

Supplementary Information

Pan-genome analysis of the genus *Finegoldia* identifies two distinct clades, strain-specific heterogeneity, and putative virulence factors

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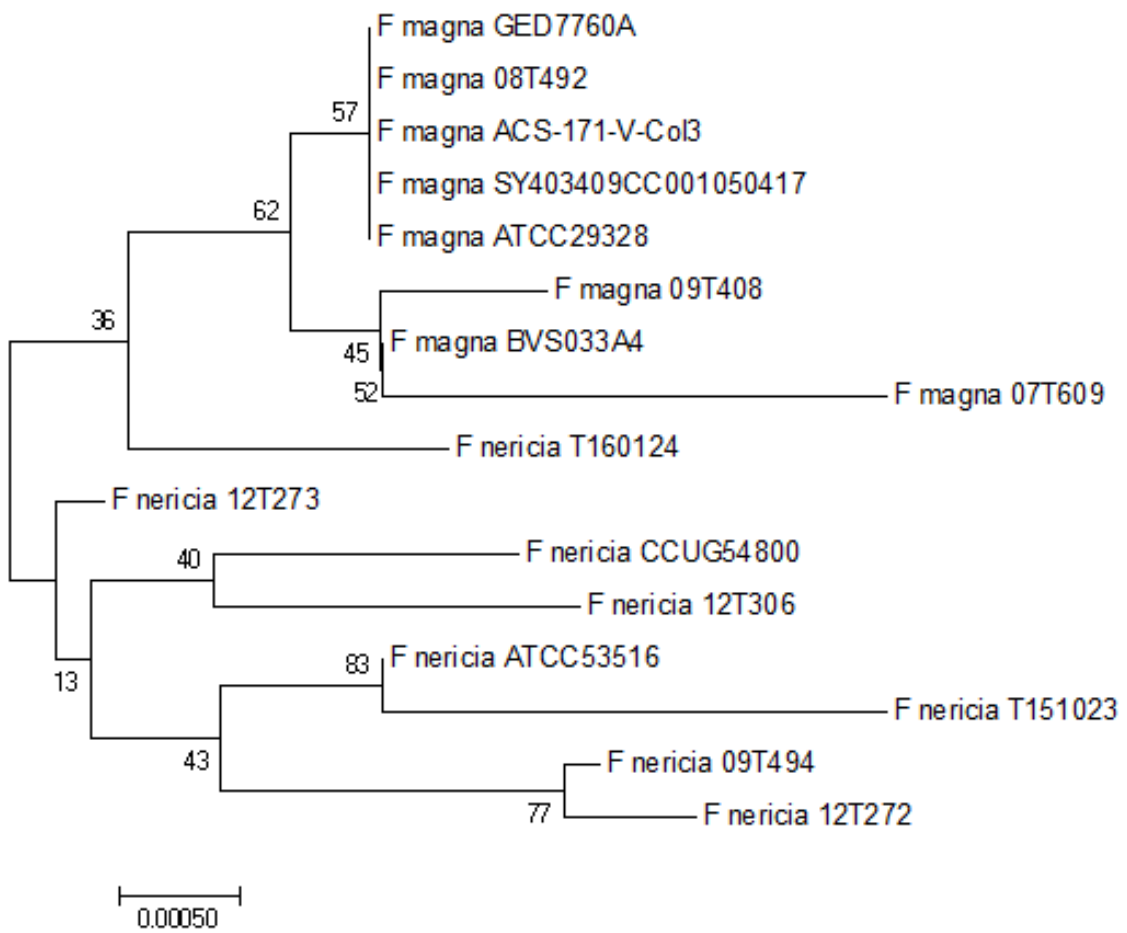


Figure S1: Phylogenetic tree of 16S rDNA sequences extracted from draft genomes of *Fingoldia*
 The analysis involved 16 nucleotide sequences. For one genome, *F. magna* ALB8, the 16S rDNA sequence is incomplete. There is an overall high similarity (in average 99%) between the 16S rDNA sequence of strains of *F. magna* and “*F. nericia*”: there are 5 to 9 SNPs in the 16S rDNA of “*F. nericia*” strains compared to the cluster of *F. magna* strains, including the reference strain *F. magna* ATCC29328. The phylogenetic analysis was done with MEGA7. The evolutionary history was inferred using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (250 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site.

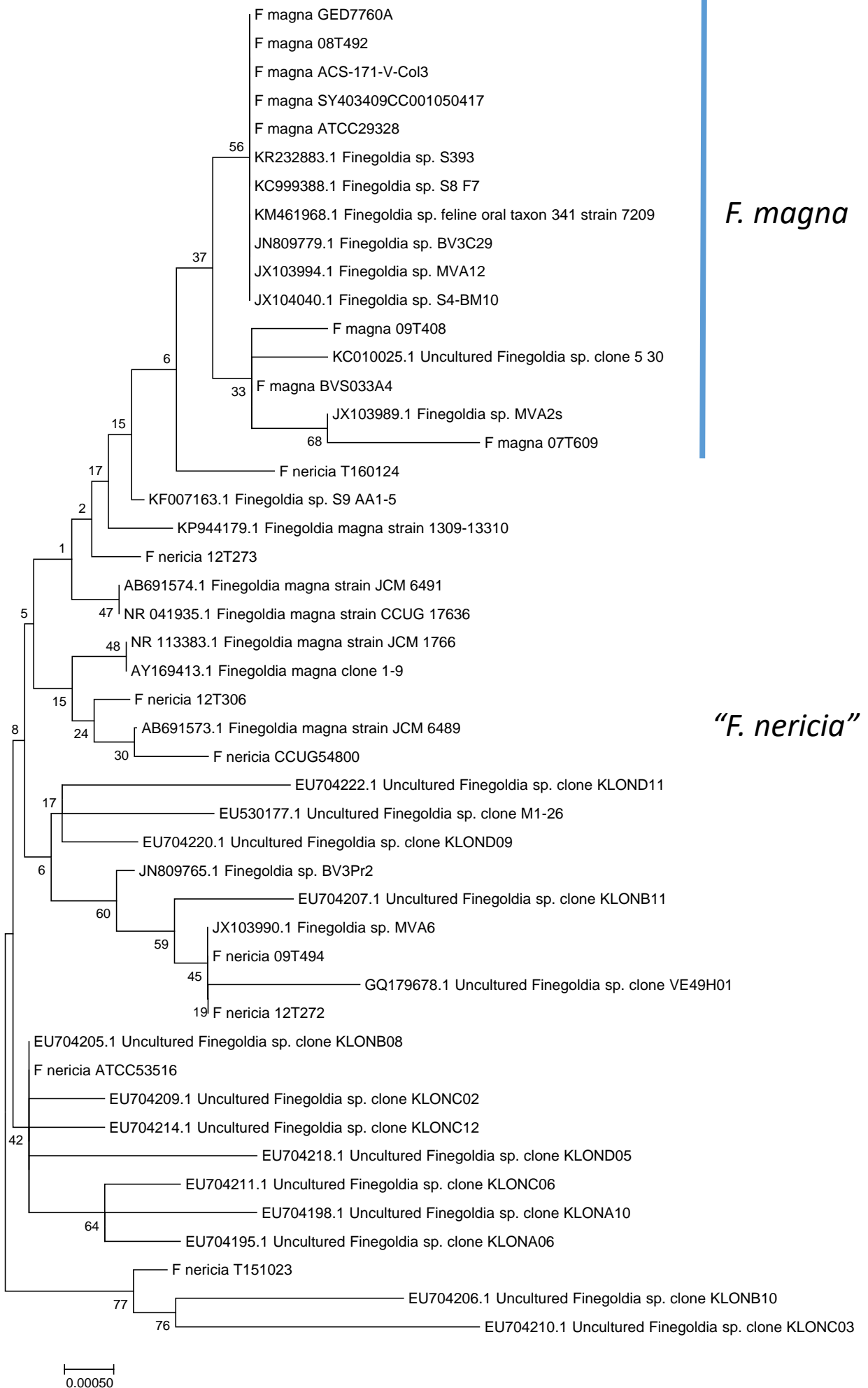


Figure S2: Phylogenetic tree of 16S rDNA sequences of *Finegoldia* isolates extracted from GenBank
 All deposited 16S rDNA sequences assigned to *Finegoldia* were taken from GenBank that had a >85% overlap with the 16S rDNA sequence (*rrnA*) of ATCC29328. 47 sequences were compared. The phylogenetic analysis was done with MEGA7. The evolutionary history was inferred using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (250 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site.

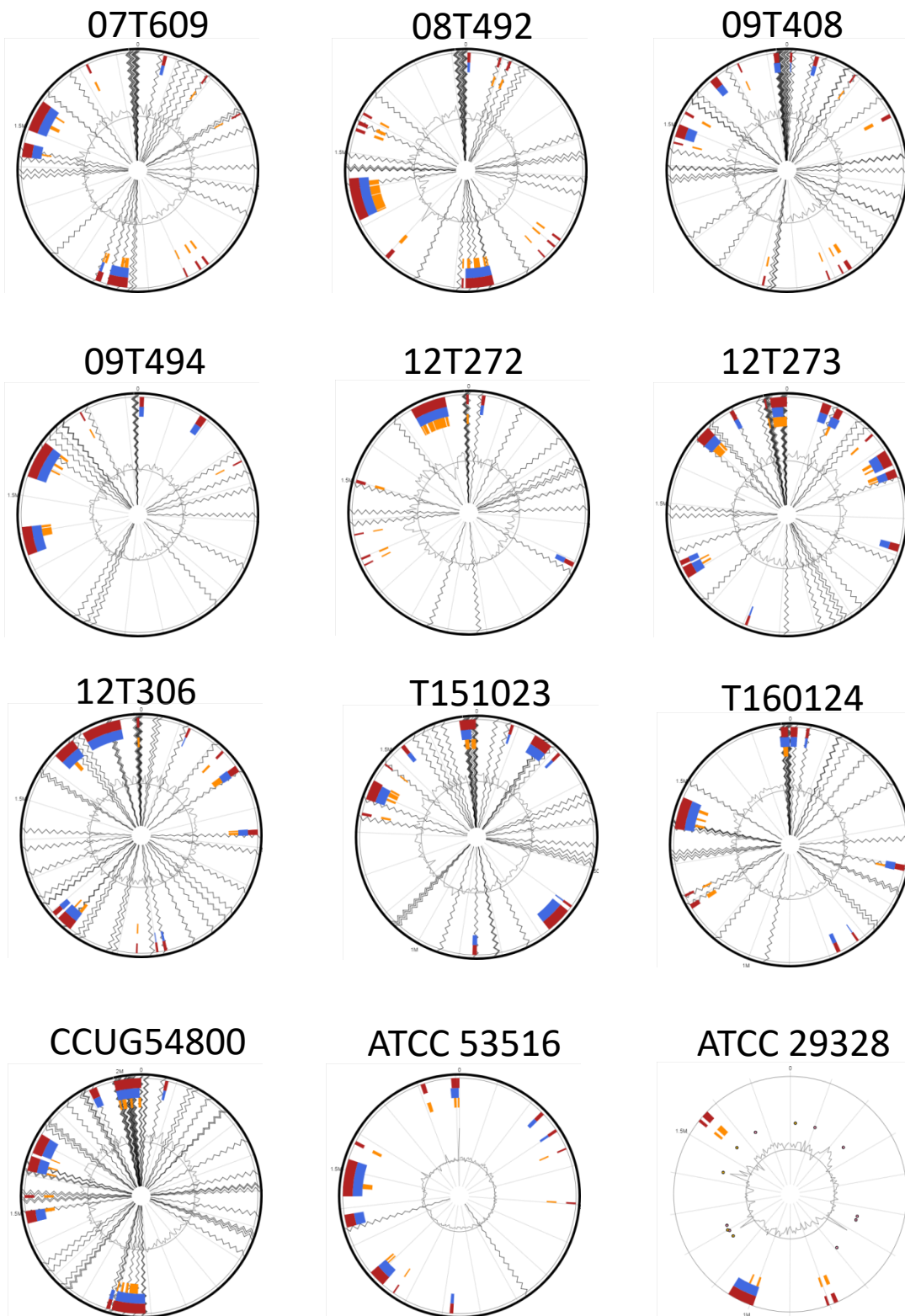


Figure S3: Predicted genomic islands in *Finnegoldia* genomes

All analyzed 12 *Finnegoldia* genomes contain predicted genomic islands, but with strain-specific differences. The color depicts the prediction method: blue, IslandPath-DIMOB; orange, SIGI-HMM and dark red, integrated. All genes found in these islands are shown in table S3.

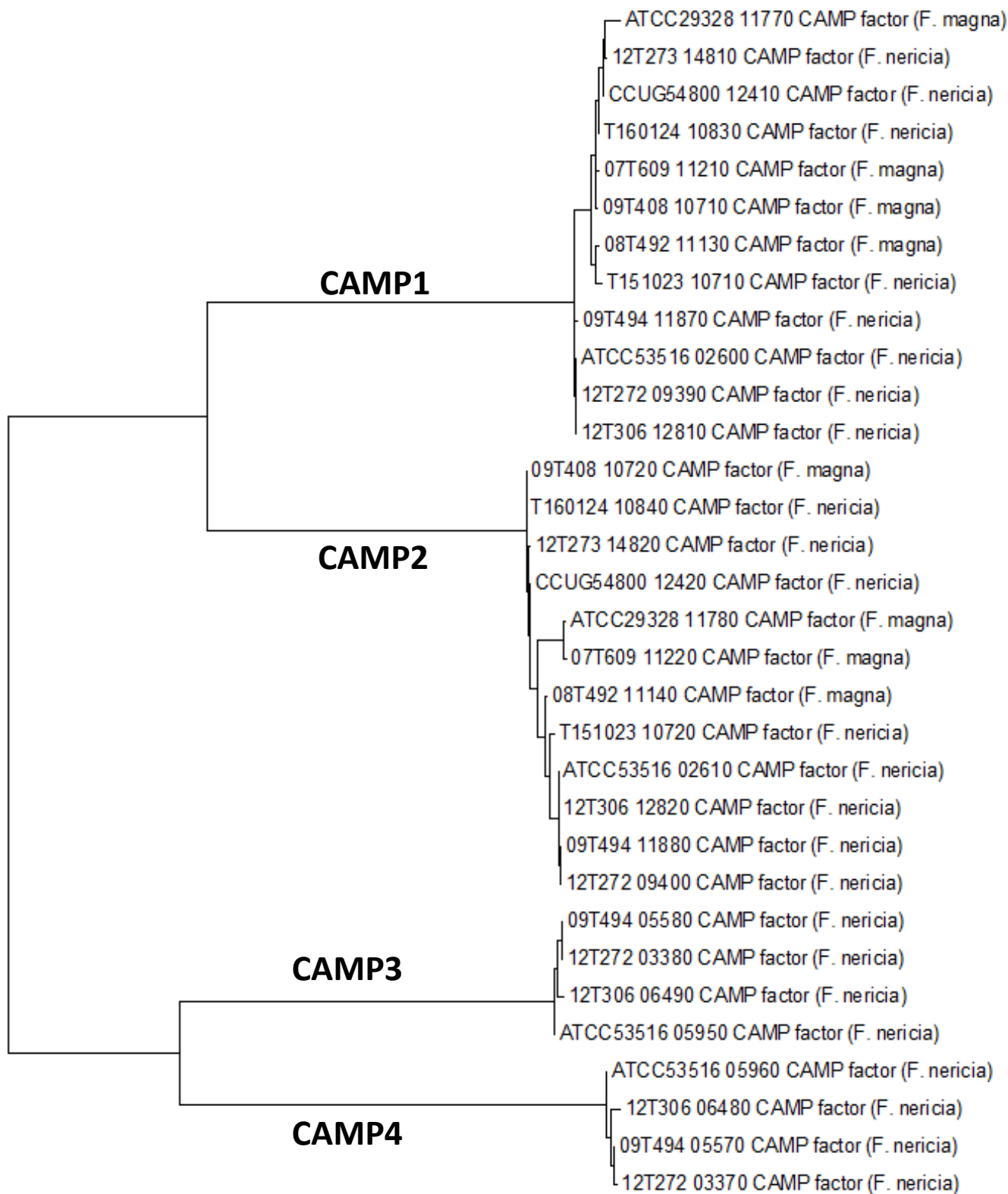


Figure S4: Phylogenetic tree of all putative CAMP factors of *Fingoldia* strains

Each strain possesses a least two distinct CAMP factors whose genes are in direct vicinity. Four out of seven "*F. nericia*" strains possess two additional CAMP factors; again, the genes are located next to each other. The tree was created in MEGA7, using the Maximum Likelihood method.

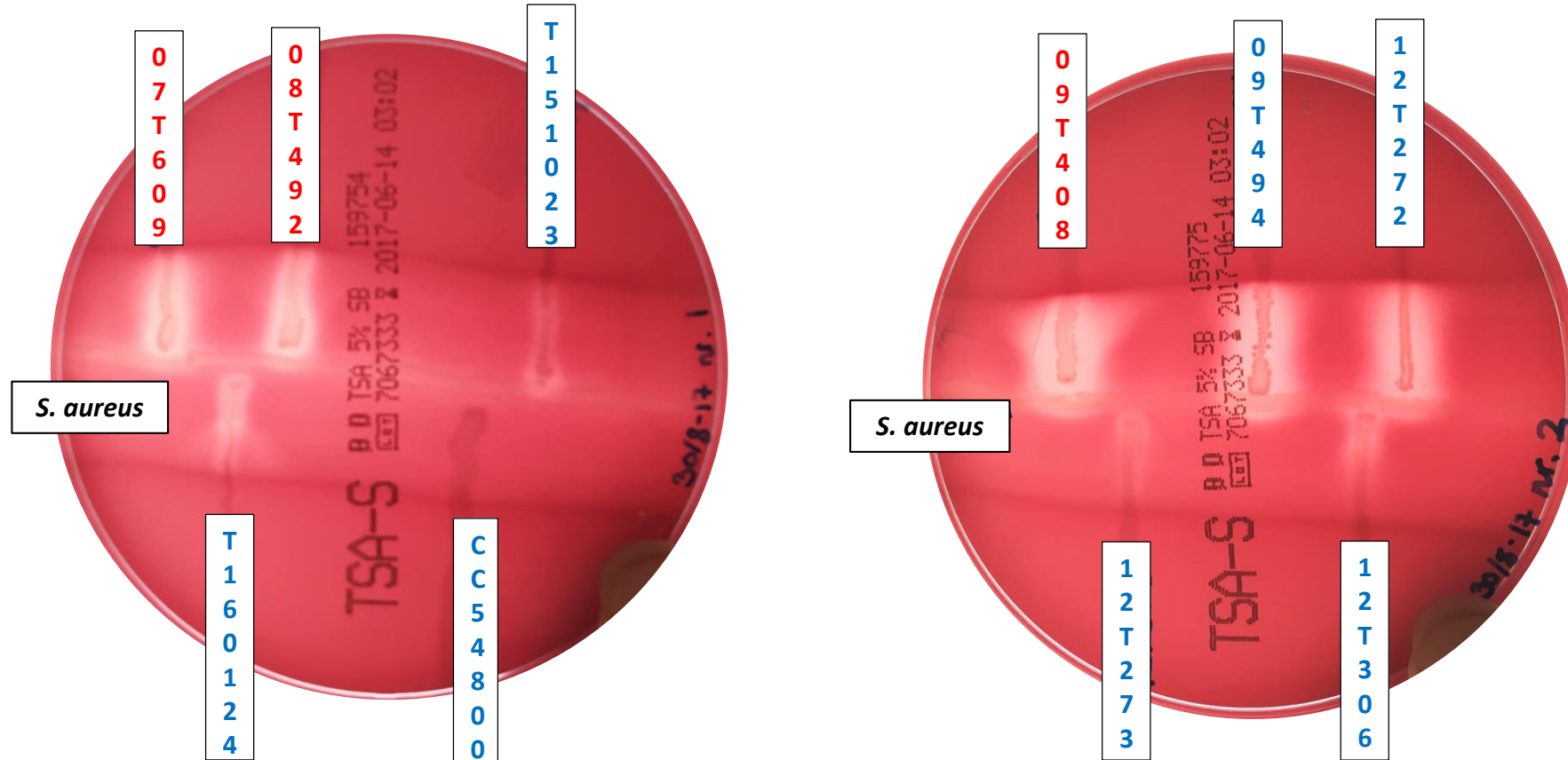


Figure S5: CAMP reaction of *Finegoldia* sp. strains at elongated cultivation time

TSA agar plates with 5% sheep blood was used. *Staphylococcus aureus* is inoculated in the middle streak. A positive CAMP test is indicated by complete erythrocyte lysis at the interface of the *Finegoldia* sp. and the *S. aureus* streaks. All three *F. magna* (in red) strains and two out of seven "*F. nericia*" (in blue) strains showed a strong positive CAMP reaction after five days of anaerobic incubation. One strain (CCUG54800) is negative in the CAMP reaction (see also Figure S6).

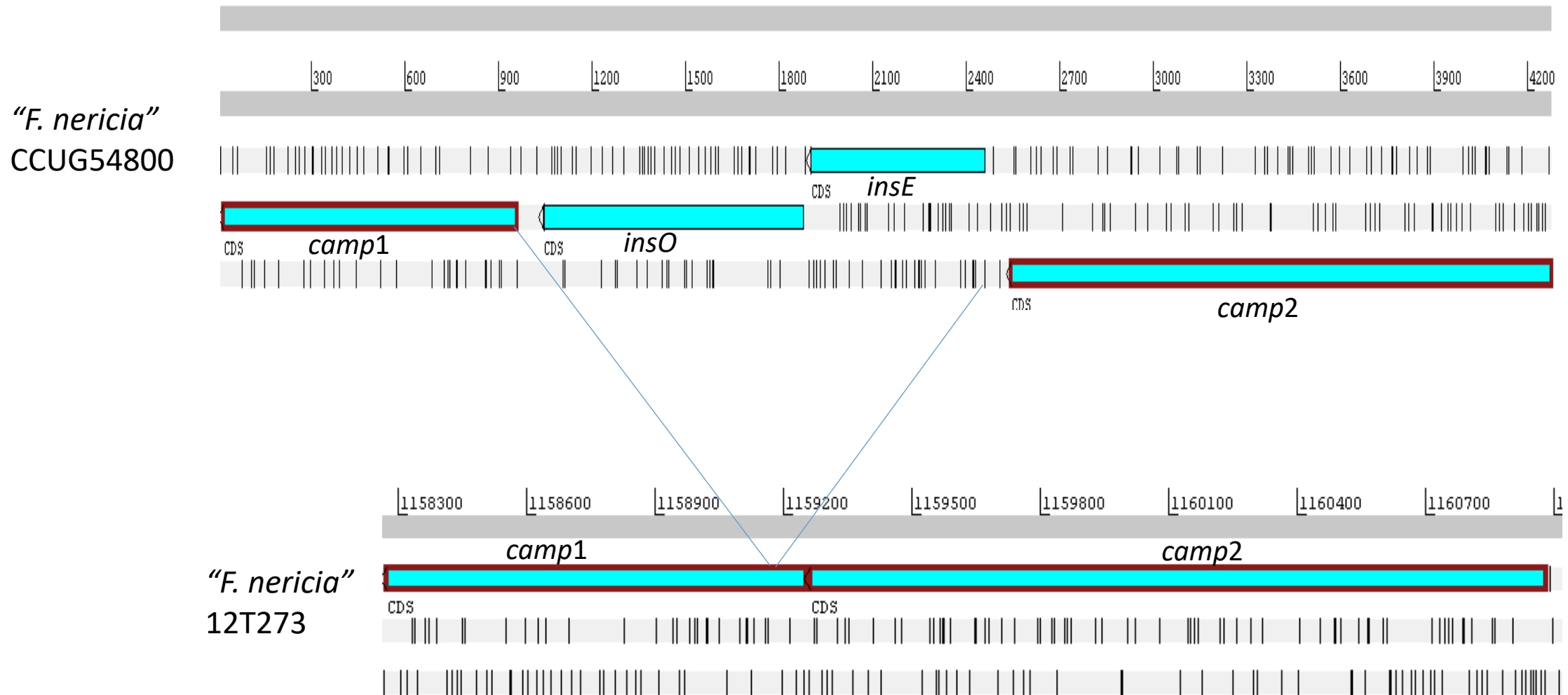


Figure S6: Insertional inactivation of *camp1* in strain CCUG54800

The genomic regions containing the *camp1* and the *camp2* gene in the “*F. nericia*” strains CCUG54800 and 12T273 are shown. A transposase-encoding mobile element is inserted in the 5’ end of *camp1* in strain CCUG54800.

Table S1: Bidirectional blast of all coding sequences of 12 *Finleigola* genomes
 The program ProteinOrtho (version 4.26) was used with the following parameters: blast-*blastp* v2.24, E-value=1e-10, alg-*aln*=0.1, coverage=0.5, percent_identity=25, adaptive_similarity=0.95, inc_pairs=1, inc_singles=1, selfblast=1, unambiguous=0)
 The Prokka annotation is shown. Highlighted in grey are the CDS with orthologs in all 12 genomes.

