGTCAGACAACCCGGA</p>	<p>dinitrogenase alpha subunit [uncultured archaeon]</p> <p>Sequence ID: dbj BAF96801.1 </p> <p>57-89</p>	<p>Uncultured microorganism clone D11 nif operon, partial sequence</p> <p>Sequence ID: gb GQ477542.1 </p> <p>1717-1817</p>
<p>50</p> <p>>1c1 HWI-ST1172:64:D1FDDACXX:8:2304:1899:78877_1:N:0:ATCATG</p> <p>ATGGAAGGTTACACACCACCGCTGTATGAGTCTCTGGGAATATTCATCCCGTTGATCGTAGTTAACTGTATTATTATCGG</p> <p>ACGGCCGAAGCCTATGGCGG</p>	<p>electron transport complex, RnfABCDGE type, E subunit [Methanohalophilus ma</p> <p>Sequence ID: ref YP_003542832.1 </p> <p>87-119</p>	<p>Methanococcoides burtonii DSM 6242, complete genome</p> <p>Sequence ID: gb CP000300.1 </p> <p>1471848-1471752</p>