Species	Protein	alg- <i>conn.</i>	Annotation	ATCC29328	ATCC35516	077609	081492	097408	097494	127272	127273	127306	CCUG54800	T151023	T160124
#12	21125 -														
12	12	1	Chromosomal replication initiator protein DnaA	ATCC29328_00010	ATCC35516_11280	077609_16840	081492_17540	097408_16640	097494_12190	127272_17700	127273_00730	127306_00150	CCUG54800_18780	T151023_00340	T160124_16570
12	12	1	DNA polymerase III subunit beta	ATCC29328_00020	ATCC35516_11270	077609_16850	081492_17550	097408_16650	097494_12200	127272_17710	127273_00740	127306_00160	CCUG54800_18790	T151023_00350	T160124_16580
12	12	1	ribosome-associated protein	ATCC29328_00030	ATCC35516_11260	077609_16860	081492_17560	097408_16660	097494_12210	127272_17720	127273_00750	127306_00170	CCUG54800_18800	T151023_00360	T160124_16590
12	12	1	DNA replication and repair protein RecF	ATCC29328_00040	ATCC35516_11250	077609_16870	081492_17570	097408_16670	097494_12220	127272_17730	127273_00760	127306_00180	CCUG54800_18810	T151023_00370	T160124_16600
12	12	1	hypothetical protein	ATCC29328_00050	ATCC35516_11240	077609_16880	081492_17580	097408_16680	097494_12230	127272_17740	127273_00770	127306_00190	CCUG54800_18820	T151023_00380	T160124_16610
12	12	1	DNA gyrase subunit B	ATCC29328_00060	ATCC35516_11230	077609_16890	081492_17590	097408_16690	097494_12240	127272_17750	127273_00780	127306_00200	CCUG54800_18830	T151023_00390	T160124_16620
12	12	1	DNA gyrase subunit A	ATCC29328_00070	ATCC35516_11220	077609_16900	081492_17600	097408_16700	097494_12250	127272_17760	127273_00790	127306_00210	CCUG54800_18840	T151023_00400	T160124_16630
12	12	1	Putative anti-sigma factor antagonist	ATCC29328_00080	ATCC35516_11210	077609_16910	081492_17610	097408_16710	097494_12260	127272_17770	127273_00800	127306_00220	CCUG54800_18850	T151023_00410	T160124_16640
12	12	1	serine protein kinase RsbW	ATCC29328_00090	ATCC35516_11200	077609_16920	081492_17620	097408_16720	097494_12270	127272_17780	127273_00810	127306_00230	CCUG54800_18860	T151023_00420	T160124_16650
24	0.167	1	RNA polymerase sigma factor SigF	ATCC29328_00100	ATCC35516_11600	077609_00300	081492_00850	097408_00820	097494_00940	127272_00900	127273_00740	127306_01010	CCUG54800_18870	T151023_00580	T160124_16660
12	12	1	Glutamine synthetase ATP-binding protein GlnA	ATCC29328_00110	ATCC35516_11190	077609_16940	081492_17640	097408_16740	097494_12280	127272_17790	127273_00820	127306_00240	CCUG54800_18880	T151023_00440	T160124_16670
12	12	1	hypothetical protein	ATCC29328_00120	ATCC35516_11170	077609_16950	081492_17650	097408_16750	097494_12290	127272_17800	127273_00830	127306_00250	CCUG54800_18890	T151023_00450	T160124_16680
24	0.167	1	Fumarate hydratase class II	ATCC29328_00130	ATCC35516_10520	077609_05000	081492_00760	097408_05110	097494_05880	127272_03880	127273_00850	127306_00260	CCUG54800_18900	T151023_00460	T160124_16690
12	12	1	hypothetical protein	ATCC29328_00140	ATCC35516_11150	077609_16970	081492_17670	097408_16770	097494_12300	127272_17810	127273_00860	127306_00270	CCUG54800_18910	T151023_00470	T160124_16700
6	7	0.241	Acetyltransferase (GNAT) family protein	ATCC29328_00150	ATCC35516_11140	077609_16980	081492_17680	097408_16780	097494_12310	127272_17820	127273_00870	127306_00280	CCUG54800_18920	T151023_00480	T160124_16710
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12	12	1	hypothetical protein	ATCC29328_00170	ATCC35516_11120	077609_17000	081492_17700	097408_16800	097494_12330	127272_17840	127273_00890	127306_00300	CCUG54800_18940	T151023_00500	T160124_16730
7	7	1	YdcA-like protein	ATCC29328_00180	ATCC35516_11110	077609_17010	081492_17710	097408_16810	097494_12340	127272_17850	127273_00900	127306_00310	CCUG54800_18950	T151023_00510	T160124_16740
11	11	1	hypothetical protein	ATCC29328_00190	ATCC35516_11100	077609_17020	081492_17720	097408_16820	097494_12350	127272_17860	127273_00910	127306_00320	CCUG54800_18960	T151023_00520	T160124_16750
11	11	1	hypothetical protein	ATCC29328_00210	ATCC35516_11090	077609_17030	081492_17730	097408_16830	097494_12360	127272_17870	127273_00920	127306_00330	CCUG54800_18970	T151023_00530	T160124_16760
12	12	1	hypothetical protein	ATCC29328_00220	ATCC35516_11080	077609_17040	081492_17740	097408_16840	097494_12370	127272_17880	127273_00930	127306_00340	CCUG54800_18980	T151023_00540	T160124_16770
12	12	1	hypothetical protein	ATCC29328_00230	ATCC35516_11070	077609_17050	081492_17750	097408_16850	097494_12380	127272_17890	127273_00940	127306_00350	CCUG54800_18990	T151023_00550	T160124_16780
12	12	1	hypothetical protein	ATCC29328_00240	ATCC35516_11060	077609_17060	081492_17760	097408_16860	097494_12390	127272_17900	127273_00950	127306_00360	CCUG54800_19000	T151023_00560	T160124_16790
12	12	1	Yvi protein family protein	ATCC29328_00250	ATCC35516_11050	077609_17070	081492_17770	097408_16870	097494_12400	127272_17910	127273_00960	127306_00370	CCUG54800_19010	T151023_00570	T160124_16800
12	12	19.123	High-affinity zinc uptake system binding-protein ATCC29328_00260	ATCC29328_00260	ATCC35516_11040	077609_17080	081492_17780	097408_16880	097494_12410	127272_17920	127273_00970	127306_00380	CCUG54800_19020	T151023_00580	T160124_16810
7	7	1	High-affinity zinc uptake system ATP-binding protein	ATCC29328_00270	ATCC35516_11030	077609_17090	081492_17790	097408_16890	097494_12420	127272_17930	127273_00980	127306_00390	CCUG54800_19030	T151023_00590	T160124_16820
7	7	1	High-affinity zinc uptake system membrane protein	ATCC29328_00280	ATCC35516_11020	077609_17100	081492_17800	097408_16900	097494_12430	127272_17940	127273_00990	127306_00400	CCUG54800_19040	T151023_00600	T160124_16830
7	7	1	hypothetical protein	ATCC29328_00290	ATCC35516_10990	077609_17110	081492_17810	097408_16910	097494_12440	127272_17950	127273_01000	127306_00410	CCUG54800_19050	T151023_00610	T160124_16840
4	4	1	hypothetical protein	ATCC29328_00300	ATCC35516_10980	077609_17120	081492_17820	097408_16920	097494_12450	127272_17960	127273_01010	127306_00420	CCUG54800_19060	T151023_00620	T160124_16850
12	12	1	Transglutaminase-like superfamily protein	ATCC29328_00310	ATCC35516_10970	077609_17130	081492_17830	097408_16930	097494_12460	127272_17970	127273_01020	127306_00430	CCUG54800_19070	T151023_00630	T160124_16860
12	12	1	molibdopterine biosynthesis-like protein MoxZ	ATCC29328_00320	ATCC35516_10960	077609_17140	081492_17840	097408_16940	097494_12470	127272_17980	127273_01030	127306_00440	CCUG54800_19080	T151023_00640	T160124_16870
12	12	1	(Hw) antiporter NhaP2	ATCC29328_00330	ATCC35516_10950	077609_17150	081492_17850	097408_16950	097494_12480	127272_17990	127273_01040	127306_00450	CCUG54800_19090	T151023_00650	T160124_16880
12	12	17.048	Ferrous-iron efflux pump FieF	ATCC29328_00340	ATCC35516_10940	077609_17160	081492_17860	097408_16960	097494_12490	127272_18000	127273_01050	127306_00460	CCUG54800_19100	T151023_00660	T160124_16890
12	12	1	PAP2 superfamily protein	ATCC29328_00350	ATCC35516_10930	077609_17170	081492_17870	097408_16970	097494_12500	127272_18010	127273_01060	127306_00470	CCUG54800_19110	T151023_00670	T160124_16900
8	8	1	hypothetical protein	ATCC29328_00360	ATCC35516_10920	077609_17180	081492_17880	097408_16980	097494_12510	127272_18020	127273_01070	127306_00480	CCUG54800_19120	T151023_00680	T160124_16910
12	12	1	Thiamine precursor transporter HmpT	ATCC29328_00370	ATCC35516_10910	077609_17190	081492_17890	097408_16990	097494_12520	127272_18030	127273_01080	127306_00490	CCUG54800_19130	T151023_00690	T160124_16920
9	9	1	Ph-type protease precursor	ATCC29328_00380	ATCC35516_10900	077609_17200	081492_17900	097408_17000	097494_12530	127272_18040	127273_01090	127306_00500	CCUG54800_19140	T151023_00700	T160124_16930
1	1	1	N-acetylmuramoyl-L-alanine amidase LytC pre	ATCC29328_00390	ATCC35516_10890	077609_17210	081492_17910	097408_17010	097494_12540	127272_18050	127273_01100	127306_00510	CCUG54800_19150	T151023_00710	T160124_16940
12	12	1	CnaB-type D-type domain protein	ATCC29328_00400	ATCC35516_10880	077609_17220	081492_17920	097408_17020	097494_12550	127272_18060	127273_01110	127306_00520	CCUG54800_19160	T151023_00720	T160124_16950
12	12	1	Putative small multi-drug export protein	ATCC29328_00410	ATCC35516_10870	077609_17230	081492_17930	097408_17030	097494_12560	127272_18070	127273_01120	127306_00530	CCUG54800_19170	T151023_00730	T160124_16960
12	12	1	Phosphoenolpyruvate carboxyltransferase	ATCC29328_00420	ATCC35516_10860	077609_17240	081492_17940	097408_17040	097494_12570	127272_18080	127273_01130	127306_00540	CCUG54800_19180	T151023_00740	T160124_16970
12	12	1	Oligonucleotide 2	ATCC29328_00430	ATCC35516_10850	077609_17250	081492_17950	097408_17050	097494_12580	127272_18090	127273_01140	127306_00550	CCUG54800_19190	T151023_00750	T160124_16980
24	0.147	1	Oligonucleotide 5, Phosphatidyl	ATCC29328_00440	ATCC35516_10840	077609_17260	081492_17960	097408_17060	097494_12590	127272_18100	127273_01150	127306_00560	CCUG54800_19200	T151023_00760	T160124_16990
12	12	1	Glutamine transport ATP-binding protein GlnA	ATCC29328_00450	ATCC35516_10830	077609_17270	081492_17970	097408_17070	097494_12600	127272_18110	127273_01160	127306_00570	CCUG54800_19210	T151023_00770	T160124_17000
12	12	1	hypothetical protein	ATCC29328_00460	ATCC35516_10820	077609_17280	081492_17980	097408_17080	097494_12610	127272_18120	127273_01170	127306_00580	CCUG54800_19220	T151023_00780	T160124_17010
12	12	1	hypothetical protein	ATCC29328_00470</											

12	12	1	Hyd family secretin protein	ATCC29328_06930	ATCC53516_14030	07769_06220	08792_06070	09748_06310	09744_07250	12772_05020	12773_09890	127306_08090	CCUG54800_07360	T51023_06600	T160124_06510
12	12	1	Hydrolytic protein	ATCC29328_06940	ATCC53516_14030	07769_06230	08792_06080	09748_06320	09744_07260	12772_05030	12773_09900	127306_08100	CCUG54800_07370	T51023_06610	T160124_06520
12	12	1	Cell division protein SepF	ATCC29328_06950	ATCC53516_14030	07769_06240	08792_06090	09748_06330	09744_07270	12772_05040	12773_09910	127306_08110	CCUG54800_07380	T51023_06620	T160124_06530
12	12	1	YGGT family protein	ATCC29328_06960	ATCC53516_14030	07769_06250	08792_06100	09748_06340	09744_07280	12772_05050	12773_09920	127306_08120	CCUG54800_07390	T51023_06630	T160124_06540
12	12	1	Hydrolytic protein	ATCC29328_06970	ATCC53516_14040	07769_06260	08792_06110	09748_06350	09744_07290	12772_05060	12773_09930	127306_08130	CCUG54800_07400	T51023_06640	T160124_06550
12	12	1	Lipotein signal peptidase	ATCC29328_06980	ATCC53516_14050	07769_06270	08792_06120	09748_06360	09744_07300	12772_05070	12773_09940	127306_08140	CCUG54800_07410	T51023_06650	T160124_06560
12	12	1	Uridine diphosphate-lyase	ATCC29328_06990	ATCC53516_14060	07769_06280	08792_06130	09748_06370	09744_07310	12772_05080	12773_09950	127306_08150	CCUG54800_07420	T51023_06660	T160124_06570
12	13 0.141	1	Putative endo-beta-N-acetylglucosaminidase	ATCC29328_07030	ATCC29328_07030	07769_06320	08792_06140	09748_06380	09744_07360	12772_05120	12773_09990	127306_08190	CCUG54800_07460	T51023_06700	T160124_06620
12	14 0.143	1	Thrombospondin precursor	ATCC29328_07040	ATCC53516_14110	07769_06330	08792_06150	09748_06390	09744_07370	12772_05130	12773_10000	127306_08200	CCUG54800_07470	T51023_06710	T160124_06630
12	12	1	Thymopoietin	ATCC29328_07080	ATCC53516_14150	07769_06370	08792_06220	09748_06430	09744_07410	12772_05170	12773_10040	127306_08240	CCUG54800_07510	T51023_06750	T160124_06670
12	12	1	Allyl hydroperoxidase reductase subunit C	ATCC29328_07090	ATCC53516_14160	07769_06380	08792_06230	09748_06440	09744_07420	12772_05180	12773_10050	127306_08250	CCUG54800_07520	T51023_06760	T160124_06680
12	12	1	Nitroreductase family protein	ATCC29328_07110	ATCC53516_14180	07769_06400	08792_06250	09748_06470	09744_07440	12772_05200	12773_10070	127306_08270	CCUG54800_07540	T51023_06780	T160124_06700
12	12	1	Molybdate-binding periplasmic protein precu	ATCC29328_07120	ATCC53516_14190	07769_06410	08792_06260	09748_06480	09744_07450	12772_05210	12773_10080	127306_08280	CCUG54800_07550	T51023_06790	T160124_06710
12	12	1	Molybdenum transport system permease prot	ATCC29328_07130	ATCC53516_14200	07769_06420	08792_06270	09748_06490	09744_07460	12772_05220	12773_10090	127306_08290	CCUG54800_07560	T51023_06800	T160124_06720
12	12	1	Fe(3+) ions import ATP-binding protein FbpC	ATCC29328_07140	ATCC53516_14210	07769_06430	08792_06280	09748_06500	09744_07470	12772_05230	12773_10100	127306_08300	CCUG54800_07570	T51023_06810	T160124_06730
12	12	1	Ribonuclease F	ATCC29328_07150	ATCC53516_14220	07769_06440	08792_06290	09748_06510	09744_07480	12772_05240	12773_10110	127306_08310	CCUG54800_07580	T51023_06820	T160124_06740
12	12	1	SrA-binding protein	ATCC29328_07160	ATCC53516_14230	07769_06450	08792_06300	09748_06520	09744_07490	12772_05250	12773_10120	127306_08320	CCUG54800_07590	T51023_06830	T160124_06750
12	12	1	Hydrolytic protein	ATCC29328_07170	ATCC53516_14240	07769_06460	08792_06310	09748_06530	09744_07500	12772_05260	12773_10130	127306_08330	CCUG54800_07600	T51023_06840	T160124_06760
12	12	1	Hydrolytic protein	ATCC29328_07180	ATCC53516_14250	07769_06470	08792_06320	09748_06540	09744_07510	12772_05270	12773_10140	127306_08340	CCUG54800_07610	T51023_06850	T160124_06770
12	12	1	Hydrolytic protein	ATCC29328_07190	ATCC53516_14260	07769_06480	08792_06330	09748_06550	09744_07520	12772_05280	12773_10150	127306_08350	CCUG54800_07620	T51023_06860	T160124_06780
12	12	1	Guanylate kinase	ATCC29328_07200	ATCC53516_14270	07769_06490	08792_06340	09748_06560	09744_07530	12772_05290	12773_10160	127306_08360	CCUG54800_07630	T51023_06870	T160124_06790
12	12	1	DNA-directed RNA polymerase subunit omega	ATCC29328_07210	ATCC53516_14280	07769_06500	08792_06350	09748_06570	09744_07540	12772_05300	12773_10170	127306_08370	CCUG54800_07640	T51023_06880	T160124_06800
12	12	1	Coenzyme A biosynthesis bifunctional protein	ATCC29328_07220	ATCC53516_14290	07769_06510	08792_06360	09748_06580	09744_07550	12772_05310	12773_10180	127306_08380	CCUG54800_07650	T51023_06890	T160124_06810
12	12	1	Primosomal protein W	ATCC29328_07230	ATCC53516_14300	07769_06520	08792_06370	09748_06590	09744_07560	12772_05320	12773_10190	127306_08390	CCUG54800_07660	T51023_06900	T160124_06820
12	12	1	Peptide deformylase 1	ATCC29328_07240	ATCC53516_14310	07769_06530	08792_06380	09748_06600	09744_07570	12772_05330	12773_10200	127306_08400	CCUG54800_07670	T51023_06910	T160124_06830
12	12	1	Methionyl-tRNA formyltransferase	ATCC29328_07250	ATCC53516_14320	07769_06540	08792_06390	09748_06610	09744_07580	12772_05340	12773_10210	127306_08410	CCUG54800_07680	T51023_06920	T160124_06840
12	12	1	Putative nuclear zinc metalloproteinase	ATCC29328_07260	ATCC53516_14330	07769_06550	08792_06400	09748_06620	09744_07590	12772_05350	12773_10220	127306_08420	CCUG54800_07690	T51023_06930	T160124_06850
12	12	1	Ribosomal RNA small subunit methyltransferase	ATCC29328_07270	ATCC53516_14340	07769_06560	08792_06410	09748_06630	09744_07600	12772_05360	12773_10230	127306_08430	CCUG54800_07700	T51023_06940	T160124_06860
12	12	1	Putative DNA-specific RNA methyltransferase	ATCC29328_07280	ATCC53516_14350	07769_06570	08792_06420	09748_06640	09744_07610	12772_05370	12773_10240	127306_08440	CCUG54800_07710	T51023_06950	T160124_06870
12	24 0.167	1	Serine/threonine phosphatase stp	ATCC29328_07290	ATCC29328_07290	07769_07069	08792_07200	09748_07069	09744_07440	12772_05370	12773_11070	127306_09280	CCUG54800_07720	T51023_06950	T160124_06870
12	12	1	Serine/threonine-protein kinase PkcK	ATCC29328_07300	ATCC53516_14370	07769_06590	08792_06440	09748_06650	09744_07620	12772_05380	12773_10260	127306_08460	CCUG54800_07730	T51023_06970	T160124_06890
12	12	1	Putative ribosome biogenesis GTPase RgaA	ATCC29328_07310	ATCC53516_14380	07769_06600	08792_06450	09748_06670	09744_07630	12772_05400	12773_10270	127306_08470	CCUG54800_07740	T51023_06980	T160124_06900
12	12	1	Ribonuclease 3 primimerase	ATCC29328_07320	ATCC53516_14390	07769_06610	08792_06460	09748_06680	09744_07640	12772_05420	12773_10290	127306_08490	CCUG54800_07750	T51023_06990	T160124_06910
12	12	1	Thiamine transporter TH1	ATCC29328_07330	ATCC53516_14400	07769_06620	08792_06470	09748_06690	09744_07650	12772_05440	12773_10300	127306_08490	CCUG54800_07760	T51023_07000	T160124_06920
12	12	1	Thiamine pyrophosphokinase	ATCC29328_07340	ATCC53516_14410	07769_06630	08792_06480	09748_06700	09744_07660	12772_05440	12773_10300	127306_08500	CCUG54800_07770	T51023_07010	T160124_06930
12	12	1	SOS ribosomal protein L28	ATCC29328_07350	ATCC53516_14420	07769_06640	08792_06490	09748_06710	09744_07670	12772_05440	12773_10310	127306_08510	CCUG54800_07780	T51023_07020	T160124_06940
12	12	1	Alkaline shock-protein 23	ATCC29328_07360	ATCC53516_14430	07769_06650	08792_06500	09748_06720	09744_07680	12772_05450	12773_10320	127306_08520	CCUG54800_07790	T51023_07030	T160124_06950
12	12	1	DACD domain protein	ATCC29328_07370	ATCC53516_14440	07769_06660	08792_06510	09748_06730	09744_07700	12772_05460	12773_10330	127306_08530	CCUG54800_07800	T51023_07040	T160124_06960
12	12	1	ATP-dependent DNA helicase RecG	ATCC29328_07380	ATCC53516_14450	07769_06670	08792_06520	09748_06740	09744_07710	12772_05470	12773_10340	127306_08540	CCUG54800_07810	T51023_07050	T160124_06970
12	12	1	Ribosomal RNA small subunit methyltransferase	ATCC29328_07390	ATCC53516_14460	07769_06680	08792_06530	09748_06750	09744_07720	12772_05480	12773_10350	127306_08550	CCUG54800_07820	T51023_07060	T160124_06980
12	12	1	Ribonucleoproteine adenylyltransferase	ATCC29328_07400	ATCC53516_14470	07769_06690	08792_06540	09748_06760	09744_07730	12772_05490	12773_10360	127306_08560	CCUG54800_07830	T51023_07070	T160124_06990
12	12	1	Hydrolytic protein	ATCC29328_07410	ATCC53516_14480	07769_06700	08792_06550	09748_06770	09744_07740	12772_05500	12773_10370	127306_08570	CCUG54800_07840	T51023_07080	T160124_07000
12	12	1	Flavodoxin	ATCC29328_07420	ATCC53516_14490	07769_06710	08792_06560	09748_06780	09744_07750	12772_05510	12773_10380	127306_08580	CCUG54800_07850	T51023_07090	T160124_07010
12	12	1	Hydrolytic protein	ATCC29328_07430	ATCC53516_14500	07769_06720	08792_06570	09748_06790	09744_07760	12772_05520	12773_10390	127306_08590	CCUG54800_07860	T51023_07100	T160124_07020
12	12	1	preprotein translocase subunit SecE	ATCC29328_07440	ATCC53516_14510	07769_06730	08792_06580	09748_06800	09744_07770	12772_05530	12773_10400	127306_08600	CCUG54800_07870	T51023_07110	T160124_07030
12	12	1	Putative H ₂ O ₂ -stimulated pyrophosphate energy	ATCC29328_07450	ATCC53516_14520	07769_06740	08792_06590	09748_06810	09744_07780	12772_05540	12773_10410	127306_08610	CCUG54800_07880	T51023_07120	T160124_07040
12	13 0.141	1	Magnesium and cobalt efflux protein CorC	ATCC29328_07460	ATCC53516_14530	07769_06750	08792_06600	09748_06820	09744_07790	12772_05550	12773_10420	127306_08640	CCUG54800_07890	T51023_07130	T160124_07050
12	12	1	Methionine aminopeptidase 1	ATCC29328_07470	ATCC53516_14540	07769_06760	08792_06610	09748_06830	09744_07800	12772_05560	12773_10430	127306_08650	CCUG54800_07900	T51023_07140	T160124_07060
12	12	1	Hydrolytic protein	ATCC29328_07480	ATCC53516_14550	07769_06770	08792_06620	09748_06840	09744_07810	12772_05570	12773_10440	127306_08660	CCUG54800_07910	T51023_07150	T160124_07070
12	12	1	Hydrolytic protein	ATCC29328_07490	ATCC53516_14560	07769_06780	08792_06630	09748_06850	09744_07820	12772_05580	12773_10450	127306_08670	CCUG54800_07920	T51023_07160	T160124_07080
12	12	1	Hydrolytic protein	ATCC29328_07500	ATCC53516_14570	07769_06790	08792_06640	09748_06860	09744_07830	12772_05590	12773_10460	127306_08680	CCUG54800_07930	T51023_07170	T160124_07090
12	12	1	Hydrolytic protein	ATCC29328_07510	ATCC53516_14580	07769_06800	08792_06650	09748_06870	09744_07840	12772_05600	12773_10470	127306_08690	CCUG54800_07940		

12	12	1	Positive regulator of sigmaE1, RseC/MucC	ATCC29238_09240	ATCC53516_16330	07769_08530	08749_08830	09740_09570	12772_07340	12773_12220	12730_10450	CCUG54800_09670	151023_08910	T160124_08830
12	12	1	RNA threonylcarbamoylase dihydrolase	ATCC29238_09250	ATCC53516_16340	07769_08540	08749_08840	09740_09580	12772_07350	12773_12230	12730_10460	CCUG54800_09680	151023_08920	T160124_08840
12	12	1	Aspartate tRNA ligase	ATCC29238_09260	ATCC53516_16350	07769_08550	08749_08850	09740_09590	12772_07360	12773_12240	12730_10470	CCUG54800_09690	151023_08930	T160124_08850
12	12	1	putative peptidoglycan biosynthesis protein N	ATCC29238_09270	ATCC53516_16360	07769_08560	08749_08860	09740_09600	12772_07370	12773_12250	12730_10480	CCUG54800_09700	151023_08940	T160124_08860
12	12	1	carbohydrate diacid transcriptional activator C	ATCC29238_09280	ATCC53516_16370	07769_08570	08749_08870	09740_09610	12772_07380	12773_12260	12730_10490	CCUG54800_09710	151023_08950	T160124_08870
12	12	1	Tetratricopeptide repeat protein	ATCC29238_09290	ATCC53516_16380	07769_08580	08749_08880	09740_09620	12772_07390	12773_12270	12730_10500	CCUG54800_09720	151023_08960	T160124_08880
12	12	1	hypothetical protein	ATCC29238_09300	ATCC53516_16390	07769_08590	08749_08890	09740_09630	12772_07400	12773_12280	12730_10510	CCUG54800_09730	151023_08970	T160124_08890
12	12	1	Arginine-tRNA ligase	ATCC29238_09310	ATCC53516_16400	07769_08600	08749_08900	09740_09640	12772_07410	12773_12290	12730_10520	CCUG54800_09740	151023_08980	T160124_08900
12	12	1	Endonuclease MutS2	ATCC29238_09320	ATCC53516_16410	07769_08610	08749_08910	09740_09650	12772_07420	12773_12300	12730_10530	CCUG54800_09750	151023_08990	T160124_08910
12	12	1	putative protease YhdU precursor	ATCC29238_09330	ATCC53516_16420	07769_08620	08749_08920	09740_09660	12772_07430	12773_12310	12730_10540	CCUG54800_09760	151023_09000	T160124_08920
12	12	1	chromosome-segregation protein	ATCC29238_09340	ATCC53516_16430	07769_08630	08749_08930	09740_09670	12772_07440	12773_12320	12730_10550	CCUG54800_09770	151023_09010	T160124_08930
12	12	1	Phenylalanine-tRNA ligase beta subunit	ATCC29238_09350	ATCC53516_16440	07769_08640	08749_08940	09740_09680	12772_07450	12773_12330	12730_10560	CCUG54800_09780	151023_09020	T160124_08940
12	12	1	Phenylalanine-tRNA ligase alpha subunit	ATCC29238_09360	ATCC53516_16450	07769_08650	08749_08950	09740_09690	12772_07460	12773_12340	12730_10570	CCUG54800_09790	151023_09030	T160124_08950
12	12	1	Kir system potassium uptake protein A	ATCC29238_09380	ATCC53516_16490	07769_08670	08749_08970	09740_09730	12772_07470	12773_12360	12730_10590	CCUG54800_09810	151023_09050	T160124_08970
12	12	1	Kir system potassium uptake protein B	ATCC29238_09390	ATCC53516_16500	07769_08680	08749_08980	09740_09740	12772_07480	12773_12370	12730_10600	CCUG54800_09820	151023_09060	T160124_08980
12	12	1	Aspartate tRNA ligase	ATCC29238_09400	ATCC53516_16510	07769_08690	08749_08990	09740_09750	12772_07490	12773_12380	12730_10610	CCUG54800_09830	151023_09070	T160124_08990
12	12	1	Putative septation protein SpvG	ATCC29238_09410	ATCC53516_16520	07769_08700	08749_09000	09740_09760	12772_07500	12773_12390	12730_10620	CCUG54800_09840	151023_09080	T160124_09000
12	12	1	Processive diacylglycerol alpha-glucosyltransferase	ATCC29238_09420	ATCC53516_16530	07769_08710	08749_09010	09740_09770	12772_07510	12773_12400	12730_10630	CCUG54800_09850	151023_09090	T160124_09010
12	12	1	TVF38/TME46 family inner membrane prote	ATCC29238_09430	ATCC53516_16540	07769_08720	08749_09020	09740_09780	12772_07520	12773_12410	12730_10640	CCUG54800_09860	151023_09100	T160124_09020
12	12	1	Alpha-monooxygenase/acylglucosyl synthase	ATCC29238_09440	ATCC53516_16550	07769_08730	08749_09030	09740_09790	12772_07530	12773_12420	12730_10650	CCUG54800_09870	151023_09110	T160124_09030
12	12	1	hypothetical protein	ATCC29238_09450	ATCC53516_16560	07769_08740	08749_09040	09740_09800	12772_07540	12773_12430	12730_10660	CCUG54800_09880	151023_09120	T160124_09040
12	12	1	Redox-sensing transcriptional repressor Rex	ATCC29238_09460	ATCC53516_16570	07769_08750	08749_09050	09740_09810	12772_07550	12773_12440	12730_10670	CCUG54800_09890	151023_09130	T160124_09050
11	11	1	Carbon starvation protein A	ATCC29238_09470	ATCC53516_16580	07769_08760	08749_09060	09740_09820	12772_07560	12773_12450	12730_10680	CCUG54800_09900	151023_09140	T160124_09060
12	12	1	chromosome-segregation protein	ATCC29238_09480	ATCC53516_16590	07769_08770	08749_09070	09740_09830	12772_07570	12773_12460	12730_10690	CCUG54800_09910	151023_09150	T160124_09070
12	12	1	Dihydrodipicolinate synthase	ATCC29238_09490	ATCC53516_16600	07769_08780	08749_09080	09740_09840	12772_07580	12773_12470	12730_10700	CCUG54800_09920	151023_09160	T160124_09080
12	12	1	phosphodiesterase	ATCC29238_09500	ATCC53516_16610	07769_08790	08749_09090	09740_09850	12772_07590	12773_12480	12730_10710	CCUG54800_09930	151023_09170	T160124_09090
12	12	1	GTP cyclohydrolase 1	ATCC29238_09510	ATCC53516_16620	07769_08800	08749_09100	09740_09860	12772_07600	12773_12490	12730_10720	CCUG54800_09940	151023_09180	T160124_09100
12	12	1	hypothetical protein	ATCC29238_09520	ATCC53516_16630	07769_08810	08749_09110	09740_09870	12772_07610	12773_12500	12730_10730	CCUG54800_09950	151023_09190	T160124_09110
12	12	1	ETfase YnfJ	ATCC29238_09530	ATCC53516_16640	07769_08820	08749_09120	09740_09880	12772_07620	12773_12510	12730_10740	CCUG54800_09960	151023_09200	T160124_09120
12	12	1	60 kDa chaperonin	ATCC29238_09540	ATCC53516_16650	07769_08830	08749_09130	09740_09890	12772_07630	12773_12520	12730_10750	CCUG54800_09970	151023_09210	T160124_09130
12	12	1	10 kDa chaperonin	ATCC29238_09550	ATCC53516_16660	07769_08840	08749_09140	09740_09900	12772_07640	12773_12530	12730_10760	CCUG54800_09980	151023_09220	T160124_09140
12	12	1	DNA-3-methyladenine glycosylase	ATCC29238_09560	ATCC53516_16670	07769_08850	08749_09150	09740_09910	12772_07650	12773_12540	12730_10770	CCUG54800_09990	151023_09230	T160124_09150
12	12	1	hypothetical protein	ATCC29238_09570	ATCC53516_16680	07769_08860	08749_09160	09740_09920	12772_07660	12773_12550	12730_10780	CCUG54800_10000	151023_09240	T160124_09160
12	12	1	Glycine-tRNA ligase	ATCC29238_09580	ATCC53516_16690	07769_08870	08749_09170	09740_09930	12772_07670	12773_12560	12730_10790	CCUG54800_10010	151023_09250	T160124_09170
12	12	1	hypothetical protein	ATCC29238_09590	ATCC53516_16700	07769_08880	08749_09180	09740_09940	12772_07680	12773_12570	12730_10800	CCUG54800_10020	151023_09260	T160124_09180
12	12	1	Protoporphyrin diacylglyceryl transferase	ATCC29238_09600	ATCC53516_16710	07769_08890	08749_09190	09740_09950	12772_07690	12773_12580	12730_10810	CCUG54800_10030	151023_09270	T160124_09190
12	12	1	transcriptional regulatory protein	ATCC29238_09610	ATCC53516_16720	07769_08900	08749_09200	09740_09960	12772_07700	12773_12590	12730_10820	CCUG54800_10040	151023_09280	T160124_09200
12	12	1	NH(3)-dependent NAD(+) synthetase	ATCC29238_09620	ATCC53516_16730	07769_08910	08749_09210	09740_09970	12772_07710	12773_12600	12730_10830	CCUG54800_10050	151023_09290	T160124_09210
12	12	1	IMPACT family member YnfZ	ATCC29238_09630	ATCC53516_16740	07769_08920	08749_09220	09740_09980	12772_07720	12773_12610	12730_10840	CCUG54800_10060	151023_09300	T160124_09220
12	12	1	Penicillin-binding protein 1A	ATCC29238_09650	ATCC53516_16760	07769_08940	08749_09240	09740_09990	12772_07740	12773_12630	12730_10860	CCUG54800_10080	151023_09320	T160124_09250
6	0.271	5	alkaline phosphatase synthesis transcriptional	ATCC29238_09670	ATCC53516_16780	07769_08960	08749_09260	09740_10000	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	LivABC system protein A	ATCC29238_09680	ATCC53516_16880	07769_08960	08749_09260	09740_10010	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	LivABC system protein B	ATCC29238_09690	ATCC53516_16890	07769_08970	08749_09270	09740_10020	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	Serine/threonine transporter SstT	ATCC29238_09700	ATCC53516_16900	07769_08980	08749_09280	09740_10030	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	N-acetyltransferase II-alanine aminotransferase	ATCC29238_09710	ATCC53516_16950	07769_08990	08749_09290	09740_10040	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	Energy-coupled prolyl cis-trans isomerase C	ATCC29238_09720	ATCC53516_16960	07769_09000	08749_09300	09740_10050	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	hypothetical protein	ATCC29238_09730	ATCC53516_16970	07769_09010	08749_09310	09740_10060	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	hypothetical protein	ATCC29238_09780	ATCC53516_17030	07769_09070	08749_09370	09740_10110	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	Phosphate regulation sensor protein PhoSR	ATCC29238_09790	ATCC53516_17040	07769_09080	08749_09380	09740_10120	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
12	12	1	Sensory transduction protein regZ	ATCC29238_09800	ATCC53516_17050	07769_09090	08749_09390	09740_10130	12772_07760	12773_12650	12730_10880	CCUG54800_10100	151023_09340	T160124_09270
24	0.167	6	FtsX-like permease family protein	ATCC29238_09810,ATCC29232	ATCC53516_17080,ATCC53516_17090	07769_09120,07769_09130	08749_09420,08749_09430	09740_10140,09740_10150	12772_08020,12772_08030	12773_12900,12773_12910	12730_11040,12730_11050	CCUG54800_10320,CCUG54800_10330	151023_09520,151023_09530	T160124_09520,T160124_09530
10	4	1	hypothetical protein	ATCC29238_09840	*	07769_09130	08749_09430	*	12772_11560	12773_12650	12730_10900	CCUG54800_10360	151023_09360	T160124_09280
10	4	1	Ura1 domain phosphatase superfamily protein	ATCC29238_09850	*	07769_09140	08749_09440	*	12772_11560	12773_12650	12730_10900	CCUG54800_10360	151023_09360	T160124_09280
4	4	1	hypothetical protein	ATCC29238_09860	*	07769_09150	08749_09450	*	12772_11560	12773_12650	12730_10900	CCUG54800_10360	151023_09360	T160124_09280
4	4.0.5	1	putative ABC transporter ATP-binding protein	ATCC29238_09870	*	07769_09160	08749_09460	*	*	*	*	*	*	*
3	3	1	putative ABC transporter permease protein	ATCC29238_09880	*	07769_09170	08749_09470	*	*	*	*	*	*	*
2	2	1	hypothetical protein	ATCC29238_09890	*	07769_09180	0874							

12	12	1	UDP-N-acetylglucosaminyl-L-glucosamine reductase	ATCC29328_11630	ATCC53516_18630	07769_10990	08749_10990	09748_10990	09748_11660	12772_09120	12773_14590	127306_12600	CCUG54800_12210	151023_10490	T160124_10610
12	12	1	Folylpolyglutamate synthase	ATCC29328_11630	ATCC53516_18630	07769_10990	08749_10990	09748_10990	09748_11660	12772_09120	12773_14590	127306_12600	CCUG54800_12210	151023_10490	T160124_10610
24	0.167	1	Peptide chain release factor 1	ATCC29328_11540	ATCC29328_11540	07769_10990	08749_10990	09748_10990	09748_11660	12772_09120	12773_14590	127306_12600	CCUG54800_12210	151023_10490	T160124_10610
12	12	1	Release factor glutamine methyltransferase	ATCC29328_11550	ATCC53516_18640	07769_11020	08749_10940	09748_10330	09748_11660	12772_09150	12773_14620	127306_12630	CCUG54800_12230	151023_10520	T160124_10640
12	12	1	hypothetical protein	ATCC29328_11560	ATCC53516_18650	07769_11030	08749_10540	09748_10940	09748_11660	12772_09150	12773_14620	127306_12630	CCUG54800_12230	151023_10520	T160124_10640
12	12	1	S05 ribosomal protein L31	ATCC29328_11570	ATCC53516_18660	07769_11040	08749_10980	09748_10550	09748_11660	12772_09150	12773_14620	127306_12630	CCUG54800_12230	151023_10520	T160124_10640
12	12	1	hypothetical protein	ATCC29328_11580	ATCC53516_18670	07769_11050	08749_10980	09748_10550	09748_11660	12772_09150	12773_14620	127306_12630	CCUG54800_12230	151023_10520	T160124_10640
12	12	1	Thio-disulfide interchange protein Dsb precu	ATCC29328_11590	ATCC53516_18680	07769_11060	08749_10980	09748_10570	09748_11660	12772_09150	12773_14620	127306_12630	CCUG54800_12230	151023_10520	T160124_10640
12	12	1	Thioredoxin	ATCC29328_11600	ATCC53516_18690	07769_11070	08749_10980	09748_10580	09748_11660	12772_09150	12773_14620	127306_12630	CCUG54800_12230	151023_10520	T160124_10640
12	12	1	hypothetical protein	ATCC29328_11650	ATCC53516_18290	07769_11090	08749_11010	09748_10590	09748_11660	12772_09230	12773_14690	127306_12700	CCUG54800_12280	151023_10590	T160124_10710
12	12	1	hypothetical protein	ATCC29328_11660	ATCC53516_18300	07769_11100	08749_11020	09748_10600	09748_11660	12772_09240	12773_14700	127306_12710	CCUG54800_12280	151023_10600	T160124_10720
12	12	1	hydroxylase A	ATCC29328_11670	ATCC53516_18310	07769_11110	08749_11030	09748_10610	09748_11660	12772_09250	12773_14710	127306_12720	CCUG54800_12310	151023_10610	T160124_10730
12	12	1	NAD(+)-translocating NADH-quinone reductase	ATCC29328_11680	ATCC53516_18320	07769_11120	08749_11040	09748_10620	09748_11660	12772_09260	12773_14720	127306_12730	CCUG54800_12310	151023_10620	T160124_10740
12	12	1	Electron transport complex protein RnfG	ATCC29328_11710	ATCC53516_18350	07769_11150	08749_11050	09748_10650	09748_11660	12772_09290	12773_14750	127306_12760	CCUG54800_12350	151023_10650	T160124_10770
12	12	1	hypothetical protein	ATCC29328_11730	ATCC53516_18370	07769_11170	08749_11070	09748_10670	09748_11660	12772_09310	12773_14770	127306_12780	CCUG54800_12370	151023_10670	T160124_10790
12	12	1	hypothetical protein	ATCC29328_11750	ATCC53516_18390	07769_11190	08749_11110	09748_10690	09748_11660	12772_09330	12773_14790	127306_12800	CCUG54800_12390	151023_10690	T160124_10810
12	12	1	N-acetylmuramoyl-L-alanine amidase LytC precu	ATCC29328_11760	ATCC53516_18400	07769_11200	08749_11120	09748_10700	09748_11660	12772_09330	12773_14800	127306_12800	CCUG54800_12410	151023_10700	T160124_10820
12	12	1	CAMP factor (Cfa)	ATCC29328_11770	ATCC53516_18410	07769_11210	08749_11130	09748_10710	09748_11660	12772_09330	12773_14810	127306_12810	CCUG54800_12410	151023_10710	T160124_10830
12	12	1	CAMP factor (Cfa)	ATCC29328_11780	ATCC53516_18420	07769_11220	08749_11140	09748_10720	09748_11660	12772_09340	12773_14820	127306_12820	CCUG54800_12420	151023_10720	T160124_10840
24	0.147	1	Papain family amino-acid aminotransferase	ATCC29328_11790	ATCC29328_11790	07769_11230	08749_11150	09748_10730	09748_11660	12772_09340	12773_14820	127306_12820	CCUG54800_12420	151023_10720	T160124_10840
12	12	1	Arginine transport ATP-binding protein ArTM	ATCC29328_11820	ATCC53516_18450	07769_11250	08749_11180	09748_10750	09748_11660	12772_09430	12773_14850	127306_12850	CCUG54800_12450	151023_10750	T160124_10870
12	12	1	Inner membrane amino-acyl ABC transporter	ATCC29328_11820	ATCC53516_18450	07769_11250	08749_11180	09748_10750	09748_11660	12772_09440	12773_14860	127306_12860	CCUG54800_12460	151023_10760	T160124_10880
12	12	1	rRNA pseudouridine synthase A	ATCC29328_11830	ATCC53516_18460	07769_11260	08749_11190	09748_10760	09748_11660	12772_09450	12773_14870	127306_12870	CCUG54800_12470	151023_10770	T160124_10890
12	12	1	Energy-coupling factor transporter transmembrane protein	ATCC29328_11840	ATCC53516_18470	07769_11270	08749_11200	09748_10770	09748_11660	12772_09460	12773_14880	127306_12880	CCUG54800_12480	151023_10780	T160124_10900
24	0.167	1	Energy-coupling factor transporter ATP-binding	ATCC29328_11850	ATCC29328_11850	07769_11280	08749_11210	09748_10780	09748_11660	12772_09460	12773_14880	127306_12880	CCUG54800_12480	151023_10780	T160124_10900
12	12	1	DNA-directed RNA polymerase subunit beta'	ATCC29328_11870	ATCC53516_18490	07769_11310	08749_11240	09748_10810	09748_11660	12772_09480	12773_14910	127306_12910	CCUG54800_12510	151023_10810	T160124_10920
12	12	1	DNA-directed RNA polymerase subunit beta	ATCC29328_11880	ATCC53516_18500	07769_11320	08749_11240	09748_10820	09748_11660	12772_09500	12773_14920	127306_12920	CCUG54800_12520	151023_10820	T160124_10940
12	12	1	AcyL-ACP thioesterase	ATCC29328_11890	ATCC53516_18510	07769_11330	08749_11250	09748_10830	09748_11660	12772_09510	12773_14930	127306_12930	CCUG54800_12530	151023_10830	T160124_10950
12	12	1	AAA-like domain protein	ATCC29328_11900	ATCC53516_18520	07769_11340	08749_11260	09748_10840	09748_11660	12772_09510	12773_14930	127306_12930	CCUG54800_12530	151023_10830	T160124_10950
12	12	1	Nurk domain protein	ATCC29328_11910	ATCC53516_18530	07769_11350	08749_11270	09748_10850	09748_11660	12772_09530	12773_14950	127306_12950	CCUG54800_12550	151023_10850	T160124_10970
12	12	1	Ribosomal RNA small subunit methyltransferase	ATCC29328_11920	ATCC53516_18540	07769_11360	08749_11280	09748_10860	09748_11660	12772_09540	12773_14960	127306_12960	CCUG54800_12560	151023_10860	T160124_10980
12	12	1	KS-glycyl-tRNA synthetase	ATCC29328_11930	ATCC53516_18550	07769_11370	08749_11290	09748_10870	09748_11660	12772_09550	12773_14970	127306_12970	CCUG54800_12570	151023_10870	T160124_10990
12	12	1	hypothetical protein	ATCC29328_11940	ATCC53516_18560	07769_11380	08749_11300	09748_10880	09748_11660	12772_09560	12773_14980	127306_12980	CCUG54800_12580	151023_10880	T160124_11000
12	12	1	hypothetical protein	ATCC29328_11950	ATCC53516_18570	07769_11390	08749_11310	09748_10890	09748_11660	12772_09570	12773_14990	127306_12990	CCUG54800_12590	151023_10890	T160124_11010
12	12	1	DNA polymerase III subunit tau	ATCC29328_11960	ATCC53516_18580	07769_11400	08749_11320	09748_10900	09748_11660	12772_09580	12773_15000	127306_13000	CCUG54800_12600	151023_10900	T160124_11020
12	12	1	hypothetical protein	ATCC29328_11970	ATCC53516_18590	07769_11410	08749_11330	09748_10910	09748_11660	12772_09590	12773_15010	127306_13010	CCUG54800_12610	151023_10910	T160124_11030
12	12	1	hypothetical protein	ATCC29328_11980	ATCC53516_18600	07769_11420	08749_11340	09748_10920	09748_11660	12772_09600	12773_15020	127306_13020	CCUG54800_12620	151023_10920	T160124_11040
12	12	1	Thymidylate kinase	ATCC29328_11990	ATCC53516_18610	07769_11430	08749_11350	09748_10930	09748_11660	12772_09610	12773_15030	127306_13030	CCUG54800_12630	151023_10930	T160124_11050
12	12	1	S05 ribosomal protein L25	ATCC29328_12000	ATCC53516_18620	07769_11440	08749_11360	09748_10940	09748_11660	12772_09620	12773_15040	127306_13040	CCUG54800_12640	151023_10940	T160124_11060
9	9	1	Sigma-factor processing regulatory protein B	ATCC29328_12010	ATCC53516_18630	07769_11450	08749_11370	09748_10950	09748_11660	12772_09630	12773_15050	*	CCUG54800_12650	*	T160124_11070
12	12	1	putative thiol peroxidase	ATCC29328_12020	ATCC53516_18640	07769_11460	08749_11380	09748_10960	09748_11660	12772_09640	12773_15060	*	CCUG54800_12660	*	T151023_10960
10	10	1	putative copper-exporting P-type ATPase V	ATCC29328_12030	ATCC53516_18650	07769_11470	08749_11390	09748_10970	09748_11660	12772_09650	12773_15070	127306_13070	CCUG54800_12670	151023_10970	T160124_11080
1	1	1	hypothetical protein	ATCC29328_12040	ATCC53516_18660	07769_11480	08749_11400	09748_10980	09748_11660	12772_09660	12773_15080	*	CCUG54800_12680	*	T160124_11090
12	12	1	D-alanyl-D-alanine carboxypeptidase	ATCC29328_12060	ATCC53516_18680	07769_11500	08749_11420	09748_11000	09748_11660	12772_09660	12773_15100	127306_13100	CCUG54800_12700	151023_11000	T160124_11120
12	12	1	UDP-N-acetyl-alpha-D-glucosamine C6 dehydratase	ATCC29328_12070	ATCC53516_18690	07769_11510	08749_11430	09748_11010	09748_11660	12772_09670	12773_15110	127306_13110	CCUG54800_12710	151023_11010	T160124_11130
12	12	1	Branched-chain-amino-acid aminotransferase	ATCC29328_12080	ATCC53516_18700	07769_11520	08749_11440	09748_11020	09748_11660	12772_09680	12773_15120	127306_13120	CCUG54800_12720	151023_11020	T160124_11140
12	12	1	ATC family protein S18	ATCC29328_12090	ATCC53516_18710	07769_11530	08749_11450	09748_11030	09748_11660	12772_09690	12773_15130	127306_13130	CCUG54800_12730	151023_11030	T160124_11150
12	13	0.141	Single-stranded DNA-binding protein ssb	ATCC29328_12100	ATCC53516_18720	07769_11540	08749_11460	09748_11040	09748_11660	12772_09700	12773_15140	127306_13140	CCUG54800_12740	151023_11040	T160124_11160
12	12	1	S05 ribosomal protein S6	ATCC29328_12110	ATCC53516_18730	07769_11550	08749_11470	09748_11050	09748_11660	12772_09710	12773_15150	127306_13150	CCUG54800_12750	151023_11050	T160124_11170
12	12	1	hypothetical protein	ATCC29328_12120	ATCC53516_18740	07769_11560	08749_11480	09748_11060	09748_11660	12772_09720	12773_15160	127306_13160	CCUG54800_12760	151023_11060	T160124_11180
12	12	1	Biotin transporter BioY	ATCC29328_12130	ATCC53516_18750	07769_11570	08749_11490	09748_11070	09748_11660	12772_09730	12773_15170	127306_13170	CCUG54800_12770	151023_11070	T160124_11190
12	12	1	isopentenyl-diphosphate delta-isomerase	ATCC29328_12140	ATCC53516_18760	07769_11580	08749_11500	09748_11080	09748_11660	12772_09740	12773_15180	127306_13180	CCUG54800_12780	151023_11080	T160124_11200
12	12</														

12	12	1	Hypothetical protein	ATCC29328_13910	ATCC53516_05040	07769_13360	08792_14460	09740_12800	09749_16430	12722_13790	12723_06410	12730_04590	CCUG54800_03840	T51023_03230	T61024_02950
12	12	1	Ribonucleoside-diphosphate reductase subunit	ATCC29328_13920	ATCC53516_05050	07769_13370	08792_14470	09740_12810	09749_16440	12722_13800	12723_06420	12730_04580	CCUG54800_03850	T51023_03220	T61024_02940
12	12	1	Maltose/maltotriose transporter ATP-binding	ATCC29328_13930	ATCC53516_05060	07769_13380	08792_14480	09740_12820	09749_16450	12722_13810	12723_06430	12730_04570	CCUG54800_03860	T51023_03210	T61024_02930
12	12	1	Putative membrane protein YnfK	ATCC29328_13940	ATCC53516_05070	07769_13390	08792_14490	09740_12830	09749_16460	12722_13820	12723_06440	12730_04560	CCUG54800_03870	T51023_03200	T61024_02920
7	9	0.445	Hypothetical protein	ATCC29328_13960	ATCC53516_05090	07769_13400	08792_14500	09740_12840	09749_16470	12722_13830	12723_06450	12730_04550	CCUG54800_03880	T51023_03190	T61024_02910
3	4	0.36	Hypothetical protein	ATCC29328_13970	*	07769_14510	08792_14510	09740_12850	09749_16480	12722_13840	12723_06460	12730_04540	CCUG54800_03890	T51023_03180	T61024_02900
1	1	1	Hypothetical protein	ATCC29328_13980	*	*	*	09740_12860	09749_16490	12722_13850	12723_06470	12730_04530	CCUG54800_03900	T51023_03170	T61024_02890
12	12	1	Coenzyme PQQ synthase protein D	ATCC29328_13990	ATCC53516_05100	07769_13410	08792_14520	09740_12870	09749_16500	12722_13860	12723_06480	12730_04520	CCUG54800_03910	T51023_03160	T61024_02880
12	12	1	OPT oligopeptide transporter protein	ATCC29328_14000	ATCC53516_05110	07769_13420	08792_14530	09740_12880	09749_16510	12722_13870	12723_06490	12730_04510	CCUG54800_03920	T51023_03150	T61024_02870
12	12	1	Hypothetical protein	ATCC29328_14010	ATCC53516_05120	07769_13430	08792_14540	09740_12890	09749_16520	12722_13880	12723_06500	12730_04500	CCUG54800_03930	T51023_03140	T61024_02860
12	12	1	Pf5-dependent dihydroxyacetone kinase, ADP	ATCC29328_14050	ATCC53516_05010	07769_13440	08792_14550	09740_12900	09749_16530	12722_13890	12723_06510	12730_04490	CCUG54800_03940	T51023_03130	T61024_02850
12	12	1	Aldehyde dehydrogenase	ATCC29328_14070	ATCC53516_05030	07769_13460	08792_14570	09740_12920	09749_16540	12722_13900	12723_06520	12730_04480	CCUG54800_03950	T51023_03120	T61024_02840
12	12	1	Tyrosine-protein kinase YwqD	ATCC29328_14080	ATCC53516_05040	07769_13470	08792_14580	09740_12930	09749_16550	12722_13910	12723_06530	12730_04470	CCUG54800_03960	T51023_03110	T61024_02830
12	15	0.145	Capular polysaccharide type 8 biosynthesis p	ATCC29328_14090	ATCC53516_05050	07769_13480	08792_14590	09740_12940	09749_16560	12722_13920	12723_06540	12730_04460	CCUG54800_03970	T51023_03100	T61024_02820
12	15	0.145	Tyrosine-protein phosphatase YwqE	ATCC29328_14100	ATCC53516_05060	07769_13490	08792_14600	09740_12950	09749_16570	12722_13930	12723_06550	12730_04450	CCUG54800_03980	T51023_03090	T61024_02810
12	12	1	Bacterial SH3 domain protein	ATCC29328_14110	ATCC53516_05070	07769_13500	08792_14610	09740_12960	09749_16580	12722_13940	12723_06560	12730_04440	CCUG54800_03990	T51023_03080	T61024_02800
3	3	1	Hypothetical protein	ATCC29328_14120	*	*	*	*	*	12722_13950	12723_06570	12730_04430	CCUG54800_04000	T51023_03070	T61024_02790
3	3	1	Hypothetical protein	ATCC29328_14130	*	*	*	*	*	12722_13960	12723_06580	12730_04420	CCUG54800_04010	T51023_03060	T61024_02780
12	12	1	Topology modulation protein	ATCC29328_14140	ATCC53516_05080	07769_13510	08792_14620	09740_12970	09749_16590	12722_13970	12723_06590	12730_04410	CCUG54800_04020	T51023_03050	T61024_02770
1	1	1	Hypothetical protein	ATCC29328_14150	*	*	*	*	*	12722_13980	12723_06600	12730_04400	CCUG54800_04030	T51023_03040	T61024_02760
6	0.167	Hypothetical protein	ATCC29328_14160	ATCC53516_05100	07769_13520	08792_14630	09740_12980	09749_16600	09749_16600	12722_13990	12723_06610	12730_04390	CCUG54800_04040	T51023_03030	T61024_02750
8	8	1	Cna protein B-type domain protein	ATCC29328_14170	ATCC53516_05110	07769_13530	08792_14640	09740_12990	09749_16610	12722_14000	12723_06620	12730_04380	CCUG54800_04050	T51023_03020	T61024_02740
12	12	1	Putative acyltransferase	ATCC29328_14180	ATCC53516_05120	07769_13540	08792_14650	09740_13000	09749_16620	12722_14010	12723_06630	12730_04370	CCUG54800_04060	T51023_03010	T61024_02730
10	10	1	Integral membrane protein (intg_mem_TP038)	ATCC29328_14190	ATCC53516_05130	07769_13550	08792_14660	09740_13010	09749_16630	12722_14020	12723_06640	12730_04360	CCUG54800_04070	T51023_03000	T61024_02720
12	12	1	Peptidase family 55I	ATCC29328_14200	ATCC53516_05140	07769_13560	08792_14670	09740_13020	09749_16640	12722_14030	12723_06650	12730_04350	CCUG54800_04080	T51023_02990	T61024_02710
5	5	1	HRAN domain protein	ATCC29328_14210	*	*	*	*	*	12722_14040	12723_06660	12730_04340	CCUG54800_04090	T51023_02980	T61024_02700
2	2	1	DnaI domain protein	ATCC29328_14220	*	*	*	*	*	12722_14050	12723_06670	12730_04330	CCUG54800_04100	T51023_02970	T61024_02690
12	12	1	Outer membrane-specific lipoprotein transport	ATCC29328_14230	ATCC53516_05150	07769_13610	08792_14680	09740_13070	09749_16650	12722_14060	12723_06680	12730_04320	CCUG54800_04110	T51023_02960	T61024_02680
12	12	1	Bacterial flagellin proteins, tetK family	ATCC29328_14250	ATCC53516_05210	07769_13630	08792_14710	09740_13090	09749_16660	12722_14070	12723_06690	12730_04310	CCUG54800_04120	T51023_02950	T61024_02670
11	11	1	Bifunctional AAC/APH	ATCC29328_14260	ATCC53516_05220	07769_13640	08792_14720	09740_13100	09749_16670	12722_14080	12723_06700	12730_04300	CCUG54800_04130	T51023_02940	T61024_02660
12	12	1	dihydropteridine reductase	ATCC29328_14270	ATCC53516_05230	07769_13650	08792_14730	09740_13110	09749_16680	12722_14090	12723_06710	12730_04290	CCUG54800_04140	T51023_02930	T61024_02650
12	12	1	Phosphoribosyltransferase	ATCC29328_14280	ATCC53516_05240	07769_13660	08792_14740	09740_13120	09749_16690	12722_14100	12723_06720	12730_04280	CCUG54800_04150	T51023_02920	T61024_02640
12	12	1	DNA alkyltransfer repair enzyme	ATCC29328_14300	ATCC53516_05300	07769_13680	08792_14760	09740_13140	09749_16710	12722_14120	12723_06740	12730_04270	CCUG54800_04160	T51023_02910	T61024_02630
12	12	1	Hypothetical protein	ATCC29328_14310	ATCC53516_05310	07769_13690	08792_14770	09740_13150	09749_16720	12722_14130	12723_06750	12730_04260	CCUG54800_04170	T51023_02900	T61024_02620
12	12	1	Putative lipid kinase YnfR	ATCC29328_14320	ATCC53516_05320	07769_13700	08792_14780	09740_13160	09749_16730	12722_14140	12723_06760	12730_04250	CCUG54800_04180	T51023_02890	T61024_02610
5	6	1	N-acetylmuramyl-L-alanine amidase LytC pre	ATCC29328_14330	ATCC53516_05330	07769_13710	08792_14790	09740_13170	09749_16740	12722_14150	12723_06770	12730_04240	CCUG54800_04190	T51023_02880	T61024_02600
4	4	1	Hypothetical protein	ATCC29328_14340	*	*	*	*	*	12722_14160	12723_06780	12730_04230	CCUG54800_04200	T51023_02870	T61024_02590
11	13	0.154	ABC transporter ATP-binding protein YnfE	ATCC29328_14350	ATCC53516_05410	07769_13720	08792_14800	09740_13180	09749_16750	12722_14170	12723_06790	12730_04220	CCUG54800_04210	T51023_02860	T61024_02580
11	11	1	Hypothetical protein	ATCC29328_14370	ATCC53516_05430	07769_13750	08792_14850	09740_13210	09749_16810	12722_14220	12723_06820	12730_04210	CCUG54800_04220	T51023_02850	T61024_02570
12	12	1	Regulatory actin-binding protein CmrR	ATCC29328_14380	ATCC53516_05440	07769_13760	08792_14860	09740_13220	09749_16820	12722_14230	12723_06830	12730_04200	CCUG54800_04230	T51023_02840	T61024_02560
12	12	1	TVPS8/MEK4 family inner membrane protein	ATCC29328_14390	ATCC53516_05450	07769_13770	08792_14870	09740_13230	09749_16830	12722_14240	12723_06840	12730_04190	CCUG54800_04240	T51023_02830	T61024_02550
12	12	1	Adenylosuccinate lyase	ATCC29328_14400	ATCC53516_05460	07769_13780	08792_14880	09740_13240	09749_16840	12722_14250	12723_06850	12730_04180	CCUG54800_04250	T51023_02820	T61024_02540
12	12	1	Phosphoribosylamine-glycine ligase	ATCC29328_14410	ATCC53516_05470	07769_13790	08792_14890	09740_13250	09749_16850	12722_14260	12723_06860	12730_04170	CCUG54800_04260	T51023_02810	T61024_02530
12	12	1	Bifunctional purine biosynthesis protein PurH	ATCC29328_14420	ATCC53516_05480	07769_13800	08792_14900	09740_13260	09749_16860	12722_14270	12723_06870	12730_04160	CCUG54800_04270	T51023_02800	T61024_02520
12	12	1	Phosphoribosyltransferase	ATCC29328_14430	ATCC53516_05490	07769_13810	08792_14910	09740_13270	09749_16870	12722_14280	12723_06880	12730_04150	CCUG54800_04280	T51023_02790	T61024_02510
12	12	1	Amidophosphoribosyltransferase precursor	ATCC29328_14440	ATCC53516_05500	07769_13820	08792_14920	09740_13280	09749_16880	12722_14290	12723_06890	12730_04140	CCUG54800_04290	T51023_02780	T61024_02500
12	12	1	Phosphoribosylaminoimidazole-succinocarbox	ATCC29328_14450	ATCC53516_05510	07769_13830	08792_14930	09740_13290	09749_16890	12722_14300	12723_06900	12730_04130	CCUG54800_04300	T51023_02770	T61024_02490
12	12	1	Hypothetical protein	ATCC29328_14460	ATCC53516_05520	07769_13840	08792_14940	09740_13300	09749_16900	12722_14310	12723_06910	12730_04120	CCUG54800_04310	T51023_02760	T61024_02480
9	9	1	Voltage-gated potassium channel KcsA	ATCC29328_14470	ATCC53516_05530	07769_13850	08792_14950	09740_13310	09749_16910	12722_14320	12723_06920	12730_04110	CCUG54800_04320	T51023_02750	T61024_02470
8	8	1	NADH oxidase	ATCC29328_14480	*	07769_13860	08792_14960	09740_13320	09749_16920	12722_14330	12723_06930	12730_04100	CCUG54800_04330	T51023_02740	T61024_02460
4	4	1	Putative aminoacyl-tRNA synthetase RctD	ATCC29328_14490	ATCC53516_05540	07769_13870	08792_14970	09740_13330	09749_16930	12722_14340	12723_06940	12730_04090	CCUG54800_04340	T51023_02730	T61024_02450
11	12	1	NADP-reducing hydrogenase subunit HndA	ATCC29328_14500	ATCC53516_05620	07769_13880	08792_14980	09740_13340	09749_16940	12722_14350	12723_06950	12730_04080	CCUG54800_04350	T51023_02720	T61024_02440
11	11	0.364	Hypothetical protein	ATCC29328_14510	ATCC53516_05630	07769_13890	08792_14990	09740_13350	09749_16950	12722_14400	12723_06960	12730_04070	CCUG54800_04360	T51023_02710	T61024_02430
4	4	1	Hypothetical protein	ATCC29328_14520	ATCC53516_05640	*	*	*	*	12722_14410	12723_06970	12730_04060	CCUG54800_04370	T51023_02700	T61024_02420
10	10	1	Hypothetical protein	ATCC29328_14530	ATCC53516_05650	07769_13910	08792_15010	09740_13360							

Table S2: CRISPR/cas systems in *Fingoldia* sp.

STRAIN NAME	SPECIES	# CRISPR	# SPACERS
07T609	<i>F. magna</i>	1	13
08T492	<i>F. magna</i>	2	6, 6
09T408	<i>F. magna</i>	3	17, 16, 12
09T494	" <i>F. nericia</i> "	1	34
12T272	" <i>F. nericia</i> "	1	41
12T273	" <i>F. nericia</i> "	0	0
12T306	" <i>F. nericia</i> "	1	82
CCUG54800	" <i>F. nericia</i> "	0	0
T151023	" <i>F. nericia</i> "	1	61
T160124	" <i>F. nericia</i> "	1	14
ATCC 29328	<i>F. magna</i>	4	14, 3, 6, 4
ATCC 53516	" <i>F. nericia</i> "	1	87
GED7760A	<i>F. magna</i>	0	0
ACS-171-V-COL3	<i>F. magna</i>	3	6, 17, 14
BVS033A4	<i>F. magna</i>	1	38
SY403409CC001050417	<i>F. magna</i>	1	11
ALB8	<i>F. magna</i>	0	0

***F. magna* 07T609: DR length: 36 Number of spacers: 13**

34785	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	ACGCGATTCTTGAGAGTGGTGCCGCTGATA	34850
34851	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TTCTCTGCTGAGGGGGCTTGAATAA	34916
34917	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	AAGTATTCCTTATCATCTTTTGCGACTGTA	34982
34983	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TACGTTGGAGGGGGAGACCGTTCGGAAGCTA	35049
35050	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	AACTCAAAAAGACGATATCAACGAACAAAT	35115
35116	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TGGATAAAAAATTCATATACATCTACACAA	35181
35182	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TGCCATGAATGTCGCCATCGATTTCATCGA	35247
35248	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	CACGGAAAACATAAAGAGTTGTACGAAAAA	35313
35314	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	GCTATACTGATATACAAAAACTACGATATC	35379
35380	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TTTGTTGCTATGTCGTTGTTGCTATCCAGGA	35446
35447	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TTATATTGCTAAAAATAATGGCGATCGGGG	35512
35513	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	TTCAACTGCATTTCTCAAATTAATAAATGT	35578
35579	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC	AAAACGGCGTATAGGGTCTCGGGGTTCCCT	35644
35645	GTTTGAGAATGATGTAATTCATATAGGTATTA AAC		35680

***F. magna* 08T492: DR length: 30 Number of spacers: 6**

7270	CTTTACATTT CAGTATGATTAGATTTTAAT	TTTCCAGGCTTTCATCCAAGCTGCTTCTAATA	7335
7336	ATTTACATTT CAGTATGAGTAGATTTTAAT	TTGGGCATTGCTGGAGCATTCTTGCTTGAAATT	7400
7401	ATTTACATTT CAGTATGAGTAAATTTTAAT	TTCTCTAATTTGTCAGGTTGGCATTAAGACAAATGCA	7465
7466	ATTTACATTT CAGTATGAGTAGATTTTAAT	ACAAATCCTCAATATTCACAATATAGTCATCAATATC	7532
7533	ATTTACATTTCAATATGAGTAGATTTTAAT	GATTTGATTAATGAAAAGACCATATTCAGAATT	7597
7598	ATTTACATTTCAATATGAGTAGATTTTAAT	TGGAGCTGGTCTTTAGGTTGAAACGACAAAGAAGA	7663
7664	ATTTACATTTCAATATGAGTAGATTTTAAT		7693

***F. magna* 08T492: DR length: 25 Number of spacers: 6**

63273	TTTTCTTATCTGTTGTAGTTTTTA	CTGGTCTACTA ACTTTGTTGTCTGAAGAA	63326
63327	GTTTATCTGCTTTTTCTGATTTTC	TAACAAGAGTTACTTTCTTTCTTTCTGCA	63380
63381	TTTTCTTGAATCTTCGGCTTTTT	CCTTAGCTTAGCTTTCAATTTCTCA	63431
63432	GCCTTTTTTCTTCATCGGCCTTTT	TCTTTGCTTCTTCAGCT	63473
63474	TTTTCTTTGCTTCTTCAGCTTTTT	TCTTTGCTTCTTCGGCTTTTTTGCTTCTTCAGCT	63533
63534	TTTTCTTTGCTTCTTCGGCTTTTT	GTTTTTCTGCCGAATTTTCAAGCCATCT	63587
63588	ACTTCTTTTCTTTTCTGCTTGT		63612

F. magna 09T408: DR length: 36 Number of spacers: 17

25488	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AAAATAACATTGAACAGTTTATACAAGCAA	25553
25554	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATTC AATTTTGAATATCCTTCTTCCGTGAT	25619
25620	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AACATCATATCCGAGAAGTAATATGGAATA	25685
25686	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	GCGTATTGAAATATCATTCCACTGTATATG	25751
25752	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATCATCGCTTACTCAGAAAAATTATTTTG	25817
25818	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TTCTTGAGTTTCTATTTGCTCATAATCAGAA	25884
25885	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATGATACGCTGAAATGGATAGCTCAGATAGG	25951
25952	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	CTGTAGACTTGAAGAATCCCATACAGGATA	26017
26018	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TAATCAAACGATTAAGAAAAAAGAGATAA	26083
26084	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TCTTTTGTGTCCTTCTATCTCTCCACCAAGA	26149
26150	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AGGATATATATCCCCTATCGACTTATCAAG	26216
26217	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AATCATAGCAAGTCTTTTAGTCTTAGTAGT	26282
26283	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	GATATTGGAGATATTGAGGACAAGGAATAT	26348
26349	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AATGCTACAAAAGATAATGGTCAAAGAGTA	26414
26415	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TTATAGGATAAAGTATTTGGGGTTAAATTGA	26480
26481	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AAAGACGGCAAGGACTTATACATACGA	26546
26547	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATGGGTTATAGAGATTCAAAAAAGTTACCG	26613
26614	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC		26649

F. magna 09T408: DR length: 30 Number of spacers: 16

55864	TGTTATACCCGCACACGCGGGGATGATCCT	ATTACCAAGAACAGTTGAAAAAATTGTATGA	55924
55925	TGTTATACCCGCACACGCGGGGATGATCCT	GCACGTTTACGGCTCACTGTATGTTGGTAGT	55985
55986	AGTTATACCCGCACACGCGGGGATGATCCT	AAAGAAAAAGTAAAAGTTGAGTAAAGTTGAGT	56046
56047	AGTTATACCCGCACACGCGGGGATGATCCT	ATCATTACTTATTTCCATAAGCCTATTAATT	56107
56108	CGTTATACCCGCACACGCGGGGATGATCCT	GATATATTGTTTATGTCATGAAGTCCGTCAT	56168
56169	TGTTATACCCGCACACGCGGGGATGATCCT		56229
56230	CGTTATACCCGCACACGCGGGGATGATCCT	GTATAAGTTTTATCTGTAAC TAAATTATCTA	56290
56291	CGTTATACCCGCACACGCGGGGATGATCCT	GTATAAGTTTTATCTGTAAC TAAATTATCTA	56351
56352	CGTTATACCCGCACACGCGGGGATGATCCT	GTATAAGTTTTATCTGTAAC TAAATTATCTA	56412
56413	CGTTATACCCGCACACGCGGGGATGATCCT	ACTTTTAGAAA CTGATG TACTAATTTTATCG	56473
56474	CGTTATACCCGCACACGCGGGGATGATCCT	GTATAAGTTTTATCTGTAAC TAAATTATCTA	56534
56535	CGTTATACCCGCACACGCGGGGATGATCCT	ACTTTTAGAAA CTGATG TACTAATTTTATCG	56595
56596	CGTTATACCCGCACACGCGGGGATGATCCT	GTATAAGTTTTATCTGTAAC TAAATTATCTA	56656
56657	CGTTATACCCGCACACGCGGGGATGATCCT	ACTTTTAGAAA CTGATG TACTAATTTTATCG	56717
56718	CGTTATACCCGCACACGCGGGGATGATCCT	TCATTAGATCATTTTACACGAATTTTACAG	56778
56779	AGTTATACCCGCACACGCGGGGATGATCCC	TGATAACCAAATAAGAAGTCGCAAAATCAA	56839
56840	CGTTATACCCGCACACGCGGGGATAATATT		56869

***F. magna* 09T408: DR length: 31 Number of spacers: 12**

8034	GATTTACATTCCATTCTGGTTAGATTTTAAT	GATTGTTTTATCATAGACTTAACCCTCTGCGT	8097
8098	TATTTACATTCCACTCTGGTTAGATTTTAAT	GAAAAAAGCGACGAAGTACAATTGAAACCTTGATGA	8165
8166	CATTTACATTCCACTCTGGTTAGATTTTAAT	AGCAGTAATAGGAGTTACAAGCTGGTATTATCA	8230
8231	AATTTACATTCCACTCTGGTTAGATTTTAAT	ACAATAGCTTTCGTTTCTGTTGCTTTTTCAAGAA	8295
8296	CATTTACATTCCACTATGGGTAGATTTTAAT	TTATCTTCTGATTCTTCTTGTCTTTTTATCAT	8360
8361	CATTTACATTCCACTATGGGTAGATTTTAAT	TTTCTACGAACCTTGCTCGCCTTGTCATACG	8424
8425	CATTTACATTCCACTATGGGTAGATTTTAAT	GTAATTTAGATATTGATGTAAAAAACATTGTTGTAA	8491
8492	TATTTACATTCCACTATGGTTAGATTTTAAT	TATCTAGATACATATCTAATATATATAATTCCT	8555
8556	TATTTACATTCCACTATGGTTAGATTTTAAT	TAAAGAAGAATTAAGACGTGCCGAAGTATCAGGTC	8621
8622	AATTTACATTCCACTCTGATTAGATTTTAAT	GAACTCAGGTGGTATTACTTTATTTAAAGAAAAGG	8687
8688	TATTTACATTCCACTATGGGTAGATTTTAAT	TAAGACAACAACCAACACTCGAAGTCGGAGAAA	8751
8752	TATTTACATTCCACTATGGGTAGATTTTAAT	CGGGTAAAGTGAGGAGTCTGCAAAGTCTGCTTGT	8817
8818	TATTTACATTCCACTATGAGTAGATTTTAAT		8848

***F. magna* ATCC29328: DR length: 36 Number of spacers: 14**

79845	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TTTATCCTCGTCAAACCTTTTTCCACACAC	79910
79911	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TATGGTGGAGATGAGGAGTATCTACGAAC	79976
79977	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AGTACGAATTTGGATTTACTCCAAACGACG	80042
80043	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AGATTAGGTGAACATACAAATACAGTTACT	80108
80109	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TCAAACCTTGATGAGGTCAAGGATTTGATTT	80174
80175	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATTTCTACACGATTTGTTTCATCATTGAA	80240
80241	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TTGCTATTTTTGTTTTAATCTTTAGTTCCG	80306
80307	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATACTGATTAATCTGAATGGTTGAGTGAT	80372
80373	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	ATTGTTTACAAGCTCCCGAATATAAGCTTG	80438
80439	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TGGTTATAAAAAACCGAAAGCAGAAGTGAA	80504
80505	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	TTTGATGACTACGAATTGCAAGCAGTGTATA	80571
80572	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	AATGATAATTTAAAAGAATACTTAATTTATA	80638
80639	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	GAGTAAAAACATAAAAAAGATTGAGTATGTTG	80704
80705	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC	CTGAAAGTTTAGGATTGACGTTGAGGACA	80770
80771	GTTTGAGAATGATGTAATTTTCATATAGGTATTA AAC		80806

***F. magna* ATCC29328: DR length: 28 Number of spacers: 3**

45598	AGGAACACCCCGCTATTGCTGGGAAAA	ATTGTGCTGTTTTAGGGCCTCCAGTATCTTCCCT	45659
45660	AGGAACACCCCGCATGTGCGGGTAAAA	CTCAACACCGTTGTGTATTACATTATAAC	45720
45721	AGAAACACCCCTGCACTTGCGGGTAAAA	CTGTGGACAAAATCTGTAACATAACAATCCTAT	45781
45782	AGAAACACCCCGCATGTGCGGGTAAAA		45810

***F. magna* ATCC29328: DR length: 28 Number of spacers: 6**

45891	TGGAACACCCCTGCTATTGCTGGTAAAA	AAGTATTATTACGAAAAGTTTATAGATAAAA	45951
45952	AGGAACACCCCGCATGTGCGGGTAAAA	TTATTGATCTCTCATTTTTAGTTCTCTT	46011
46012	AGGAACACCCCGCTTTTGCGGGTAAAA	CTTATTGTTGAAATTATCTTTGTTTTAGAGTT	46072
46073	AGAAATACCCCGCATGTGCGGGTAAACA	TGCTGTGTCAAATGCAAAAAGAAGATGTTTTAAAT	46134
46135	AGGAACACCCCGCATGTGCGGGTAAAA	CATAAAGTTATAATTATAATCTTTTTTATAAC	46195
46196	AGGAACACCCCGCTTGTGCGGGTAAAA	TCATAGATACTTTTTCGCTCCTTGAAATAATC	46256
46257	AGAAACACCCCGCTTGTGCGGGTAAAC		46284

***F. magna* ATCC29328: DR length: 25 Number of spacers: 4**

79988	AACACCCCGCTTGTGCGGGTAAAA	TTTTATTTAGAACTAACTGAGTCAGGCAACAGG	80045
80046	AACACCCCTCGCTTGTGCGGGTAAAA		80106
80107	AACACCCCGCCTGTGCGGGTAATA	TTAATTAAGGAATAGTTTTTCATCAGAAAACGCCATCGCCATCAGG	80175
80176	AACACACTCGCTTGTGCGAGTAAAA	TAAAAAAAATTTAGGAAATGGTGTTATGAGACAGA	80235
80236	AACACACTCGCCATTGCGAGAAATA		80260

F. magna ALB8: none

F. magna GED7760A: none

***F. magna* ACS-171-V-Col3: DR length: 30 Number of spacers: 6**

28319	CTTTCATTCCACTCTAGTTAGATTTTAAT	ATAATATCGTGTTAACTTCTGAGTTAATATAAT	28382
28383	ATTTACATTTAGTATGAGTAGATTTTAAT	CACGTGACTGGCAAGATTGTAAAAATCGATGAAT	28447
28448	ATTTACATTCCACTATGGTTAGATTTTAAT	ACGACCTTGTCTTGTATGATTGAGTCTTTTGAAT	28512
28513	ATTTACATTCCACTCTAGTTAGATTTTAAT	GCTTTCCCTTGCCTTCTACACCGTATTAGCGTACGG	28579
28580	ATTTACATTCCACTCTGGTTAGATTTTAAT	GATAGTTTCAGATAAAGGAACCAGCTTTTCAAGAAA	28645
28646	ATTTACATTCCACTCTGGTTAGATTTTAAC	GTACATGCTCACTGTTGGAAAACATGGCAAAAAGG	28710
28711	ATTTACATTTAGTATGAGTAGATTTTAAT		28741

F. magna ACS-171-V-Col3: DR length: 30 Number of spacers: 17

28841	ATTACATTCCACTATGGGTAGATTTTAAT	ATAAACACAAAGTATCGAATTACAAAGATAGATGT	28905
28906	ATTACATTCCACTCCGGTTATATTTAAT	ACTTACTTGAATTCGGACACATTTCTGCAAACCAATA	28972
28973	ATTACATTCCACTCTGGTTAGATTTAAT	TTGAAGACATAATCGAGACGATTAAGGATGAGAC	29036
29037	ATTTTCATTCCACTCTGGTTAGATTTAAT	TAAAGATACTACAAGAAGATACTTAACTAAGAACAT	29102
29103	ATTACATTCCACTCTGGTTAGATTTAAT	GAGGTGGTTATCTCATGATAGAACTAGGTTTTCAAGA	29170
29171	ATTACATTCCACTCTGGTTAGATTTAAT	TTTGCTTTCGCAGTATCCACAGTGAGTGTGCTCCAAT	29238
29239	ATTACATTTCAGTATGATTAGATTTAAT	TCATATGATAACCTTTTATAGCTAAATCAAATT	29302
29303	ATTTACATTTCAGTATGAGTAGATTTAAT	ATAATGATTATGTTGTGGATATTGACACACTACCAA	29368
29369	ATTACATTTCAGTATGAGTAGATTTAAT	TTGGATTAACCTTACTGCAATTGAAGTAACTTCCCC	29434
29435	ATTACATTTCAGTATGAGTAGATTTAAT	TTAAAAATTTAAATAATACGCTTGATAAAAACTTTT	29501
29502	ATTACATTTCAGTATGAGTAGATTTAAT	CAGAGTTGAAAATAAAGAACTAAGTTTACAACCTTA	29567
29568	ATTACATTTCAGTATGAGTAGATTTAAT	CTCAAGGAGCGATCTCTATAAACAAGCTAATA	29632
29633	ATTACATTTCAGTATGAGTAGATTTAAT	GAACGATCAAGAAATACGATAATTGGATAGCTCAG	29698
29699	ATTACATTTCAGTATGAGTAGATTTAAT	TGCTTTCGCAGTAGACACAGTCAAGTATGCTCCGAT	29764
29765	ATTACATTTCAGTATGAGTAGATTTAAT	AACGGCCATGAAAAGTAAGTGAATGACCTTGTAAG	29829
29830	ATTACATTTCAGTATGAGTAGATTTAAT	GGATTGACCTTGTCAGACTTCAATGACCTAACCGT	29894
29895	ATTACATTTCAGTATGAGTAGATTTAAT	CGTTCATATCTTTTTCAAAGTCGTTTGATGAGCTATT	29961
29962	ATTACATTTCAGTATGAGTAGATTTAAT		29991

F. magna ACS-171-V-Col3: DR length: 36 Number of spacers: 14

11866	ATTTAATACCTATATGAAATTACATCATTCTCAAAC	TGATTGAGCAAATAACGAAAGAGACAAAAG	11931
11932	GTTAATACCTATATGAAATTACATCATTCTCAAAC		11997
11998	GTTAATACCTATATGAAATTACATCATTCTCAAAC	CATAATAGTACCTGTTAAAATCTTCTATAAA	12064
12065	GTTAATACCTATATGAAATTACATCATTCTCAAAC	ATTTGATGTTGATTGTTTCTTTATCGACA	12130
12131	GTTAATACCTATATGAAATTACATCATTCTCAAAC	TCCCAAATCCGAACTTATCTCTCAGTACCA	12196
12197	GTTAATACCTATATGAAATTACATCATTCTCAAAC	GCAAAAAGATAATAAAAAAATACCCCGTGT	12262
12263	GTTAATACCTATATGAAATTACATCATTCTCAAAC	TAAAACATTGAAATACACTACAGAGAGTC	12328
12329	GTTAATACCTATATGAAATTACATCATTCTCAAAC	TCATCATAGTTGCAAATCCTCAATGTTTACA	12395
12396	GTTAATACCTATATGAAATTACATCATTCTCAAAC	TGATTTCGAAAATATCTGTTCTAAAT	12461
12462	GTTAATACCTATATGAAATTACATCATTCTCAAAC	ACTGAAAAAGAGATTTTCTAGATTATATAGCA	12527
12528	GTTAATACCTATATGAAATTACATCATTCTCAAAC	CTCTAGTTTGTTCGTTAGAAACACGTTCTT	12593
12594	GTTAATACCTATATGAAATTACATCATTCTCAAAC	TAAGTTCAAGCACCGCAGGTTCTTTGTCTT	12659
12660	GTTAATACCTATATGAAATTACATCATTCTCAAAC	TTAAAATGTAATGGTATGAATTTTCTAATT	12725
12726	GTTAATACCTATATGAAATTACATCATTCTCAAAC	CCAACATGCAAATGTTAGCTGATTTATAC	12791
12792	GTTAATACCTATATGAAATTACATCATTCTCAAAC		12827

F. magna BVS033A4: DR length: 30

Number of spacers: 38

106	CTTTACATCCCCTCTAGTTAGATTTAAT	ATTGTTTCAAATACACACCCTTATGTTAAAGGCT	171
172	ATTTACATTCCACTATGGGTAGATTTAAT	CCAGTTGCTACATTTGTTGCTATTACTTATTGGTA	236
237	ATTTACATTCCACTATGGGTAGATTTAAT	AGTGTTCGGGCTTATAATGTTGGTGTGTTGGTGT	302
303	ATTTACATTCCACTATGGGTAGATTTAAT	TTAATTGAATAGAATACTTTATTCGGATATTTATC	367
368	ATTTACATTCCACTATGGGTAGATTTAAT	AGCGTATTTCCAAGAAGTGCTGCACCTCCTGTGCGT	433
434	ATTTACATTCCACTCTGGTTAGATTTAAT	CCTCAAAGAACTAATCTTTTTTCGCTCCCTGCCTC	499
500	ATTTACATTCCACTCTGGTTAGATTTAAT	AGGGATAAAGATGGCAAAAACATCAAGGTTCCGCT	564
565	ATTTACATTCCACTCTGGTTAGATTTAAT	GGATTTTATGATTTAAAATTTATTGATGAAGAAGAT	630
631	ATTTACATTCCACTCTGGTTAGATTTAAT	TCCAAGCCAAAAAAGCTCCAGCAATTCGAGACCCAC	697
698	ATTTACATTCCACTCTGGTTAGATTTAAT	ATGTGACCTGCCTTGATTCTAGTTGCATTAGCTCT	763
764	ATTTACATTCCACTCTGGTTAGATTTAAT	ACAATTTTTATTGAAGTTGAACCTATTAATCAAAA	829
830	ATTTACATTCCACTCTGGTTAGATTTAAT	TTAATTTAAAAAAAATTCTCTCAGTTTTCATC	893
894	ATTTACATTCCACTCTGGTTAGATTTAAT	TCAATCGACAGTTCAGATAAAGATTACTTCGAGGAT	959
960	ATTTACATTCCACTCTGGTTAGATTTAAT	AAAGCTCCAATCAGATTTTTACTGTCTCGATTAAGACC	1027
1028	ATTTACATTCCACTCTGGTTAGATTTAAT	AAAAAGATGCAATCAGATTATCTTGCATAGTACAA	1092
1093	ATTTACATTCCACTCTGGTTAGATTTAAT	CGAAGACGGTGAAATCTTGTTAAAGATATTACTCT	1158
1159	ATTTACATTCCACTCTGGTTAGATTTAAT	AAGGCTAAGGAGGGCTCACAATGAAAGAAAAAT	1222
1223	ATTTACATTCCACTCTGGTTAGATTTAAT	TACTATTGTGATGATTTCCAGCTAATGGATTGTG	1287
1288	ATTTACATTCCACTCTGGTTAGATTTAAT	TGTTTTATATCCAGTAACTAAATCTTTGATATCATG	1353
1354	ATTTACATTCCACTCTGGTTAGATTTAAT	GTCAATCCTTGAGTTGAACCTTGCCTGAAGCTTA	1417
1418	ATTTACATTCCACTCTGGTTAGATTTAAT	AAGCAAATTATACCAAAGTTCGACTTAGCTATAAA	1482
1483	ATTTACATTCCACTCTGGTTAGATTTAAT	TGATGCAGTGGGAGGACAAAATTGAACGTGTTAATAT	1548
1549	ATTTACATTCCACTCTGGTTAGATTTAAT	CTTGTAATTGCACCTAAAAAAGTGGCAGAAGCTACT	1614
1615	ATTTACATTCCACTCTGGTTAGATTTAAT		1679
1680	ATTTACATTCCACTCTGGTTAGATTTAAT	TTTTAACTTGCCTTGCTTCTCTGCAAATCCCTC	1746
1747	ATTTACATTCCACTCTGGTTAGATTTAAT	ATGTATTTTAGTACGTCATCGCTAAATGTTTTTCTC	1813
1814	ATTTACATTCCACTCTGGTTAGATTTAAT	TTAAACAGTTTTCTTCATAGCTAACATACTGTTTACT	1880
1881	ATTTACATTCCACTCTGGTTAGATTTAAT	CGACAATATCTGTACCATTAGTCGGTACTATAGCAGC	1947
1948	ATTTACATTCCACTCTGGTTAGATTTAAT	TATCAACTCATGTTCAATCATGACATCTGATTAAT	2013
2014	ATTTACATTCCACTCTGGTTAGATTTAAT	AAAAGAATAAGTGCAAAATGAGTATTAATGAACTAT	2080
2081	ATTTACATTCCACTCTGGTTAGATTTAAT	TAGATTCCGAAAGCAACTGGAACTCTAATAGAT	2147
2148	ATTTACATTCCACTCTGGTTAGATTTAAT	CTTACATGGTCTTAAAAATTATCCAAATTAAGT	2212
2213	ATTTACATTCCACTCTGGTTAGATTTAAT	AAGAAAAGTTATTAAGAAGAGGTCGTAGCTTTCTAC	2279
2280	ATTTACATTCCACTCTGGTTAGATTTAAT	TTTTGTATTGATAATTTTCAATTGTTGAAATCTTTAAT	2347
2348	ATTTACATTCCACTCTGGTTAGATTTAAT	GAAGGGAAAGCAGGTAAGGTTTCAAGCATTCAAAG	2412
2413	ATTTACATTCCACTCTGGTTAGATTTAAT	GGATTTGACGAAAAATCCAACCTGGGAGGATGCGAC	2477
2478	ATTTACATTCCACTCTGGTTAGATTTAAT	TCGTTAATTTCTTATATTTTGTATTAATGAA	2541
2542	ATTTACATTCCACTCTGGTTAGATTTAAT	TTGTACTATATCCTCGAATAGTCAATTTAAAATT	2606
2607	ATTTACATTCCACTCTGGTTAGATTTAAT		2636

***F. magna* SY403409CC001050417: DR length: 36 Number of spacers: 11**

17675	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TGCATTCTCCCATATCAGCATCTGCCAA	17740
17741	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	ACATTTTTTAATTTGAGAAATGCAGTTGAA	17806
17807	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TGTCCTTTTTCAGAATTATCTCTTTTTCC	17872
17873	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TTCTGTAAAGTCTTCATTGTCTAACAATT	17938
17939	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	GAACGATAAGCTACCATATCCGTTTTTGTC	18005
18006	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TGTCCTTTTTCAGAATTATCTCTTTTTCCG	18071
18072	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TTTCGCTTCGTACTTCTTACCATCGAACA	18137
18138	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TGCTGTAATACTATCGTACTCACTTTGTG	18203
18204	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	ATCGATTTCGGCACTGATGTTCAAATAACT	18269
18270	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	ACCTTAGGACCAACAGGACCAGTTTTCCG	18335
18336	GTTTAATACCTATATGAAATTACATCATTCTCAAAC	TTAGCATGTAGTATCCACTGACGTAGTTG	18401
18402	GTTTAATACCTATATGAAATTACATCATTCTCAAAC		18437

***"F. nericia"* 09T494: DR length: 30 Number of spacers: 34**

36946	ATTTACATTCCAATATGGGTGGATTTAAT	TGGGGCGTAGCTGGTGCCTTTTAGCTGGAAAT	37010
37011	ATTTACATTCCACTTTGGGTAGATTTAAT	CAAGTCATATTCAAACTGGATCATGCGAAAAAGA	37074
37075	ATTTACATTCCACTTTGGGTAGATTTAAT	AATGAATCCTTGAGCGCCTTGAAGTCCGGGGTCTCCT	37142
37143	ATTTACATTTCAATATGAGTAGATTTAAT	AAGAGTTAAAAGAGGAGATGTGAGTCAATGTAGCTT	37208
37209	ATTTACATTTCAGTATGATTAGATTTAAT	GGAGCAATACGAATTGCAAACCTCAAAGAAGAGTGA	37273
37274	ATTTACATTTCAGTATGAATAGTTTAAATG	CTTCTGGACCAACCTTTAACCCTTTATTCCA	37337
37338	ATTTACATTCCATTCTGGTTAGATTTAAT	GTCATGAGTGGACATATAACTTGAAGCTCAAAAA	37401
37402	ATTTACATTCCACTCTGGTTAGATTTAAT	GAAGTTGTGGATAGCAGAAATCAAAGGGCATCTTA	37466
37467	ATTTACATTCCACTCTGGGTAGATTTAAT	TAAATTGCTTTGTGGATATCAGAAAATGTTACGATA	37532
37533	CTTTACATTCCATTCTGGTTAGATTTAAT	AGGAAGTTACCAGTTTAGGGAACAAGAATTCACAT	37598
37599	CTTTACATTCCATTCTGGTTAGATTTAAT	AAGTGGCAAAGACGGACAACCTCCATCTGGGTTAGT	37664
37665	CTTTACATTCCATTCTGGTTAGATTTAAT	AAGTTAATCCCCCTTGACCATCTTCTTATATAAAAA	37731
37732	CTTTACATTCCATTCTGGTTAGATTTAAT	TTATCTTCAAGGTTTGAGGGGATATAATGCAAGTCT	37797
37798	CTTTACATTCCATTCTGGTTAGATTTAAT	TTTACTTGAAATCTTTATCAACATCAATTAATTA	37863
37864	CTTTACATTCCATTCTGGTTAGATTTAAT	TTCTGCTGAATGTGTTACCAACAATTGCAAAGATT	37929
37930	CTTTACATTCCATTCTGGTTAGATTTAAT	TTTAGGACTTGGTGCTAACATTATGAGTGGAAATTT	37995
37996	CTTTACATTCCATTCTGGTTAGATTTAAT	TTTCCAGTGAAGCTAGCTTCAATTAACCTGATTAAGT	38061
38062	CTTTACATTCCATTCTGGTTAGATTTAAT	TTTACTTGAAATCTTTATCAACATGAATTAATTA	38127
38128	CTTTACATTCCATTCTGGTTAGATTTAAT	GAATAGAAAATCAACAATTATTTCAAACAGAAAATA	38193
38194	CTTTACATTCCATTCTGGTTAGATTTAAT	TTCTCCAAAGTCAAATTTTTCAGTTTTGAAAATTGAT	38260
38261	CTTTACATTCCATTCTGGTTAGATTTAAT	TCAATCATTTTCGTAATAATCAATAATTTTAAAGT	38325

38326	CTTTACATTCCATTCTGGTTAGATTTAAT	AACTTGAACAGAATATCCGTATCCCTCCTCTGTGAT	38391
38392	CTTTACATTCCATTCTGGTTAGATTTAAT	CAAACAAGGTCAAAGATAGGATTAAGTGGAATAC	38457
38458	CTTTACATTCCATTCTGGTTAGATTTAAT		38523
38524	CTTTACATTCCATTCTGGTTAGATTTAAT	TTCAATTTGAGTGTGTTACCAATAATTGCAAAGATTT	38589
38590	CTTTACATTCCATTCTGGTTAGATTTAAT	CTCTTTTCTTTAGTGAATCATATTCAAGTTTTCG	38655
38656	CTTTACATTCCATTCTGGTTAGATTTAAT	TAAATAGGACACAAAGAGATTATCTCACTACAAG	38720
38721	CTTTACATTCCATTCTGGTTAGATTTAAT	CTTTTATACTAAAATCTTCAATATCAAAATATAT	38784
38785	CTTTACATTCCATTCTGGTTAGATTTAAT	TTGTCTTGTCTGTGTTTTCTCTTTTCGTAGAT	38850
38851	CTTTACATTCCATTCTGGTTAGATTTAAT	TTTACCCCATATAATTTACATATGTTTTATCATAAAT	38916
38917	CTTTACATTCCATTCTGGTTAGATTTAAT	TCTTTCTTACTATAACTTATTATACCTT	38982
38983	CTTTACATTCCATTCTGGTTAGATTTAAT	TCTAATGCAAACGGTCTAAATTTTTTGGTTTTGG	39048
39049	CTTTACATTCCATTCTGGTTAGATTTAAT	CTTTGTTAAGCTTAAAGCTTGGAGAATATCTAATAAA	39115
39116	CTTTACATTCCATTCTGGTTAGATTTAAT	AATAATTTTTAATGTATAATGAACTTGATTATTAT	39181
39182	CTTTACATTCCATTCTGGTTAGATTTAAT		39211

"F. nericia" 12T272: DR length: 30 Number of spacers: 41

68572	ATTTACATTCCATTCTGGTTGATTTAAT	TAAAAATAGACAATGGCAAGAGGGCAAGAGATCTCA	68638
68639	ATTTACATTCCATTTGGTTGATTTGAT	CAGTAAGTTGCGTTGTAGTTACTTTTCTATGAAG	68703
68704	ATTTAAATTTTCATTATGAGTAGGTTTAAAT	TGTCTTTTAAAGTCCA TAGAACCTGCTATCGTATATTACATT CACATAATATG	68789
68790	ATTTACATTCCACTCTGGTTAGATTTAAT	TGAAGTATTGTATACTTTTAAATCTATTAGCTATCAC	68856
68857	ATTTACATTCCACTTTGGTTAAATTTAAT	TATATTCTTGCCAAGTAAACTTTTAAAAGTTCAAAA	68922
68923	ATTCACATTCCATTCTGGTTAAATTTAAT	TCATAAAGAATTTACCAATATTTATATAATCATT	68987
68988	ATTTACATTCCACTCTGGTTAAATTTAAT	CCCTCATCTGTGATAGGGTAAATAAAAATAACTGTA	69052
69053	ATTTACATTCCACTCTGGTTAAATTTAAT	ATATTTACCACCATAATTTACATAAGTTTGATTATAGAT	69121
69122	ATTTACATTCCACTCTGGTTAAATTTAAT	TCTACATTTAAAACCTCTTTATATATTTGCTCTTGTG	69188
69189	ATTTACATTCCACTCTGGTTAAATTTAAT	ATGGTTATTGAAAAAGATGACGGTGGCTCTGGTGGT	69254
69255	ATTTACATTCCACTCTGGTTAAATTTAAT	TGAGGATAAGGTAATGTCGAATTTAGTATTGATATT	69320
69321	ATTTACATTCCACTCTGGTTAAATTTAAT	AACAATCGTGACGTACCCGCACAGCTTAGAGTGAA	69385
69386	ATTTACATTCCACTCTGGTTAAATTTAAT	CCATATTCTGTCCCCTTCGCCATTATCCAAGGAAG	69451
69452	ATTTACATTCCACTCTGGTTAAATTTAAT	AATGAAAAAACAAAATCCTAGACGTTATCAAGTCGC	69517
69518	ATTTACATTCCACTCTGGTTAAATTTAAT	TGGAAGGTAAAAGCATTGCTAACATTACAAGAG	69581
69582	ATTTACATTCCACTCTGGTTAAATTTAAT	AAAGCTAAAAGCGGAGCAATAACAGCCAAAATAAC	69646
69647	ATTTACATTCCACTCTGGTTAAATTTAAT	CTTTAGCTGGATAGGATTTGACCATGAGCAGAG	69714
69715	ATTTACATTCCACTCTGGTTAAATTTAAT	ATATAATCATAACTGTACTTTGTAATTTCAA	69780
69781	ATTTACATTCCACTCTGGTTAAATTTAAT	TTTTTATATAAAGAAGACGGTCAAGGTGGTTTGAC	69845
69846	ATTTACATTCCACTCTGGTTAAATTTAAT	CAAACTTTTAAAAATTTGACCTTTTCGTATTGCCAT	69911

69912	ATTACATTCCACTCTGGTTAAATTTAAT	GTGCTTGATAAATTTGTGCATAATCATTAACTAA	69976
69977	ATTACATTCCACTCTGGTTAAATTTAAT	TAAATTGTTTTATTATTTTCATTAATCCAGTTATTA	70042
70043	ATTACATTCCACTCTGGTTAAATTTAAT	TCACCTAAAAAATGTTATTTAAATCATCTATTCTT	70107
70108	ATTACATTCCACTCTGGTTAAATTTAAT		70173
70174	ATTACATTCCACTCTGGTTAAATTTAAT	TGGAACAAAAAATTGGCAGTAGAAAATTTGACGGAACATTAC	70245
70246	ATTACATTCCACTCTGGTTAAATTTAAT	TTCCAGTTGGTAGTTTATAATTTAACATAATAGC	70310
70311	ATTACATTCCACTCTGGTTAAATTTAAT	CAATAAAATTGTCTATATGTGATATTTTCGTTTACTAA	70377
70378	ATTACATTCCACTCTGGTTAAATTTAAT	ATTGTTATTAATTTACCTTGCATTTTATCAATGAT	70443
70444	ATTACATTCCACTCTGGTTAAATTTAAT	TATTATACCAAGTTTACCTAAATTTGAT	70508
70509	ATTACATTCCACTCTGGTTAAATTTAAT	TAAGCCATTCTTTTAGGTCTTTGATGCCTCAAGAGA	70574
70575	ATTACATTCCACTCTGGTTAAATTTAAT	TCATTAAAGCAATGCTAATCTGTAAGTA	70639
70640	ATTACATTCCACTCTGGTTAAATTTAAT	CTGAACTCATAAATTGAAATAATAGGTCAACTTCGTT	70706
70707	ATTACATTCCACTCTGGTTAAATTTAAT	GTAGCTTTTCCATCTCTGTAGAGTTCTACTTCTATT	70772
70773	ATTACATTCCACTCTGGTTAAATTTAAT	CTTGGTATTATCAGAAATACTTCTCTAGCAACA	70837
70838	ATTACATTCCACTCTGGTTAAATTTAAT	TCATTTGCAATTGCTCAACTTACGAAGAAAGTTTT	70903
70904	ATTACATTCCACTCTGGTTAAATTTAAT	TCAGTTTTAACAACTGCAAGAAAATCATCCCACATAAATTC	70974
70975	ATTACATTCCACTCTGGTTAAATTTAAT	TACATTTTCTCCAAGTAGATTGGGTCTATACTGTG	71039
71040	ATTACATTCCACTCTGGTTAAATTTAAT	GTTGTACTTTCTTCTACTGTATCAACAAGTGT	71104
71105	ATTACATTCCACTCTGGTTAAATTTAAT	CCCAATGTTTCGTGTGCTCCAAGTGAATAATT	71168
71169	ATTACATTCCACTCTGGTTAAATTTAAT	ATTTATATTACCCTTGATTTCTTTATTTTGAAAAAC	71234
71235	ATTACATTCCACTCTGGTTAAATTTAAT	GTTGTACTTTCTTCTACTGTATCAACAAGTGT	71299
71300	ATTACATTCCACTCTGGTTAAATTTAAT		71329

"F. nerica" 12T273: none

"F. nerica" 12T306: DR length: 30 Number of spacers: 82

14108	ATTAATCTATCCAGAGTGAATGTAAT	TTGTCCCATATCGTTAATAAATGTTGAAAATTTTG	14173
14174	ATTAATCTATCCAGAGTGAATGTAAT	CTACTAAAAATGATGAAATATGAGAAATGAAAT	14239
14240	ATTAATCTATCCAGAGTGAATGTAAT	CTTGTGTGTGTTAATATCATTGTCATTTTCAATAA	14308
14309	ATTAATCTATCCAGAGTGAATGTAAT	ATGATATATAGCAACTGTAAAAATGCTTCCCT	14372
14373	ATTAATCTATCCAGAGTGAATGTAAT	GAAACAAACAAAAATATTGTTTTAATTTTGACAA	14437
14438	ATTAATCTATCCAGAGTGAATGTAAT	AACCTAACATTTGTTGATAATTTGTATTAATAAATC	14505
14506	ATTAATCTATCCAGAGTGAATGTAAT	AATGGTAATATTAGTGTCGATAATTTAAAGAAATTA	14571
14572	ATTAATCTATCCAGAGTGAATGTAAT	ACATAGTACCTAGTTTTCAATTTCTTTAAATA	14636
14637	ATTAATCTATCCAGAGTGAATGTAAT	CTATATCAATTATATTATACATTATCTCAATTAACAAA	14704
14705	ATTAATCTATCCAGAGTGAATGTAAT	ACAGTAAATGTTTTGAAAACTTGAACCTTTACAACCA	14773
14774	ATTAATCTATCCAGAGTGAATGTAAT	AAATCAAGTGGTAATACAGATTGGCAAAAAAGTTAAC	14839

14840	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TTAGTAAATGAAATTAGTCACATAGATAATTTTGT	14904
14905	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TTTAAATCTTTATAACAAGTATATAATACATTTATA	14970
14971	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TACTACAAGTTAATGTATAATCTTGTATAGTTTATAG	15037
15038	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATGGCAATACGAAAAGGTCAAGTTTTCAAAGTTTAAAT	15106
15107	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TTTATTTAAGTGACCGTAAACTGATAAATATTTAT	15171
15172	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GAACAACTTGAAAATGGATAATAAATATTACCAAATT	15238
15239	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TATGGTAAATACAGTATCGATAATCTTAAAAAATTAA	15305
15306	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TACTCATTTTTTGAAAAGCTTGTAATCTCTAAAC	15371
15372	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TGAATATTAACATATATAAAGTGAACCCATCTTTTAT	15439
15440	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	AAGAAATAATTTATTGAGGAATGGTGCTAAAAAAGA	15506
15507	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TTAGTAAACGAAATATCACATATAGACAATTTTAT	15571
15572	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GATAGTATTGACCCTTTATTTAGAAAAAATGTTAAA	15639
15640	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ACAATAAAATTTATTGAATTTTATGATATGATTGA	15704
15705	ATTAAAATCTATCCAGAGTGGAAATGTAAAT		15769
15770	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	CTAAATGTTCCGTCAAATTTACGACTCTAGTTTTGTT	15838
15839	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GAATTTATGTGGGACGATTTCTAGCAGTTGTGA	15903
15904	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ACACCAAAGTAGCTTTTTTAAATCATATCCC	15967
15968	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TCTGGATTGTGGGTTAATATCGTCAGCTATTTTAC	16034
16035	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TTTATCTGAAAAAATGTTGAATTTAAATGGATAT	16100
16101	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	AATTTCCACGCCAAAAAAGCCCTGCGATTCCAA	16164
16165	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TCCATACCCAATAGTGAATTTGCAACGCAAAAG	16230
16231	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATTTTAATTTGAATAGAGGGTAAATGTTTCATCTTAA	16297
16298	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATTTAATTATGTGTGCTACATCAACTATTTACTCATT	16364
16365	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	AGTTTTGTCCAGATTTTATTACAAATACTAACCA	16429
16430	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GTTTTAGCAAATCCTCCGTAAAATTGATAAAATTTTGT	16498
16499	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GAATATCAGCTAAAAGCGTCTAAGAAATGGTATAA	16563
16564	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TAAATCTAAATAAATTTCAAATTCATATACTCT	16627
16628	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	AAAGTTGAATATTATAACACGCTTGAGTTAATGAAC	16693
16694	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATATTAATGGTATATATTTGCTATTCAACCTCTG	16759
16760	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATAAATCGTTATATTTAACCCTAAATCAATACTTT	16825
16826	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATTGCACGTGAAATATTAGCACATAAGTTTTTCATC	16891
16892	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	CTTTATAGTATAATTTTATAAGTTAAAGTGAGT	16957
16958	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GAATTTTGTTTTCGTTTTAAAAATAATTTAATTA	17023
17024	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATAAGAAAAAATATTATACAACGTAATTATATCACG	17089
17090	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	GAATTTTTGTTTTCGTTTTAAAAATAATTTAATTTAG	17156
17157	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	CAACGAACAAAAAGAAGATGGAACAAGCAAGGTTAA	17222
17223	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TTTTTTGGGAAAATGTGAATTTGTTTTGTTTTTTC	17287
17288	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	ATCTCTAGAATTAACAAGATCTGACACTCATCAA	17352
17353	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	CAAGAAACACCATTTGGAATAGTTATAGACGTTA	17417
17418	ATTAAAATCTATCCAGAGTGGAAATGTAAAT	TAATTAGATACCACCTATCATATCATTTTCTTTATT	17483

17484	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATGAATATAAAGATTATAAAAATAGTAATAAGAGAT	17548
17549	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATTTAACCTAATACTTTATCTTATAACTATTAT	17612
17613	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATCGTTGCCCTTACGTGTTTTTGACAAGTGAAGAAA	17678
17679	ATTAAAATCTATCCAGAGTGGAATGTAAAT	GACGAAAAATACAAAGGTATTATATTTACTACTA	17742
17743	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATATATAATAAAACATATGTCAACTATGGGGGCAA	17807
17808	ATTAAAATCTATCCAGAGTGGAATGTAAAT	GAATTTTCGACTCTCATAATCTCTTTAAAGTCTCAT	17874
17875	ATTAAAATCTATCCAGAGTGGAATGTAAAT	TTGTAAGTGTGTCCAGCTTTTAAGATATATTGAAATAA	17942
17943	ATTAAAATCTATCCAGAGTGGAATGTAAAT	TTTGTTATTAATTTGTGGCGTAACTATGTCTTAA	18007
18008	ATTAAAATCTATCCAGAGTGGAATGTAAAT	CTTAAAAGACATTAAGAGGGATTAATAATAGATGG	18073
18074	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATTAATGACATAATCAAATTTACACGAAGAACGTT	18138
18139	ATTAAAATCTATCCAGAGTGGAATGTAAAT	TTAAAAGTGAATGAAATGTTTGTGTGCAAGATAT	18203
18204	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATGTTTTAATAGCGAATTCAAAAAGTTGTTTGA	18267
18268	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ACATATTTAAAAGTAAATAAGCAATTCTGTGAAAGA	18333
18334	ATTAAAATCTATCCAGAGTGGAATGTAAAT	GCTATTATGCTAAATTATCCTTTACCTGTGGATA	18398
18399	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATAGACTCTTTAAATACCTTGAATATCTTCATT	18463
18464	ATTAAAATCTATCCAGAGTGGAATGTAAAT	TCCAAAACCTCGTTTTGAAAATCAAGCAGGTGTCCCT	18529
18530	ATTAAAATCTATCCAGAGTGGAATGTAAAT	AGAACAGTTGTTGATACAGTAGAAGAAAGTACAAC	18594
18595	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATCATTGATAAAAATGCAAAATGAAATTAATAACAA	18659
18660	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ACAAATCCTGATGGCTCTTGCCATCATTACCAC	18723
18724	ATTAAAATCTATCCAGAGTGGAATGTAAAT	AAAGACAGTAACACGATTTATTCATTACGGAGTAG	18789
18790	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATTTTTGATTTACATGTCATGGCAAGGTTACAAT	18854
18855	ATTAAAATCTATCCAGAGTGGAATGTAAAT	ATTTCTCCGACTTCCAATGTTGGTTGCTTACGAATAA	18921
18922	ATTAAAATTTAACCAGAGTGGAATGTAAAT	TTACACAGAAAAGTACTAACAATGCGACTGACTGG	18987
18988	ATTAAAATTTAACCAGAGTGGAATGTAAAT	AAGAACAATTGTGTCGGAATAGGTAAGTTTCCTGATA	19054
19055	ATTAAAATTTAACCAGAGTGGAATGTAAAT	GATGGAGTGGAGGCTTTTATGTTTTTGATATATCTAT	19121
19122	ATTAAAATTTAACCAGAGTGGAATGTAAAT	ATTTAAACTAAAGGAAGTGAGGATATGCAACAAAC	19186
19187	ATTAAAATTTAACCAGAGTGGAATGTAAAT	GTTGGCTTGGGAATTGCAGGTGCTTTTTGGCTTGGAA	19254
19255	ATTAAAATCTACCCAGAGTGGAATGTAAAT	TTCTCAACATCAATCAAATTCAGTGTAGCTTTGA	19318
19319	ATTAAAATCTACCCAGAGTGGAATGTAAAT	GGGAAAACCTGGTGCAACTGGACCATAAGGACCACCAGGG	19387
19388	ATTAAAATTTAACCATAGTGGAATGTAAAT	AGTACTACATCTTCTACATCATAAAAAATCTTTTGC	19452
19453	ATTAAAATCTACTCATACTGAAATGTAAAT	ACGATTAGTGGTATTGATAAGGATATGGGAGTAGT	19517
19518	ATTAAAATTTAACCAAAGTGGAATGTAAAT		19547

"*F. nericia*" CCUG54800: none

"F. nericia" T151023: DR length: 30

Number of spacers: 61

11514	ATTTACATTCCAATATGGGTAAATTTTAAT	CACAATATGAATTAGATCCTTACTAGGTACAAGG	11578
11579	ATTTACATTCCACTCTGGGTAAATTTTAAT	CGTCGTTTGTATCATAATAGCCCAATCTACATA	11642
11643	TTTACATTCCATTCTGGTTAAACTTTAAT	ACAACACCGAAAGCATTGTTCTTTTTATGTCTCG	11707
11708	ATTTACATTCCATTCTGGTTAAATTTTAAT	AATAAGAGGTGTTAAATAGTGATATATCTTTTTAC	11772
11773	ATTTACATTCCACTCTGGTTAAATTTTAAT	ATATGAACAAGTATTACAGAAAACACAAAACAATGGT	11839
11840	ATTTACATTCCATTCTGGTTAAATTTTAAT	GACATAAAGGCAACGCTCGGAACAGTCGCTCCAGT	11904
11905	ATTTACATTCCAATCTGGGTAAATTTTAAC	GATATGGCTGAAAAGTATTTGGGAAATGGCAGACGA	11970
11971	ATTTACATTTCAATATGAGTAGATTTTAAT	GTAATGATTGATAAGTAGTATCTAAAATATCATC	12035
12036	CTTTACATTTCAATATGAGTAGATTTTAAT	GCAATTATCCAGTCGCCTGGCTTGATGTCAATCTC	12100
12101	TTTACATTTCAATATGAGTAGATTTTAAT	CTGATACGGGCACITTTCTTTTCAGACTTCCAACGC	12166
12167	TTTACATTTTCAGTATGAGTAGATTTTAAT	TAATAAATTAATCCGCCAATACCTGCGAATATCAAA	12232
12233	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TACAGATAGTTCTAGTAATCTCAAGTATTAATTTAG	12301
12302	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CTTGTGCTATGATATAAGCTTTTTGGTATTCTTCATCA	12369
12370	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TAGAATAGAGGTAATAATATGATATATCTTTTTAC	12434
12435	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TTTAGCATGATTTTCATCAAGTGTTCATTTTTGCT	12499
12500	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GCAAGTGCTGAAGAAATCGCAGGAGTTCAGAAGCGGC	12567
12568	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CAATTTTGTACAGATTCGACAATAATATATAGCC	12635
12636	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TACTACAGATAAAAAACGCAAAAAGTTTTCTGAAC	12701
12702	ATTTACATTTTCAGTATGAGTAGATTTTAAT	AAGACAGTAACACGATTTATTTTCATAACGGAGTAGT	12767
12768	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GGACTTGAAAAAGAGTTGACGTATTCAAGCACTAG	12832
12833	ATTTACATTTTCAGTATGAGTAGATTTTAAT	AAACTAACAAGGTTGCACTCTCAAGTGCAAGTGA	12897
12898	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GAGGTTAGATTTATGTTTAAGATTGAAAGAAAAGA	12962
12963	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TGAAGAAGATCATTACATCAAGCCAATCCAAAAAT	13027
13028	ATTTACATTTTCAGTATGAGTAGATTTTAAT		13092
13093	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CTTATTTGCATAAGTGTTCATATCTTACCTACATAG	13159
13160	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CAAATAAACTTGTGAATTTGTAAGAGCCTTGTCTTC	13226
13227	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CTCAACTCAATGGGAGATGCAATGACTGCATCATC	13293
13294	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GATTGGATTAATTCCTTACTCAGCACAGAAAAT	13357
13358	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CACAGATAATACCATGTTTTAAGTTACAGATCA	13421
13422	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GTAGTTTCCCAAAAACCTCGTCTATGTTTGCAAATGA	13487
13488	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TAGCTTCTGGCTATTAACITTTGATGCTTSC	13551
13552	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GCAATGAGTTCAGTAGGTATTGAAGCTGAAGCAGG	13616
13617	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TACCATCAAGTTACGAAGTCTCCAATGTAGTCGCTC	13682
13683	ATTTATATTTTCAGTATGAGTAGATTTTAAT	CGTCTGAATCCCTTTGATTTATTGATAAAGAGTTG	13747
13748	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GAAAAGATATGGGTCTATATATTGTTCCGGGGGT	13813
13814	ATTTACATTTTCAGTATGAGTAGATTTTAAT	AAATAATCAGTTTTTCATTGTTCTGAAGGTTAATTTT	13879
13880	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CAGATAGTGTCTACATCTGTTTCTCAAAGCAT	13943
13944	ATTTACATTTTCAGTATGAGTAGATTTTAAT	GTCAATTCCTTCATGAATTGCAAGTGGCGCTTCATA	14009
14010	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TGAGGATATGAGGGTCAAAGGAATTTCTGATTTAAC	14075

14076	ATTTACATTT CAGTATGAGTAGATTTTAAT	GCTGTGAGGTTTGTGTTTCGCCCATGTCTATCA	14139
14140	ATTTACATTT CAGTATGAGTAGATTTTAAT	CGAGACACTGGTGGTCGTGGTGAAGTTACAATCAA	14204
14205	ATTTACATTT CAGTATGAGTAGATTTTAAT	ACACGAAGAGCCTAGTTTATAGGCCTTTTCTTAGG	14271
14272	ATTTACATTT CAGTATGAGTAGATTTTAAT	AGATATTATCATCATAATCGTCATCTCCACGATG	14337
14338	ATTTACATTT CAGTATGAGTAGATTTTAAT	ATGGCTGCTGTGGATACATTTTTGGTACTATATT	14402
14403	ATTTACATTT CAGTATGAGTAGATTTTAAT	TATACAATATTTTGTAGATTTTGCAGTAAGTTATCT	14468
14469	ATTTACATTT CAGTATGAGTAGATTTTAAT	TGTTTAATTCTCGAGACTGGCAAGCATGTAAAAAC	14533
14534	ATTTACATTT CAGTATGAGTAGATTTTAAT	GCATAGAATAGAGGGAAAGATGATTTATTTATTTAC	14599
14600	ATTTACATTT CAGTATGAGTAGATTTTAAT	TTTAATAATCGTCTTCTTTTAATTGTTATGAAAA	14664
14665	ATTTACATTT CAGTATGAGTAGATTTTAAT	CCCTGCTGCAATTAAGACCAACTCACATCTTCTGC	14730
14731	ATTTACATTT CAGTATGAGTAGATTTTAAT	TTATTAACCTTGATTGTGAAGTCTTTAACAGA	14793
14794	ATTTACATTT CAGTATGAGTAGATTTTAAT	GTGTGAAAGGAAGTTAATATGGAGAATTTATTAAT	14858
14859	ATTTACATTT CAGTATGAGTAGATTTTAAT	CCAACATCAGTCTTTTAATCATTGCTTGAAGT	14923
14924	ATTTACATTT CAGTATGAGTAGATTTTAAT	TGGCATTGTTATAAGTTCGTGAGTCTGGAAACTC	14989
14990	ATTTACATTT CAGTATGAGTAGATTTTAAT	GATGGATAAATTGCTCTGGTAGTGTGAGACTCGAAA	15055
15056	ATTTACATTT CAGTATGAGTAGATTTTAAT	TCACCTGATCATTAGTTTATATATGATAGTAA	15120
15121	ATTTACATTT CAGTATGAGTAGATTTTAAT	AATTAGTAGTACTTTAGATAATAAACTACGAAATA	15185
15186	ATTTACATTT CAGTATGAGTAGATTTTAAT	TGCCTATATCTGAAATGGTGGAAATTTTGATTTA	15250
15251	ATTTACATTT CAGTATGAGTAGATTTTAAT	TCTTCGGTGGTGGATTCAAAGAAAACTATCGGCTAT	15317
15318	ATTTACATTT CAGTATGAGTAGATTTTAAT	TTGGAAAGCTTGGCAAGATTAAGATGAAATTAAT	15381
15382	ATTTACATTT CAGTATGAGTAGATTTTAAT	ATATGTTGGACAAAGGACACACTTTTGATTATATCTT	15448
15449	ATTTACATTT CAGTATGAGTAGATTTTAAT	TCGGCTTTGGATAAAACATTTCTCGGTTATATAAAC	15514
15515	ATTTACATTT CAGTATGAGTAGATTTTAAT		15544

"F. nericia" T160124: DR length: 31

Number of spacers: 14

49457	GATTTACATTTCACTCTGGGTAGATTTTAAT	AATAGTTGCGCCAACATACTCAACACTACTAATAC	49522
49523	TATTTACATTTCACTCTGGGTAGATTTTAAT	TTACTAGAAGCTATCTGAACATAAATGTCGAAGA	49587
49588	CATTTACATTTCACTCTGGTTAAATTTTAAT	CATTTCTGCTGCTGCTTATTATCAGGTCTATAG	49653
49654	TATTTACATTTCACTCTGGTTAAATTTTAAT	GTATAATAAATCCAGCTGATCTCCCTCTATATG	49721
49722	ACTTTACATTTCACTCTGGTTAAATTTTAAT	TCAAATTGGATCATGGTTTGAAGTAAATTCAAAA	49787
49788	CCTTTACATTTCACTCTGGTTAAATTTTAAT	CCGATTAATTCAAGTCCTTTGTTACCTCTTTTG	49852
49853	TATTTACATTTCAATATGGTTAGATTTTAAT	AATGATATGCGGTGTACAAAGATGACAAGTTTGAGT	49919
49920	TATTTACATTTCAATATGGTTAGATTTTAAT	GAGAGGCCGAAGAAAAGGAAGAGGTCTTGTAATG	49985
49986	TATTTACATTTCAATATGGTTAGATTTTAAT	TCGCTTTCGAGTATCCACAGTCAAGTATGCTCCAA	50052
50053	TATTTACATTTCAATATGGTTAGATTTTAAT	CTAATCTTCAAGTATTTCTGGGAGCTGTTCGA	50116
50117	GATTTACATTTCAATATGGTTAGATTTTAAT	TTCATGAGTGCAGCACATGTGTCCAGTACTGT	50181
50182	AATTTACATTTCAATATAGTTAGATTTTAAT	GACAAAAACGCAAAAAGCTTTTTGAATCTAGATA	50246

50247	CATTACATTCCAATATGGTTAGATTTTAAT	AATACACGTCCGATGTAGTTTTCTTCGGCGAAAA	50311
50312	TATTACATTCCAATATGGTTAGATTTTAAT	AGAGCACCTTATAAGTTGATACTCAATTCAACTT	50376
50377	AATTACATTCCAATATGGTTAGATTTTAAT		50407

"F. nericia" ATCC53516: DR length: 30 Number of spacers: 87

985861	ATTTAAATTCATTCTGGTAAGATTTTAAT	CAATTGTAACAGACTACAACGTATAGCTTTGATAA	985926
985927	ATTTACATTCCACTCTGGGTAGATTTTAAT	CCAATTTTTGTTTACCTTTTTCAAAAAAGTTACCTTT	985993
985994	ATTTACATTCCACTCTGGATAGATTTTAAT	CTGGACAAGATAAGTTAACCATATTAGCAGAAATATT	986060
986061	ATTTACATTCCACTATGGTTAAATTTTAAT	AACAGTGGATCTTTTTCTTTACTTTTGTA AACAT	986125
986126	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TCCACCAAATACAACGCAGTGTCCCTCTTTTCTTC	986191
986192	ATTTACATTTTCAGTATGAATAGATTTTAAT	AGCGTATCAAGAAATACGATATTTGGATAGCTCAC	986256
986257	ATTTACATTTTCAGTATGAGTAGATTTTAAT	TAGCGCGGGTAAGGCTATAATTGATGGATTCTTAAA	986322
986323	ATTTACAATTCAGTATGAGTAGATTTTAAT	CCTAAATCTAACCCGTCAACGGTAACCGCCTTAT	986388
986389	ATTTACATTTTCAGTATGAGTAGATTTTAAT	AGACACTTGAGAAAAATCAAGTGAAAGGAGAAATA	986454
986455	ATTTACATTCCACTCTGGGTAGATTTTAAT	ATTAATCGTGAAATTGACAAAGGCCAAAACATTAAC	986519
986520	ATTTACATTCCACTCTGGGTAGATTTTAAT	TCTGTACTATAACCCCTGATCTGTAATTTAAAATT	986584
986585	ATTTACATTCCACTCTGGGTAGATTTTAAT	CGAATTGGAATGGGTAATATTCTAGGTGGAACACT	986649
986650	ATTTACATTCCACTCTGGGTAGATTTTAAT	TGATAGCAACGACTTGCAGAATATCACAATTGTGCA	986715
986716	ATTTACATTCCACTCTGGGTAGATTTTAAT	TAGGTCTTATTGTTCTAGAGATATCAGAATCGATATC	986782
986783	ATTTACATTCCACTCTGGATAGATTTTAAT	GTTTCGATACCTAATCCAACCTACGCCGATGTTGTC	986847
986848	ATTTACATTCCACTGTGGTTAAATTTTAAT	TTTAGGAACAGTAGCACCTGTCGGCTTGGGAATTGC	986913
986914	ATTTACATTTTCAGTATGAGTAGATTTTAAT	CAATTCGAATAGTAAGGCTTGGTAGGGCTATGG	986978
986979	ATTTACATTTTCAGTATGAATAGATTTTAAT	GCATAAGCTTCAGAACTCTATAGTCTTCCAACT	987043
987044	CTTTACATTTTCAGTATGAATAGATTTTAAT	TCCAATCGCAACTTTTGTGCGATCACGTATTGGTA	987109
987110	CTTTACATTTTCAGTATGAATAGATTTTAAT	AACGAATATGAGATGGACAAAAAAGACGATGAGAA	987174
987175	CTTTACATTTTCAGTATGAATAGATTTTAAT	TGCGTTAAAGCAATTTGCTATTACTTCTCTTTGGA	987240
987241	CTTTACATTTTCAGTATGAATAGATTTTAAT	ATTGAAGTAATCTTGATGTTTTCTTGAGCTAATAT	987306
987307	CTTTACATTTTCAGTATGAATAGATTTTAAT	GGACGAATTGTCAATATGCAATTAGCACTATATCAGA	987373
987374	CTTTACATTTTCAGTATGAATAGATTTTAAT		987437
987438	CTTTACATTTTCAGTATGAATAGATTTTAAT	TCAATGAATCATCTAGCCCTTTTATATCCACTCTAA	987503
987504	CTTTACATTTTCAGTATGAATAGATTTTAAT	GATATGAGCGATGAAAACCTCGGAGCAAATTTGAG	987568
987569	CTTTACATTTTCAGTATGAATAGATTTTAAT	GGTTTTAGTTATGATTTATCTTTTTACTGGTACTCC	987634
987635	CTTTACATTTTCAGTATGAATAGATTTTAAT	AATGGAAATTTTTCTTTTATAATCAAATTTTTTA	987698
987699	ATTTACATTTTCAGTATGAATAGATTTTAAT	GCAGTGTCTTATACCTCTGCATACTGGGCTAACGT	987765
987766	ATTTACATTTTCAGTATGAATAGATTTTAAT	GTTTTGTGCTTTAATTTCAACAGTATCACATGCTAG	987832
987833	ATTTACATTCCAGTATGATTAGATTTTAAT	TCGATATGTTAGTACTCACTAATTAAGATAT	987898
987899	ATTTACATTCCAGTATGATTAGATTTTAAT	AGTGTTCGTA AATAGTAGAGAAGCAATATTAAGTT	987963

987964	ATTACATTCCAGTATGATTAGATTTAAT	ATAAACTCAGAATTTTTACTTATAAAAAAAGCT	988028
988029	ATTACATTCCAGTATGATTAGATTTAAT	GGTTTAAATTATGCTTTGAGATTAT	988084
988085	TAAAACATTCCAGTATGATTAGATTTAAT	TTTTTGTGCTTTACTTGCTACAGTAAGCCATGCGAG	988150
988151	ATTACATTCCATTCTGGTTGGATTTAAT	AATGATTGGTGGAGGAGTTCTATTAATCGTAATGGC	988216
988217	ATTACATTCCATTCTGGTTGGATTTAAT	TCTACAAAAAAGTTGGTAGCACATCAACATTTGT	988282
988283	ATTACATTCCATTCTGGTTGGATTTAAT	CTTTTTAAGTGCAGATTGATTCCTTCGGAACGTC	988349
988350	ATTACATTCCATTCTGGTTGGATTTAAT	TGCGACTGGTGCAGGATATTTCTATGAGTTGAAGTC	988415
988416	ATTACATTCCATTCTGGTTGGATTTAAT	TATCAACATTAAGCGTGTTCGTTACTACTTTTAG	988482
988483	ATTACATTCCATTCTGGTTGGATTTAAT	TATAATAGTTTGATAAAATTTCAAGAGGAGTATCAA	988549
988550	ATTACATTCCATTCTGGTTGGATTTAAT	AATAAGTGATTCGCAATGAAAGTCAGTGAGACAAC	988615
988616	ATTACATTCCATTCTGGTTGGATTTAAT	TCTGATAATTTACTTTATGTTGTTTCATAAAGGC	988681
988682	ATTACATTCCACTCTGGGTAGATTTAAT	TAATTTTTGCAAGTTGGTCTAAGTCTTTGGAATTTTT	988748
988749	ATTACATTCCACTCTGGGTAGATTTAAT	TATAAAAACTTTAATACATCATAAGAATAAAAA	988813
988814	ATTACATTCCACTCTGGGTAGATTTAAT	AGAATAGGAGGAAAACTTTGATATATCTTTTAC	988877
988878	ATTACATTCCACTCTGGGTAGATTTAAT	ATGTGAACCTACCATCATCTTCTACGCATAAGCCTC	988944
988945	ATTACATTCCACTCTGGGTAGATTTAAT	AAAGAAATACAGCCGTTAAAGTATGATTGGGAGTATA	989011
989012	ATTACATTCCACTCTGGGTAGATTTAAT	CATCCATCATTTGTTGAATTTTCAAAGCATTGATA	989076
989077	ATTACATTCCACTCTGGGTAGATTTAAT	TCCGTTTAGTCGATAAAAAGTAAACTCGCTGTTTTC	989142
989143	ATTACATTCCACTCTGGGTAGATTTAAT	TTCATCTTTTTCTTTTTTAACTTATCCTTATAGT	989207
989208	ATTACATTCCACTCTGGGTAGATTTAAT	ATGTTTAGGTGGAGATAAATTTTTCAGTTTATAATAA	989273
989274	ATTACATTCCACTCTGGGTAGATTTAAT	TTATAATTTTAAAGCACATTTCTCTCAATCTTAGGT	989340
989341	ATTACATTCCACTCTGGGTAGATTTAAT	GTGAGGTTTTGTATGATTTATTTACTGGAAGTCC	989408
989409	ATTACATTCCACTCTGGGTAGATTTAAT	TCTGATGGAGGAGATAATGATATTTATTATTCTGA	989473
989474	ATTACATTCCACTCTGGGTAGATTTAAT	CCAAAGCGGCATTTAAAGACTTAAAGGAGAATC	989537
989538	ATTACATTCCACTCTGGGTAGATTTAAT	AAAGAATCTCTTCGATTTTCAAGTTAGAACAAC	989602
989603	ATTACATTCCACTCTGGGTAGATTTAAT	CAAGCTAAAAAAGCTCCAGCAATCCAAGTCCCAC	989667
989668	ATTACATTCCACTCTGGGTAGATTTAAT	CACATCTGCAAGATTTTATCTCTTGATAAATAATATC	989734
989735	ATTACATTCCACTCTGGGTAGATTTAAT	CCCATAAACTAAAAATTTCAACCATCTCAGATAT	989798
989799	ATTACATTCCACTCTGGGTAGATTTAAT	CCAAGCCAAGAAAGCCCCAGCAATTCGAGTCCGAC	989864
989865	ATTACATTCCACTCTGGGTAGATTTAAT	AAATGAATCTCTCGCATTTAAGATTAGAACAAC	989930
989931	ATTACATTCCACTCTGGGTAGATTTAAT	ATATCATACGGCGATAATGCTAGAGTTACTGAGCT	989995
989996	ATTACATTCCACTCTGGGTAGATTTAAT	GATGCAGTCGCGAGTTCAATAAAAAATTTGCGATTTA	990062
990063	ATTACATTCCACTCTGGGTAGATTTAAT	AGCAAGAAATGTCATTGGCTCACTTGGATTAAGTGT	990128
990129	ATTACATTCCACTCTGGGTAGATTTAAT	TTTACCGCATTTTGGAAATGCTTGACCTACAGCCTG	990193
990194	ATTACATTCCACTCTGGGTAGATTTAAT	TTTTTCCATGTAATCATTTAACGTCTCTGCTGAATA	990259
990260	ATTACATTCCACTCTGGGTAGATTTAAT	AAACTCAAATTATCCCGATAAGTCATTCTTACAAA	990325
990326	ATTACATTCCACTCTGGGTAGATTTAAT	CAATGAAAGAGAAAAAACCCTTCTATAAGAAAGTA	990390
990391	ATTACATTCCACTCTGGGTAGATTTAAT	ACGCTCTTTTTATCTAAAATTGCGTTGAAATAAAT	990456
990457	ATTACATTCCACTCTGGGTAGATTTAAT	TACTACATCAACAGAAAAAGATTACAAAAATATTTGG	990523
990524	ATTACATTCCACTCTGGGTAGATTTAAT	TCCCTGCGTTGTTTACGTCTGAGTAAGGTAAGTCCG	990588

990589	ATTACATTCCACTCTGGGTAGATTTAAT	TTGAATAATATTTTTAAAGTGTTCAATCTTTTGAT	990654
990655	ATTACATTCCACTCTGGGTAGATTTAAT	TTAACAGTTGGCGAAAAAATACTATCGAAATTG	990718
990719	ATTACATTCCACTCTGGGTAGATTTAAT	TTAGATGTTAGTTACAACACATTAGCAAGCTATCGAACAA	990788
990789	ATTACATTCCACTCTGGGTAGATTTAAT	AATGAATCTCTACGCATTTAAGATTTGAACATAT	990853
990854	ATTACATTCCACTCTGGGTAGATTTAAT	TGAATTTGTTGTATCTGAAACATAAATTATCTAAATT	990919
990920	ATTACATTCCACTCTGGGTAGATTTAAT	AAGTCTTCATGGCAGTATAAGACGGAAGACGAACAA	990985
990986	ATTACATTCCACTCTGGGTAGATTTAAT	GATTCATCAAAGATAAAGTATCTTTCAAATCAAA	991050
991051	ATTACATTCCACTCTGGGTAGATTTAAT	AATCAAAAAGCATTTTTTAAACAACACGTTTGATGT	991115
991116	ATTACATTCCACTCTGGGTAGATTTAAT	GCACAACCTGAGGATTACTCTGTAAAAGCTAGAAAA	991181
991182	ATTACATTCCACTCTGGGTAGATTTAAT	TCATAATTAAATCTATCCATGCCGATCGCTTATCAAA	991248
991249	ATTACATTCCACTCTGGGTAGATTTAAT	TCAAGCTTTTTGCCAAGAAGTCTTTCCTGCTCTG	991312
991313	ATTACATTCCACTCTGGGTAGATTTAAT	CTCTACTTGACCAGCAGCATTTAATCTTAATTT	991376
991377	ATTACATTCCACTCTGGGTAGATTTAAT	GTATGATCCAATGAGTTCTCTTTACGAGTCCGT	991441
991442	ATTACATTCCACTCTGGGTAGATTTAAT	TAGAGCCTTGTTCTTGCTATGATATACGCTTTT	991508
991509	ATTACATTCCACTCTGGGTAGATTTAAT	TTGGGTAAAAGAAGCGTTAGAAATAGCAATGAAAAA	991574
991575	ATTACATTCCACTCTGGGTAGATTTAAT		991604

Table S3A: Predicted genomic islands in the genome of *F. magna* 07T609

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
65901	75199	9298	OXZ41700.1	B9N58_00255	65901	66770	1	hypothetical protein
65901	75199	9298	OXZ41701.1	B9N58_00260	66757	68745	1	exopolyphosphatase
65901	75199	9298	OXZ41702.1	B9N58_00265	68726	69172	1	50S ribosomal protein L9
65901	75199	9298	OXZ41703.1	B9N58_00270	69205	70542	1	replicative DNA helicase
65901	75199	9298	OXZ41704.1	B9N58_00275	70539	71102	1	N-acetyltransferase
65901	75199	9298	OXZ41705.1	B9N58_00280	71107	71865	1	DNA replication protein
65901	75199	9298	OXZ41706.1	B9N58_00285	71868	72845	1	DNA replication protein DnaC
65901	75199	9298	OXZ41707.1	B9N58_00290	72842	73486	1	NAD(P)H-hydrate epimerase
65901	75199	9298	OXZ41708.1	B9N58_00295	73987	74529	1	ECF transporter S component
65901	75199	9298	OXZ41709.1	B9N58_00300	74513	75199	1	radical SAM protein
185658	190851	5193	OXZ41632.1	B9N58_00840	185658	186299	-1	hemolysin III
185658	190851	5193	OXZ41633.1	B9N58_00845	186453	186956	1	acetyltransferase
185658	190851	5193	OXZ41634.1	B9N58_00850	186956	187690	1	hydrolase
185658	190851	5193	OXZ41524.1	B9N58_00855	190276	190851	1	cell filamentation protein Fic
313682	318134	4452	OXZ41489.1	B9N58_01405	313682	314023	1	plasmid mobilization relaxosome protein MobC
313682	318134	4452	OXZ41490.1	B9N58_01410	314128	314343	1	transcriptional regulator
313682	318134	4452	OXZ41491.1	B9N58_01415	314350	315393	1	DNA (cytosine-5-)-methyltransferase
313682	318134	4452	OXZ41492.1	B9N58_01420	315397	316479	1	restriction endonuclease
313682	318134	4452	OXZ41493.1	B9N58_01425	316524	318134	1	ABC transporter ATP-binding protein
733227	739719	6492	OXZ41083.1	B9N58_03590	733227	733925	1	DNA-binding response regulator
733227	739719	6492	OXZ41084.1	B9N58_03595	733966	734550	1	peptidylprolyl isomerase
733227	739719	6492	OXZ41085.1	B9N58_03600	734552	735184	1	thymidine kinase
733227	739719	6492	OXZ41086.1	B9N58_03605	735206	735676	-1	S-ribosylhomocysteine lyase
733227	739719	6492	OXZ41087.1	B9N58_03610	735685	736788	-1	rod shape-determining protein RodA
733227	739719	6492	OXZ41088.1	B9N58_03615	736863	737696	1	endonuclease IV
733227	739719	6492	OXZ41089.1	B9N58_03620	737677	738303	1	endonuclease III
733227	739719	6492	OXZ41090.1	B9N58_03625	738371	739291	1	aspartate carbamoyltransferase
733227	739719	6492	OXZ41091.1	B9N58_03630	739291	739719	1	aspartate carbamoyltransferase regulatory subunit
756103	762234	6131	OXZ41108.1	B9N58_03715	756103	757791	1	hypothetical protein
756103	762234	6131	OXZ41109.1	B9N58_03720	757802	758599	1	pyruvate, phosphate dikinase regulatory protein
756103	762234	6131	OXZ41110.1	B9N58_03725	758683	760116	1	serine/threonine protein kinase
756103	762234	6131	OXZ41111.1	B9N58_03730	760118	760792	1	protein phosphatase
756103	762234	6131	OXZ41112.1	B9N58_03735	760849	762234	1	MiaB
795264	799700	4436	OXZ41144.1	B9N58_03900	795264	795599	-1	histidine triad nucleotide-binding protein
795264	799700	4436	OXZ41145.1	B9N58_03905	795646	796938	-1	methylthiotransferase MtaB
795264	799700	4436	OXZ41146.1	B9N58_03910	796938	797663	-1	rRNA methyltransferase
795264	799700	4436	OXZ41147.1	B9N58_03915	797656	798582	-1	50S ribosomal protein L11 methyltransferase
795264	799700	4436	OXZ41148.1	B9N58_03920	798582	799700	-1	molecular chaperone DnaJ
954114	1006418	52304	OXZ40898.1	B9N58_04620	954114	955391	-1	ABC transporter permease
954114	1006418	52304	OXZ40899.1	B9N58_04625	955589	955876	-1	cupin
954114	1006418	52304	OXZ40900.1	B9N58_04630	955944	956516	-1	uracil-DNA glycosylase
954114	1006418	52304		B9N58_04635	956655	956857	-1	hypothetical protein
954114	1006418	52304		B9N58_04640	956885	957130	-1	hypothetical protein
954114	1006418	52304		B9N58_04645	957132	957936	-1	ABC transporter
954114	1006418	52304		B9N58_04650	957923	958642	-1	iron ABC transporter permease
954114	1006418	52304	OXZ40901.1	B9N58_04655	958702	959460	-1	SAM-dependent methyltransferase
954114	1006418	52304	OXZ40902.1	B9N58_04660	959555	960148	1	transcriptional regulator
954114	1006418	52304	OXZ40903.1	B9N58_04665	960299	960490	-1	hypothetical protein
954114	1006418	52304		B9N58_04670	960685	961231	1	transposase
954114	1006418	52304	OXZ40904.1	B9N58_04675	961267	962100	1	hypothetical protein
954114	1006418	52304	OXZ40905.1	B9N58_04680	962331	963533	-1	ABC transporter substrate-binding protein
954114	1006418	52304	OXZ40906.1	B9N58_04685	963533	963958	-1	FMN-binding domain-containing protein
954114	1006418	52304	OXZ40907.1	B9N58_04690	963955	964674	-1	GTPase
954114	1006418	52304	OXZ40908.1	B9N58_04695	964686	965834	-1	ABC transporter permease
954114	1006418	52304	OXZ40909.1	B9N58_04700	965824	967107	-1	ABC transporter permease
954114	1006418	52304	OXZ40910.1	B9N58_04705	967116	968378	-1	hypothetical protein
954114	1006418	52304	OXZ40911.1	B9N58_04710	968435	969100	-1	hypothetical protein
954114	1006418	52304	OXZ40912.1	B9N58_04715	969110	970447	-1	iron transporter
954114	1006418	52304	OXZ40913.1	B9N58_04720	970450	971127	-1	ABC transporter ATP-binding protein
954114	1006418	52304	OXZ40914.1	B9N58_04725	971127	971522	-1	hypothetical protein
954114	1006418	52304	OXZ40915.1	B9N58_04730	971537	971719	-1	ferrous iron transporter B
954114	1006418	52304	OXZ40916.1	B9N58_04735	971967	972197	-1	ferrous iron transport protein A
954114	1006418	52304	OXZ40917.1	B9N58_04740	972495	972602	-1	replication initiator domain protein A
954114	1006418	52304	OXZ40875.1	B9N58_04745	973855	974205	-1	hypothetical protein
954114	1006418	52304	OXZ40876.1	B9N58_04750	974230	974955	-1	ABC transporter permease
954114	1006418	52304	OXZ40877.1	B9N58_04755	974939	975823	-1	multidrug ABC transporter ATP-binding protein
954114	1006418	52304	OXZ40878.1	B9N58_04760	975801	976043	-1	hypothetical protein
954114	1006418	52304	OXZ40879.1	B9N58_04765	976036	976434	-1	hypothetical protein
954114	1006418	52304	OXZ40880.1	B9N58_04770	976565	977170	-1	DNA-binding response regulator
954114	1006418	52304	OXZ40881.1	B9N58_04775	977142	978689	-1	hypothetical protein
954114	1006418	52304	OXZ40882.1	B9N58_04780	978977	979633	-1	DNA-binding protein
954114	1006418	52304	OXZ40883.1	B9N58_04785	979677	987320	-1	DNA helicase
954114	1006418	52304	OXZ40884.1	B9N58_04790	987403	989616	-1	hypothetical protein
954114	1006418	52304	OXZ40885.1	B9N58_04795	989652	990614	-1	DNA (cytosine-5-)-methyltransferase

954114	1006418	52304	OXZ40886.1	B9N58_04800	990607	992328	-1 DNA topoisomerase III
954114	1006418	52304	OXZ40887.1	B9N58_04805	992392	993258	-1 bacteriocin
954114	1006418	52304	OXZ40888.1	B9N58_04810	993273	995696	-1 copper amine oxidase
954114	1006418	52304	OXZ40889.1	B9N58_04815	995683	995922	-1 hypothetical protein
954114	1006418	52304	OXZ40890.1	B9N58_04820	995937	998516	-1 hypothetical protein
954114	1006418	52304	OXZ40891.1	B9N58_04825	998524	1000947	-1 conjugal transfer protein TraE
954114	1006418	52304		B9N58_04830	1002140	1002496	-1 hypothetical protein
954114	1006418	52304	OXZ40837.1	B9N58_04835	1002498	1002788	-1 hypothetical protein
954114	1006418	52304	OXZ40838.1	B9N58_04840	1002798	1003661	-1 hypothetical protein
954114	1006418	52304	OXZ40839.1	B9N58_04845	1003672	1003887	-1 conjugal transfer protein
954114	1006418	52304	OXZ40840.1	B9N58_04850	1003889	1004200	-1 single-stranded DNA-binding protein
954114	1006418	52304		B9N58_04855	1004396	1005864	-1 hypothetical protein
954114	1006418	52304	OXZ40841.1	B9N58_04860	1005882	1006418	-1 ClbS/DfsB family four-helix bundle protein
956655	968378	11723		B9N58_04635	956655	956857	-1 hypothetical protein
956655	968378	11723		B9N58_04640	956885	957130	-1 hypothetical protein
956655	968378	11723		B9N58_04645	957132	957936	-1 ABC transporter
956655	968378	11723		B9N58_04650	957923	958642	-1 iron ABC transporter permease
956655	968378	11723	OXZ40901.1	B9N58_04655	958702	959460	-1 SAM-dependent methyltransferase
956655	968378	11723	OXZ40902.1	B9N58_04660	959555	960148	1 transcriptional regulator
956655	968378	11723	OXZ40903.1	B9N58_04665	960299	960490	-1 hypothetical protein
956655	968378	11723		B9N58_04670	960685	961231	1 transposase
956655	968378	11723	OXZ40904.1	B9N58_04675	961267	962100	1 hypothetical protein
956655	968378	11723	OXZ40905.1	B9N58_04680	962331	963533	-1 ABC transporter substrate-binding protein
956655	968378	11723	OXZ40906.1	B9N58_04685	963533	963958	-1 FMN-binding domain-containing protein
956655	968378	11723	OXZ40907.1	B9N58_04690	963955	964674	-1 GTPase
956655	968378	11723	OXZ40908.1	B9N58_04695	964686	965834	-1 ABC transporter permease
956655	968378	11723	OXZ40909.1	B9N58_04700	965824	967107	-1 ABC transporter permease
956655	968378	11723	OXZ40910.1	B9N58_04705	967116	968378	-1 hypothetical protein
970450	979633	9183	OXZ40913.1	B9N58_04720	970450	971127	-1 ABC transporter ATP-binding protein
970450	979633	9183	OXZ40914.1	B9N58_04725	971127	971522	-1 hypothetical protein
970450	979633	9183	OXZ40915.1	B9N58_04730	971537	971719	-1 ferrous iron transporter B
970450	979633	9183	OXZ40916.1	B9N58_04735	971967	972197	-1 ferrous iron transport protein A
970450	979633	9183	OXZ40917.1	B9N58_04740	972495	972602	-1 replication initiator domain protein A
970450	979633	9183	OXZ40875.1	B9N58_04745	973855	974205	-1 hypothetical protein
970450	979633	9183	OXZ40876.1	B9N58_04750	974230	974955	-1 ABC transporter permease
970450	979633	9183	OXZ40877.1	B9N58_04755	974939	975823	-1 multidrug ABC transporter ATP-binding protein
970450	979633	9183	OXZ40878.1	B9N58_04760	975801	976043	-1 hypothetical protein
970450	979633	9183	OXZ40879.1	B9N58_04765	976036	976434	-1 hypothetical protein
970450	979633	9183	OXZ40880.1	B9N58_04770	976565	977170	-1 DNA-binding response regulator
970450	979633	9183	OXZ40881.1	B9N58_04775	977142	978689	-1 hypothetical protein
970450	979633	9183	OXZ40882.1	B9N58_04780	978977	979633	-1 DNA-binding protein
1022942	1030690	7748	OXZ40859.1	B9N58_04950	1022942	1023106	-1 hypothetical protein
1022942	1030690	7748	OXZ40860.1	B9N58_04955	1023211	1023579	-1 hypothetical protein
1022942	1030690	7748	OXZ40874.1	B9N58_04960	1023590	1023787	-1 hypothetical protein
1022942	1030690	7748	OXZ40861.1	B9N58_04965	1023879	1025384	-1 cardiolipin synthase
1022942	1030690	7748	OXZ40862.1	B9N58_04970	1025449	1026423	-1 choloylglycine hydrolase
1022942	1030690	7748	OXZ40863.1	B9N58_04975	1026718	1027017	-1 hypothetical protein
1022942	1030690	7748	OXZ40864.1	B9N58_04980	1027079	1028539	-1 conjugal transfer protein TraA
1022942	1030690	7748	OXZ40865.1	B9N58_04985	1028618	1028806	-1 hypothetical protein
1022942	1030690	7748	OXZ40866.1	B9N58_04990	1028781	1029101	-1 hypothetical protein
1022942	1030690	7748	OXZ40867.1	B9N58_04995	1029212	1030690	-1 Lsa family ABC-F type ribosomal protection protein
1028781	1037345	8564	OXZ40865.1	B9N58_04985	1028618	1028806	-1 hypothetical protein
1028781	1037345	8564	OXZ40866.1	B9N58_04990	1028781	1029101	-1 hypothetical protein
1028781	1037345	8564	OXZ40867.1	B9N58_04995	1029212	1030690	-1 Lsa family ABC-F type ribosomal protection protein
1028781	1037345	8564	OXZ40868.1	B9N58_05000	1030738	1032408	-1 recombinase
1028781	1037345	8564	OXZ40869.1	B9N58_05005	1032451	1033029	-1 conjugal transfer protein TraG
1028781	1037345	8564	OXZ40870.1	B9N58_05010	1033022	1033756	-1 phage antirepressor Ant
1028781	1037345	8564	OXZ40871.1	B9N58_05015	1033753	1034238	-1 conjugal transfer protein
1028781	1037345	8564	OXZ40872.1	B9N58_05020	1034231	1035058	-1 nucleoside triphosphate hydrolase
1028781	1037345	8564	OXZ40873.1	B9N58_05025	1035055	1035828	-1 replication initiator protein A
1028781	1037345	8564	OXZ40720.1	B9N58_05030	1037160	1037345	-1 hypothetical protein
1033022	1037345	4323	OXZ40869.1	B9N58_05005	1032451	1033029	-1 conjugal transfer protein TraG
1033022	1037345	4323	OXZ40870.1	B9N58_05010	1033022	1033756	-1 phage antirepressor Ant
1033022	1037345	4323	OXZ40871.1	B9N58_05015	1033753	1034238	-1 conjugal transfer protein
1033022	1037345	4323	OXZ40872.1	B9N58_05020	1034231	1035058	-1 nucleoside triphosphate hydrolase
1033022	1037345	4323	OXZ40873.1	B9N58_05025	1035055	1035828	-1 replication initiator protein A
1033022	1037345	4323	OXZ40720.1	B9N58_05030	1037160	1037345	-1 hypothetical protein
1424435	1460901	36466	OXZ40485.1	B9N58_06810	1423846	1424445	-1 capsular biosynthesis protein
1424435	1460901	36466	OXZ40486.1	B9N58_06815	1424435	1425073	-1 capsular biosynthesis protein
1424435	1460901	36466	OXZ40487.1	B9N58_06820	1425075	1425854	-1 capsular biosynthesis protein
1424435	1460901	36466	OXZ40488.1	B9N58_06825	1425855	1426277	-1 enterotoxin
1424435	1460901	36466	OXZ40489.1	B9N58_06830	1426458	1426982	1 DNA topology modulation protein FlaR
1424435	1460901	36466	OXZ40490.1	B9N58_06835	1427098	1434705	-1 hypothetical protein
1424435	1460901	36466	OXZ40491.1	B9N58_06840	1435350	1440322	-1 hypothetical protein
1424435	1460901	36466	OXZ40350.1	B9N58_06845	1441323	1444408	-1 hypothetical protein
1424435	1460901	36466	OXZ40351.1	B9N58_06850	1444520	1449238	-1 hypothetical protein
1424435	1460901	36466	OXZ40352.1	B9N58_06855	1450091	1450546	-1 IS200/IS605 family transposase
1424435	1460901	36466	OXZ40353.1	B9N58_06860	1450748	1452637	-1 cell wall protein

1424435	1460901	36466	OXZ40354.1	B9N58_06865	1453409	1453840	-1 GNAT family N-acetyltransferase
1424435	1460901	36466	OXZ40355.1	B9N58_06870	1453866	1454564	-1 hypothetical protein
1424435	1460901	36466	OXZ40356.1	B9N58_06875	1454564	1455283	-1 peptidase S51
1424435	1460901	36466	OXZ40357.1	B9N58_06880	1456188	1459541	-1 ABC transporter permease
1424435	1460901	36466	OXZ40358.1	B9N58_06885	1459543	1460244	-1 macrolide ABC transporter ATP-binding protein
1424435	1460901	36466	OXZ40359.1	B9N58_06890	1460356	1460901	1 TetR family transcriptional regulator
1435350	1440322	4972	OXZ40491.1	B9N58_06840	1435350	1440322	-1 hypothetical protein
1494017	1575399	81382	OXZ40386.1	B9N58_07025	1494017	1494325	-1 exosortase
1494017	1575399	81382	OXZ40387.1	B9N58_07030	1494330	1495001	-1 ATPase
1494017	1575399	81382	OXZ40388.1	B9N58_07035	1495202	1496740	-1 hypothetical protein
1494017	1575399	81382	OXZ40389.1	B9N58_07040	1496916	1498424	-1 AAA family ATPase
1494017	1575399	81382	OXZ40390.1	B9N58_07045	1499168	1500058	-1 methionine sulfoxide reductase
1494017	1575399	81382	OXZ40391.1	B9N58_07050	1500214	1500705	-1 protein-S-isoprenylcysteine methyltransferase
1494017	1575399	81382	OXZ40392.1	B9N58_07055	1500719	1501657	-1 esterase
1494017	1575399	81382	OXZ40393.1	B9N58_07060	1501726	1502352	-1 hypothetical protein
1494017	1575399	81382	OXZ40394.1	B9N58_07065	1502380	1502988	-1 SAM-dependent methyltransferase
1494017	1575399	81382	OXZ40395.1	B9N58_07070	1503208	1504962	-1 hypothetical protein
1494017	1575399	81382	OXZ40396.1	B9N58_07075	1505329	1505835	-1 hypothetical protein
1494017	1575399	81382	OXZ40397.1	B9N58_07080	1505846	1506592	-1 alpha/beta hydrolase
1494017	1575399	81382	OXZ40398.1	B9N58_07085	1506627	1507460	-1 SAM-dependent methyltransferase
1494017	1575399	81382	OXZ40399.1	B9N58_07090	1507482	1508108	-1 hypothetical protein
1494017	1575399	81382	OXZ40400.1	B9N58_07095	1508325	1509689	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40401.1	B9N58_07100	1509683	1510372	-1 cobalt ABC transporter permease
1494017	1575399	81382	OXZ40402.1	B9N58_07105	1510372	1510956	-1 hypothetical protein
1494017	1575399	81382	OXZ40480.1	B9N58_07110	1511016	1512359	-1 MATE family efflux transporter
1494017	1575399	81382	OXZ40403.1	B9N58_07115	1512371	1514092	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40404.1	B9N58_07120	1514076	1515830	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40405.1	B9N58_07125	1515991	1516983	1 AraC family transcriptional regulator
1494017	1575399	81382		B9N58_07130	1517161	1517348	1 cell filamentation protein
1494017	1575399	81382	OXZ40406.1	B9N58_07135	1517574	1518278	-1 hypothetical protein
1494017	1575399	81382	OXZ40407.1	B9N58_07140	1518287	1519039	-1 hypothetical protein
1494017	1575399	81382	OXZ40408.1	B9N58_07145	1519041	1519934	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40409.1	B9N58_07150	1520063	1520758	1 DNA-binding response regulator
1494017	1575399	81382	OXZ40410.1	B9N58_07155	1520760	1522055	1 two-component sensor histidine kinase
1494017	1575399	81382		B9N58_07160	1522098	1522384	-1 hypothetical protein
1494017	1575399	81382		B9N58_07165	1522760	1523472	-1 hypothetical protein
1494017	1575399	81382	OXZ40411.1	B9N58_07170	1523525	1525261	-1 multidrug ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40412.1	B9N58_07175	1525254	1526975	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40413.1	B9N58_07180	1526987	1528438	-1 ABC transporter
1494017	1575399	81382	OXZ40414.1	B9N58_07185	1528440	1529111	-1 cobalt transporter
1494017	1575399	81382	OXZ40415.1	B9N58_07190	1529108	1529698	-1 hypothetical protein
1494017	1575399	81382	OXZ40416.1	B9N58_07195	1529765	1530742	-1 AraC family transcriptional regulator
1494017	1575399	81382	OXZ40417.1	B9N58_07200	1530752	1531336	-1 TetR family transcriptional regulator
1494017	1575399	81382		B9N58_07205	1531537	1531919	-1 AraC family transcriptional regulator
1494017	1575399	81382	OXZ40418.1	B9N58_07210	1532893	1533549	-1 hypothetical protein
1494017	1575399	81382	OXZ40419.1	B9N58_07215	1533798	1534394	-1 hypothetical protein
1494017	1575399	81382	OXZ40420.1	B9N58_07220	1534396	1534854	-1 hypothetical protein
1494017	1575399	81382	OXZ40421.1	B9N58_07225	1535164	1536900	-1 multidrug ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40422.1	B9N58_07230	1536893	1538611	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40423.1	B9N58_07235	1538616	1539212	-1 TetR family transcriptional regulator
1494017	1575399	81382	OXZ40424.1	B9N58_07240	1539506	1539811	1 plasmid mobilization relaxosome protein MobC
1494017	1575399	81382		B9N58_07245	1539864	1540352	1 relaxase
1494017	1575399	81382	OXZ40425.1	B9N58_07250	1540435	1542969	-1 DEAD/DEAH box helicase
1494017	1575399	81382	OXZ40426.1	B9N58_07255	1542972	1543805	-1 hypothetical protein
1494017	1575399	81382	OXZ40427.1	B9N58_07260	1543842	1544003	-1 transcriptional regulator
1494017	1575399	81382		B9N58_07265	1544226	1544567	-1 hypothetical protein
1494017	1575399	81382	OXZ40428.1	B9N58_07270	1544618	1544866	-1 hypothetical protein
1494017	1575399	81382	OXZ40429.1	B9N58_07275	1544863	1545450	-1 transcriptional regulator
1494017	1575399	81382	OXZ40430.1	B9N58_07280	1545949	1547625	-1 recombinase family protein
1494017	1575399	81382	OXZ40431.1	B9N58_07285	1548719	1549651	-1 AraC family transcriptional regulator
1494017	1575399	81382	OXZ40432.1	B9N58_07290	1549648	1551039	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40433.1	B9N58_07295	1551033	1551728	-1 ABC transporter permease
1494017	1575399	81382		B9N58_07300	1551728	1552309	-1 hypothetical protein
1494017	1575399	81382	OXZ40434.1	B9N58_07305	1552320	1554041	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40435.1	B9N58_07310	1554038	1555786	-1 ABC transporter ATP-binding protein
1494017	1575399	81382	OXZ40436.1	B9N58_07315	1556431	1556901	-1 replication protein
1494017	1575399	81382	OXZ40437.1	B9N58_07320	1556986	1557597	-1 SAM-dependent methyltransferase
1494017	1575399	81382	OXZ40438.1	B9N58_07325	1557801	1558328	-1 conjugal transfer protein
1494017	1575399	81382	OXZ40439.1	B9N58_07330	1558760	1560394	-1 MobA/MobL protein
1494017	1575399	81382	OXZ40440.1	B9N58_07335	1560740	1561030	-1 hypothetical protein
1494017	1575399	81382	OXZ40441.1	B9N58_07340	1561269	1561748	1 AraC family transcriptional regulator
1494017	1575399	81382	OXZ40442.1	B9N58_07345	1562009	1562503	-1 hypothetical protein
1494017	1575399	81382	OXZ40443.1	B9N58_07350	1562933	1563151	-1 transcriptional regulator
1494017	1575399	81382	OXZ40444.1	B9N58_07355	1563269	1563427	-1 hypothetical protein
1494017	1575399	81382	OXZ40445.1	B9N58_07360	1563429	1563740	-1 single-stranded DNA-binding protein
1494017	1575399	81382	OXZ40446.1	B9N58_07365	1563943	1564251	-1 hypothetical protein
1494017	1575399	81382	OXZ40447.1	B9N58_07370	1564280	1564468	-1 hypothetical protein
1494017	1575399	81382	OXZ40448.1	B9N58_07375	1564741	1566234	-1 23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD

1494017	1575399	81382 OXZ40449.1	B9N58_07380	1566327	1568123	-1 ABC transporter
1494017	1575399	81382 OXZ40450.1	B9N58_07385	1568116	1569876	-1 multidrug ABC transporter ATP-binding protein
1494017	1575399	81382 OXZ40451.1	B9N58_07390	1569851	1570327	-1 MarR family transcriptional regulator
1494017	1575399	81382 OXZ40452.1	B9N58_07395	1570494	1571795	-1 phosphomethylpyrimidine synthase
1494017	1575399	81382 OXZ40453.1	B9N58_07400	1571976	1572890	-1 cyclic pyranopterin monophosphate synthase MoaC
1494017	1575399	81382 OXZ40454.1	B9N58_07405	1572892	1573839	-1 GTP 3',8-cyclase MoaA
1494017	1575399	81382 OXZ40455.1	B9N58_07410	1573927	1575102	-1 hypothetical protein
1494017	1575399	81382 OXZ40456.1	B9N58_07415	1575118	1575399	-1 hypothetical protein
1520063	1530742	10679 OXZ40409.1	B9N58_07150	1520063	1520758	1 DNA-binding response regulator
1520063	1530742	10679 OXZ40410.1	B9N58_07155	1520760	1522055	1 two-component sensor histidine kinase
1520063	1530742	10679	B9N58_07160	1522098	1522384	-1 hypothetical protein
1520063	1530742	10679	B9N58_07165	1522760	1523472	-1 hypothetical protein
1520063	1530742	10679 OXZ40411.1	B9N58_07170	1523525	1525261	-1 multidrug ABC transporter ATP-binding protein
1520063	1530742	10679 OXZ40412.1	B9N58_07175	1525254	1526975	-1 ABC transporter ATP-binding protein
1520063	1530742	10679 OXZ40413.1	B9N58_07180	1526987	1528438	-1 ABC transporter
1520063	1530742	10679 OXZ40414.1	B9N58_07185	1528440	1529111	-1 cobalt transporter
1520063	1530742	10679 OXZ40415.1	B9N58_07190	1529108	1529698	-1 hypothetical protein
1520063	1530742	10679 OXZ40416.1	B9N58_07195	1529765	1530742	-1 AraC family transcriptional regulator
1556431	1561748	5317 OXZ40436.1	B9N58_07315	1556431	1556901	-1 replication protein
1556431	1561748	5317 OXZ40437.1	B9N58_07320	1556986	1557597	-1 SAM-dependent methyltransferase
1556431	1561748	5317 OXZ40438.1	B9N58_07325	1557801	1558328	-1 conjugal transfer protein
1556431	1561748	5317 OXZ40439.1	B9N58_07330	1558760	1560394	-1 MobA/MobL protein
1556431	1561748	5317 OXZ40440.1	B9N58_07335	1560740	1561030	-1 hypothetical protein
1556431	1561748	5317 OXZ40441.1	B9N58_07340	1561269	1561748	1 AraC family transcriptional regulator
1717729	1724002	6273 OXZ39742.1	B9N58_08075	1716944	1717747	-1 ABC transporter ATP-binding protein
1717729	1724002	6273 OXZ39743.1	B9N58_08080	1717729	1717866	-1 nitrate ABC transporter substrate-binding protein
1717729	1724002	6273 OXZ39744.1	B9N58_08085	1717906	1718529	-1 ABC transporter permease
1717729	1724002	6273 OXZ39745.1	B9N58_08090	1718490	1718999	-1 hypothetical protein
1717729	1724002	6273 OXZ39746.1	B9N58_08095	1719051	1719266	-1 hypothetical protein
1717729	1724002	6273 OXZ39747.1	B9N58_08100	1719259	1719450	-1 hypothetical protein
1717729	1724002	6273	B9N58_08105	1719930	1720375	1 hypothetical protein
1717729	1724002	6273	B9N58_08110	1720544	1720825	-1 type I restriction endonuclease
1717729	1724002	6273 OXZ39748.1	B9N58_08115	1720890	1721873	-1 hypothetical protein
1717729	1724002	6273 OXZ39749.1	B9N58_08120	1721866	1722477	-1 hypothetical protein
1717729	1724002	6273 OXZ39750.1	B9N58_08125	1722803	1724002	-1 sugar ABC transporter ATP-binding protein

Table S3B: Predicted genomic islands in the genome of *F. magna* 08T492

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
4466	13082	8616	OXZ39870.1	B9N56_00035	4466	5335	1	hypothetical protein
4466	13082	8616	OXZ39871.1	B9N56_00040	5322	7310	1	exopolyphosphatase
4466	13082	8616	OXZ39872.1	B9N56_00045	7291	7737	1	50S ribosomal protein L9
4466	13082	8616	OXZ39873.1	B9N56_00050	7771	9108	1	replicative DNA helicase
4466	13082	8616	OXZ39874.1	B9N56_00055	9105	9668	1	GNAT family N-acetyltransferase
4466	13082	8616	OXZ39875.1	B9N56_00060	9673	10431	1	DNA replication protein
4466	13082	8616	OXZ39876.1	B9N56_00065	10434	11411	1	DNA replication protein DnaC
4466	13082	8616	OXZ39877.1	B9N56_00070	11408	12052	1	NAD(P)H-hydrate epimerase
4466	13082	8616	OXZ39878.1	B9N56_00075	12540	13082	1	ECF transporter S component
4466	13082	8616	OXZ39879.1	B9N56_00080	13066	13752	1	radical SAM protein
89839	96411	6572	OXZ39971.1	B9N56_00550	89839	91074	1	peptidoglycan-binding protein
89839	96411	6572	OXZ39695.1	B9N56_00615	95728	96003	-1	hypothetical protein
89839	96411	6572		B9N56_00620	96091	96411	-1	hypothetical protein
117178	124321	7143	OXZ39693.1	B9N56_00665	117178	117819	-1	hemolysin III
117178	124321	7143	OXZ39697.1	B9N56_00670	117972	118475	1	acetyltransferase
117178	124321	7143	OXZ39694.1	B9N56_00675	118475	119209	1	hydrolase
117178	124321	7143	OXZ39623.1	B9N56_00680	121747	122322	1	cell filamentation protein Fic
117178	124321	7143	OXZ39624.1	B9N56_00685	123705	124082	-1	death-on-curing protein
117178	124321	7143	OXZ39625.1	B9N56_00690	124079	124321	-1	prevent-host-death protein
675820	682312	6492	OXZ38460.1	B9N56_03450	675820	676518	1	DNA-binding response regulator
675820	682312	6492	OXZ38461.1	B9N56_03455	676559	677143	1	peptidylprolyl isomerase
675820	682312	6492	OXZ38462.1	B9N56_03460	677145	677777	1	thymidine kinase
675820	682312	6492	OXZ38463.1	B9N56_03465	677799	678269	-1	S-ribosylhomocysteine lyase
675820	682312	6492	OXZ38464.1	B9N56_03470	678278	679381	-1	rod shape-determining protein RodA
675820	682312	6492	OXZ38465.1	B9N56_03475	679456	680289	1	endonuclease
675820	682312	6492	OXZ38466.1	B9N56_03480	680270	680896	1	endonuclease III
675820	682312	6492	OXZ38467.1	B9N56_03485	680964	681884	1	aspartate carbamoyltransferase
675820	682312	6492	OXZ38468.1	B9N56_03490	681884	682312	1	subunit
698698	704829	6131	OXZ38485.1	B9N56_03575	698698	700386	1	hypothetical protein
698698	704829	6131	OXZ38486.1	B9N56_03580	700397	701194	1	pyruvate, phosphate dikinase regulatory protein
698698	704829	6131	OXZ38487.1	B9N56_03585	701278	702711	1	serine/threonine protein kinase
698698	704829	6131	OXZ38488.1	B9N56_03590	702713	703387	1	protein phosphatase
698698	704829	6131	OXZ38489.1	B9N56_03595	703444	704829	1	methylthiotransferase MiaB
737859	742292	4433	OXZ38521.1	B9N56_03760	737859	738194	-1	histidine triad nucleotide-binding protein
737859	742292	4433	OXZ38522.1	B9N56_03765	738241	739533	-1	C(2)-methylthiotransferase MtaB
737859	742292	4433	OXZ38523.1	B9N56_03770	739533	740258	-1	rRNA methyltransferase
737859	742292	4433	OXZ38524.1	B9N56_03775	740251	741174	-1	50S ribosomal protein L11 methyltransferase
737859	742292	4433	OXZ38525.1	B9N56_03780	741174	742292	-1	molecular chaperone DnaJ
892629	969377	76748	OXZ38269.1	B9N56_04475	892629	893906	-1	ABC transporter permease
892629	969377	76748	OXZ38270.1	B9N56_04480	894104	894391	-1	cupin
892629	969377	76748	OXZ38271.1	B9N56_04485	894459	895031	-1	uracil-DNA glycosylase
892629	969377	76748		B9N56_04490	895170	895373	-1	hypothetical protein
892629	969377	76748		B9N56_04495	895401	895646	-1	hypothetical protein
892629	969377	76748	OXZ38277.1	B9N56_04500	895648	896451	-1	ABC transporter
892629	969377	76748		B9N56_04505	896438	897157	-1	iron ABC transporter permease
892629	969377	76748	OXZ38272.1	B9N56_04510	897217	897975	-1	SAM-dependent methyltransferase
892629	969377	76748	OXZ38273.1	B9N56_04515	898070	898663	1	transcriptional regulator
892629	969377	76748	OXZ38274.1	B9N56_04520	899200	899384	1	transposase
892629	969377	76748	OXZ38150.1	B9N56_04525	900561	900788	1	transposase
892629	969377	76748	OXZ38148.1	B9N56_04530	900860	901066	1	hypothetical protein
892629	969377	76748	OXZ38149.1	B9N56_04535	901178	901694	1	IS3 family transposase
892629	969377	76748	OXZ38116.1	B9N56_04540	902695	902868	1	transposase
892629	969377	76748	OXZ38117.1	B9N56_04545	903099	904301	-1	ABC transporter substrate-binding protein
892629	969377	76748	OXZ38118.1	B9N56_04550	904301	904726	-1	FMN-binding domain-containing protein
892629	969377	76748	OXZ38119.1	B9N56_04555	904723	905442	-1	GTPase
892629	969377	76748	OXZ38120.1	B9N56_04560	905454	906602	-1	ABC transporter permease
892629	969377	76748	OXZ38121.1	B9N56_04565	906592	907875	-1	ABC transporter permease
892629	969377	76748	OXZ38122.1	B9N56_04570	907884	909146	-1	hypothetical protein
892629	969377	76748	OXZ38123.1	B9N56_04575	909203	909868	-1	hypothetical protein
892629	969377	76748	OXZ38124.1	B9N56_04580	909878	911215	-1	iron transporter
892629	969377	76748	OXZ38125.1	B9N56_04585	911218	911895	-1	ABC transporter ATP-binding protein
892629	969377	76748	OXZ38126.1	B9N56_04590	911895	912290	-1	hypothetical protein
892629	969377	76748		B9N56_04595	912333	912488	-1	hypothetical protein
892629	969377	76748	OXZ38127.1	B9N56_04600	912490	912732	-1	FeoA family protein
892629	969377	76748	OXZ38128.1	B9N56_04605	912736	912966	-1	ferrous iron transport protein A
892629	969377	76748	OXZ38129.1	B9N56_04610	913264	913371	-1	replication initiator domain protein A
892629	969377	76748	OXZ38130.1	B9N56_04615	913454	913726	-1	hypothetical protein
892629	969377	76748	OXZ38131.1	B9N56_04620	913799	914245	-1	methionine--tRNA ligase subunit beta
892629	969377	76748	OXZ38132.1	B9N56_04625	914402	915637	-1	site-specific integrase
892629	969377	76748	OXZ38133.1	B9N56_04630	915715	915924	-1	excisionase
892629	969377	76748		B9N56_04635	916360	916769	-1	RNA polymerase subunit sigma
892629	969377	76748	OXZ38134.1	B9N56_04640	916727	916840	-1	RNA polymerase subunit sigma-70

892629	969377	76748 OXZ38135.1	B9N56_04645	917089	918438	-1 MATE family efflux transporter
892629	969377	76748 OXZ38136.1	B9N56_04650	918475	920208	-1 multidrug ABC transporter ATP-binding protein
892629	969377	76748 OXZ38137.1	B9N56_04655	920205	921947	-1 ABC transporter ATP-binding protein
892629	969377	76748 OXZ38138.1	B9N56_04660	921983	923374	-1 ABC transporter ATP-binding protein
892629	969377	76748 OXZ38139.1	B9N56_04665	923367	924068	-1 cobalt ABC transporter permease
892629	969377	76748 OXZ38140.1	B9N56_04670	924093	924674	-1 hypothetical protein
892629	969377	76748 OXZ38141.1	B9N56_04675	924692	925303	-1 TetR family transcriptional regulator
892629	969377	76748 OXZ38142.1	B9N56_04680	925615	925971	1 plasmid mobilization relaxosome protein MobC
892629	969377	76748 OXZ38143.1	B9N56_04685	925973	927304	1 endonuclease
892629	969377	76748	B9N56_04690	927390	928475	1 IS256 family transposase
892629	969377	76748 OXZ38144.1	B9N56_04695	928580	930070	-1 hypothetical protein
892629	969377	76748 OXZ38145.1	B9N56_04700	930073	930783	-1 hypothetical protein
892629	969377	76748 OXZ38146.1	B9N56_04705	930784	931362	-1 hypothetical protein
892629	969377	76748 OXZ38147.1	B9N56_04710	931377	933107	-1 hypothetical protein
892629	969377	76748	B9N56_04715	934372	936342	-1 DNA helicase
892629	969377	76748 OXZ37671.1	B9N56_04720	936329	937294	-1 DNA (cytosine-5-)-methyltransferase
892629	969377	76748 OXZ37672.1	B9N56_04725	937287	939008	-1 DNA topoisomerase III
892629	969377	76748 OXZ37673.1	B9N56_04730	939097	940080	-1 hypothetical protein
892629	969377	76748 OXZ37674.1	B9N56_04735	940073	940684	-1 hypothetical protein
892629	969377	76748 OXZ37675.1	B9N56_04740	940758	941630	-1 bacteriocin
892629	969377	76748 OXZ37676.1	B9N56_04745	941645	943228	-1 copper amine oxidase
892629	969377	76748 OXZ37677.1	B9N56_04750	943215	943454	-1 hypothetical protein
892629	969377	76748 OXZ37678.1	B9N56_04755	943469	946048	-1 hypothetical protein
892629	969377	76748 OXZ37679.1	B9N56_04760	946056	948479	-1 conjugal transfer protein TraE
892629	969377	76748 OXZ37680.1	B9N56_04765	948370	948780	-1 PrgI family protein
892629	969377	76748 OXZ37681.1	B9N56_04770	948782	949072	-1 hypothetical protein
892629	969377	76748 OXZ37682.1	B9N56_04775	949082	949945	-1 hypothetical protein
892629	969377	76748	B9N56_04780	949956	950039	-1 hypothetical protein
892629	969377	76748 OXZ37683.1	B9N56_04785	950043	951689	-1 recombinase RecB
892629	969377	76748 OXZ37684.1	B9N56_04790	951693	951917	-1 hypothetical protein
892629	969377	76748 OXZ37685.1	B9N56_04795	952071	952772	-1 replisome organizer
892629	969377	76748 OXZ37686.1	B9N56_04800	952860	953855	-1 DNA-binding protein
892629	969377	76748 OXZ37687.1	B9N56_04805	953989	954186	-1 hypothetical protein
892629	969377	76748 OXZ37640.1	B9N56_04810	955228	955558	-1 nickase
892629	969377	76748 OXZ37641.1	B9N56_04815	955872	956186	-1 hypothetical protein
892629	969377	76748	B9N56_04820	956305	956403	-1 hypothetical protein
892629	969377	76748 OXZ37642.1	B9N56_04825	956449	957852	-1 ABC transporter
892629	969377	76748 OXZ37643.1	B9N56_04830	957857	958549	-1 hypothetical protein
892629	969377	76748 OXZ37644.1	B9N56_04835	958530	959117	-1 hypothetical protein
892629	969377	76748 OXZ37645.1	B9N56_04840	959141	960874	-1 ABC transporter ATP-binding protein
892629	969377	76748 OXZ37646.1	B9N56_04845	960862	962601	-1 ABC transporter ATP-binding protein
892629	969377	76748 OXZ37647.1	B9N56_04850	962906	963277	-1 transcriptional regulator
892629	969377	76748	B9N56_04855	963398	963598	-1 hypothetical protein
892629	969377	76748 OXZ37648.1	B9N56_04860	963602	963820	-1 transcriptional regulator
892629	969377	76748 OXZ37649.1	B9N56_04865	964132	965991	-1 group II intron reverse transcriptase/maturase
892629	969377	76748 OXZ37650.1	B9N56_04870	966714	966845	-1 hypothetical protein
892629	969377	76748 OXZ37651.1	B9N56_04875	966847	967158	-1 single-stranded DNA-binding protein
892629	969377	76748 OXZ37652.1	B9N56_04880	967354	968823	-1 hypothetical protein
892629	969377	76748 OXZ37653.1	B9N56_04885	968841	969377	-1 CibS/DfsB family four-helix bundle protein
895170	899384	4214	B9N56_04490	895170	895373	-1 hypothetical protein
895170	899384	4214	B9N56_04495	895401	895646	-1 hypothetical protein
895170	899384	4214 OXZ38277.1	B9N56_04500	895648	896451	-1 ABC transporter
895170	899384	4214	B9N56_04505	896438	897157	-1 iron ABC transporter permease
895170	899384	4214 OXZ38272.1	B9N56_04510	897217	897975	-1 SAM-dependent methyltransferase
895170	899384	4214 OXZ38273.1	B9N56_04515	898070	898663	1 transcriptional regulator
895170	899384	4214 OXZ38274.1	B9N56_04520	899200	899384	1 transposase
902695	909146	6451 OXZ38116.1	B9N56_04540	902695	902868	1 transposase
902695	909146	6451 OXZ38117.1	B9N56_04545	903099	904301	-1 ABC transporter substrate-binding protein
902695	909146	6451 OXZ38118.1	B9N56_04550	904301	904726	-1 FMN-binding domain-containing protein
902695	909146	6451 OXZ38119.1	B9N56_04555	904723	905442	-1 GTPase
902695	909146	6451 OXZ38120.1	B9N56_04560	905454	906602	-1 ABC transporter permease
902695	909146	6451 OXZ38121.1	B9N56_04565	906592	907875	-1 ABC transporter permease
902695	909146	6451 OXZ38122.1	B9N56_04570	907884	909146	-1 hypothetical protein
921983	941630	19647 OXZ38138.1	B9N56_04660	921983	923374	-1 ABC transporter ATP-binding protein
921983	941630	19647 OXZ38139.1	B9N56_04665	923367	924068	-1 cobalt ABC transporter permease
921983	941630	19647 OXZ38140.1	B9N56_04670	924093	924674	-1 hypothetical protein
921983	941630	19647 OXZ38141.1	B9N56_04675	924692	925303	-1 TetR family transcriptional regulator
921983	941630	19647 OXZ38142.1	B9N56_04680	925615	925971	1 plasmid mobilization relaxosome protein MobC
921983	941630	19647 OXZ38143.1	B9N56_04685	925973	927304	1 endonuclease
921983	941630	19647	B9N56_04690	927390	928475	1 IS256 family transposase
921983	941630	19647 OXZ38144.1	B9N56_04695	928580	930070	-1 hypothetical protein
921983	941630	19647 OXZ38145.1	B9N56_04700	930073	930783	-1 hypothetical protein
921983	941630	19647 OXZ38146.1	B9N56_04705	930784	931362	-1 hypothetical protein
921983	941630	19647 OXZ38147.1	B9N56_04710	931377	933107	-1 hypothetical protein
921983	941630	19647	B9N56_04715	934372	936342	-1 DNA helicase
921983	941630	19647 OXZ37671.1	B9N56_04720	936329	937294	-1 DNA (cytosine-5-)-methyltransferase

921983	941630	19647	OXZ37672.1	B9N56_04725	937287	939008	-1 DNA topoisomerase III
921983	941630	19647	OXZ37673.1	B9N56_04730	939097	940080	-1 hypothetical protein
921983	941630	19647	OXZ37674.1	B9N56_04735	940073	940684	-1 hypothetical protein
921983	941630	19647	OXZ37675.1	B9N56_04740	940758	941630	-1 bacteriocin
953989	963820	9831	OXZ37687.1	B9N56_04805	953989	954186	-1 hypothetical protein
953989	963820	9831	OXZ37640.1	B9N56_04810	955228	955558	-1 nickase
953989	963820	9831	OXZ37641.1	B9N56_04815	955872	956186	-1 hypothetical protein
953989	963820	9831		B9N56_04820	956305	956403	-1 hypothetical protein
953989	963820	9831	OXZ37642.1	B9N56_04825	956449	957852	-1 ABC transporter
953989	963820	9831	OXZ37643.1	B9N56_04830	957857	958549	-1 hypothetical protein
953989	963820	9831	OXZ37644.1	B9N56_04835	958530	959117	-1 hypothetical protein
953989	963820	9831	OXZ37645.1	B9N56_04840	959141	960874	-1 ABC transporter ATP-binding protein
953989	963820	9831	OXZ37646.1	B9N56_04845	960862	962601	-1 ABC transporter ATP-binding protein
953989	963820	9831	OXZ37647.1	B9N56_04850	962906	963277	-1 transcriptional regulator
953989	963820	9831		B9N56_04855	963398	963598	-1 hypothetical protein
953989	963820	9831	OXZ37648.1	B9N56_04860	963602	963820	-1 transcriptional regulator
974719	979692	4973	OXZ37660.1	B9N56_04920	974719	975048	-1 hypothetical protein
974719	979692	4973	OXZ37661.1	B9N56_04925	975133	975546	-1 RNA polymerase subunit sigma-70
974719	979692	4973	OXZ37662.1	B9N56_04930	975834	977216	-1 MATE family efflux transporter
974719	979692	4973	OXZ37663.1	B9N56_04935	977218	979692	-1 phosphoenolpyruvate synthase
1190641	1202413	11772	OXZ37235.1	B9N56_05920	1190641	1190955	1 conjugal transfer protein
1190641	1202413	11772	OXZ37236.1	B9N56_05925	1190971	1191357	1 conjugal transfer protein
1190641	1202413	11772		B9N56_05930	1191386	1192771	1 ATP-binding protein
1190641	1202413	11772		B9N56_05935	1192774	1192927	1 conjugal transfer protein
1190641	1202413	11772	OXZ37237.1	B9N56_05940	1192950	1194155	1 Cro/Ci family transcriptional regulator
1190641	1202413	11772	OXZ37238.1	B9N56_05945	1194198	1194419	1 hypothetical protein
1190641	1202413	11772	OXZ37239.1	B9N56_05950	1194536	1195033	1 antirestriction protein ArdA
1190641	1202413	11772	OXZ37240.1	B9N56_05955	1195008	1195514	1 conjugal transfer protein
1190641	1202413	11772	OXZ37241.1	B9N56_05960	1195498	1197945	1 ATP/GTP-binding protein
1190641	1202413	11772	OXZ37242.1	B9N56_05965	1197948	1200125	1 hypothetical protein
1190641	1202413	11772	OXZ37243.1	B9N56_05970	1200122	1201123	1 peptidase P60
1190641	1202413	11772	OXZ37244.1	B9N56_05975	1201120	1202052	1 conjugal transfer protein
1190641	1202413	11772	OXZ37245.1	B9N56_05980	1202297	1202413	1 peptide
1317420	1321668	4248	OXZ37344.1	B9N56_06535	1317420	1318223	-1 DNA-binding protein
1317420	1321668	4248	OXZ37345.1	B9N56_06540	1318413	1319933	-1 conjugal transfer protein
1317420	1321668	4248	OXZ37346.1	B9N56_06545	1319926	1321668	-1 recombinase
1317420	1321668	4248	OXZ37347.1	B9N56_06550	1321661	1323379	-1 recombinase
1318413	1431755	113342	OXZ37345.1	B9N56_06540	1318413	1319933	-1 conjugal transfer protein
1318413	1431755	113342	OXZ37346.1	B9N56_06545	1319926	1321668	-1 recombinase
1318413	1431755	113342	OXZ37347.1	B9N56_06550	1321661	1323379	-1 recombinase
1318413	1431755	113342	OXZ37348.1	B9N56_06555	1323478	1323645	-1 aminoacyl-tRNA hydrolase
1318413	1431755	113342	OXZ37349.1	B9N56_06560	1324114	1324521	-1 RNA polymerase subunit sigma
1318413	1431755	113342	OXZ37350.1	B9N56_06565	1325321	1326664	-1 MATE family efflux transporter
1318413	1431755	113342	OXZ37351.1	B9N56_06570	1326676	1328424	-1 ABC transporter ATP-binding protein
1318413	1431755	113342	OXZ37352.1	B9N56_06575	1328378	1330132	-1 ABC transporter ATP-binding protein
1318413	1431755	113342	OXZ37353.1	B9N56_06580	1330281	1331240	1 AraC family transcriptional regulator
1318413	1431755	113342	OXZ37354.1	B9N56_06585	1331302	1332690	-1 ABC transporter ATP-binding protein
1318413	1431755	113342	OXZ37355.1	B9N56_06590	1332701	1333357	-1 cobalt transporter
1318413	1431755	113342	OXZ37356.1	B9N56_06595	1333359	1333940	-1 hypothetical protein
1318413	1431755	113342	OXZ37357.1	B9N56_06600	1333951	1337238	-1 hypothetical protein
1318413	1431755	113342	OXZ37358.1	B9N56_06605	1337255	1338298	-1 hypothetical protein
1318413	1431755	113342	OXZ37359.1	B9N56_06610	1338295	1339740	-1 hypothetical protein
1318413	1431755	113342	OXZ37360.1	B9N56_06615	1339749	1341164	-1 hypothetical protein
1318413	1431755	113342	OXZ37361.1	B9N56_06620	1341167	1342213	-1 hypothetical protein
1318413	1431755	113342	OXZ37362.1	B9N56_06625	1342235	1345675	-1 hypothetical protein
1318413	1431755	113342	OXZ37363.1	B9N56_06630	1345688	1347274	-1 2,3-dihydroxybenzoate-AMP ligase
1318413	1431755	113342	OXZ37364.1	B9N56_06635	1347271	1347957	-1 4-phosphopantetheinyl transferase
1318413	1431755	113342	OXZ37365.1	B9N56_06640	1347959	1348699	-1 thioesterase
1318413	1431755	113342	OXZ37366.1	B9N56_06645	1348820	1349788	-1 3-deoxy-7-phosphoheptulonate synthase
1318413	1431755	113342	OXZ37367.1	B9N56_06650	1349804	1350232	-1 type II 3-dehydroquinate dehydratase
1318413	1431755	113342	OXZ37368.1	B9N56_06655	1350210	1351451	-1 shikimate dehydrogenase
1318413	1431755	113342	OXZ37369.1	B9N56_06660	1351474	1352553	-1 chorismate synthase
1318413	1431755	113342	OXZ37426.1	B9N56_06665	1352540	1353832	-1 3-phosphoshikimate 1-carboxyvinyltransferase
1318413	1431755	113342	OXZ37370.1	B9N56_06670	1353829	1354875	-1 3-dehydroquinate synthase
1318413	1431755	113342	OXZ37371.1	B9N56_06675	1354879	1356240	-1 salicylate synthase
1318413	1431755	113342	OXZ37372.1	B9N56_06680	1356436	1356828	-1 transcriptional regulator
1318413	1431755	113342	OXZ37373.1	B9N56_06685	1357265	1357633	1 plasmid mobilization relaxosome protein MobC
1318413	1431755	113342	OXZ37374.1	B9N56_06690	1357633	1359003	1 endonuclease
1318413	1431755	113342	OXZ37375.1	B9N56_06695	1359062	1359808	-1 ABC transporter permease
1318413	1431755	113342	OXZ37376.1	B9N56_06700	1359823	1360515	-1 ABC transporter permease
1318413	1431755	113342	OXZ37377.1	B9N56_06705	1360517	1361431	-1 bacitracin ABC transporter ATP-binding protein
1318413	1431755	113342	OXZ37378.1	B9N56_06710	1361446	1362603	-1 hypothetical protein
1318413	1431755	113342	OXZ37379.1	B9N56_06715	1362607	1363914	-1 hypothetical protein
1318413	1431755	113342	OXZ37380.1	B9N56_06720	1364553	1364984	-1 hypothetical protein
1318413	1431755	113342	OXZ37381.1	B9N56_06725	1364997	1365260	-1 hypothetical protein
1318413	1431755	113342	OXZ37382.1	B9N56_06730	1365254	1365823	-1 hypothetical protein

1318413	1431755	113342	B9N56_06735	1366162	1366485	1 relaxase
1318413	1431755	113342 OXZ37383.1	B9N56_06740	1366606	1366953	-1 DUF3784 domain-containing protein
1318413	1431755	113342 OXZ37384.1	B9N56_06745	1366961	1368337	-1 hypothetical protein
1318413	1431755	113342 OXZ37385.1	B9N56_06750	1368347	1369141	-1 hypothetical protein
1318413	1431755	113342 OXZ37386.1	B9N56_06755	1369131	1370177	-1 hypothetical protein
1318413	1431755	113342 OXZ37387.1	B9N56_06760	1370179	1371825	-1 hypothetical protein
1318413	1431755	113342 OXZ37388.1	B9N56_06765	1372083	1372292	-1 hypothetical protein
1318413	1431755	113342 OXZ37389.1	B9N56_06770	1372602	1374263	-1 ABC transporter permease
1318413	1431755	113342 OXZ37390.1	B9N56_06775	1374256	1374522	-1 protein
1318413	1431755	113342 OXZ37391.1	B9N56_06780	1374524	1376713	-1 radical SAM protein
1318413	1431755	113342 OXZ37392.1	B9N56_06785	1376700	1376882	-1 hypothetical protein
1318413	1431755	113342	B9N56_06790	1377012	1377617	-1 DNA-binding response regulator
1318413	1431755	113342 OXZ37393.1	B9N56_06795	1377589	1379136	-1 hypothetical protein
1318413	1431755	113342 OXZ37394.1	B9N56_06800	1379450	1380544	-1 single-stranded DNA-binding protein
1318413	1431755	113342 OXZ37395.1	B9N56_06805	1380577	1390998	-1 conjugal transfer protein
1318413	1431755	113342 OXZ37396.1	B9N56_06810	1391191	1391517	-1 terminase large subunit
1318413	1431755	113342 OXZ37397.1	B9N56_06815	1391859	1393565	-1 DNA topoisomerase III
1318413	1431755	113342 OXZ37398.1	B9N56_06820	1393635	1394474	-1 abortive phage infection protein
1318413	1431755	113342 OXZ37399.1	B9N56_06825	1394467	1395060	-1 abortive phage infection protein
1318413	1431755	113342 OXZ37400.1	B9N56_06830	1395375	1396253	-1 bacteriocin
1318413	1431755	113342 OXZ37401.1	B9N56_06835	1396269	1398623	-1 copper amine oxidase
1318413	1431755	113342 OXZ37402.1	B9N56_06840	1398620	1398877	-1 hypothetical protein
1318413	1431755	113342 OXZ37403.1	B9N56_06845	1398897	1401860	-1 hypothetical protein
1318413	1431755	113342 OXZ37404.1	B9N56_06850	1401870	1402835	-1 site-specific DNA-methyltransferase
1318413	1431755	113342 OXZ37405.1	B9N56_06855	1402807	1405302	-1 DUF87 domain-containing protein
1318413	1431755	113342 OXZ37406.1	B9N56_06860	1405299	1405637	-1 conjugal transfer protein
1318413	1431755	113342 OXZ37407.1	B9N56_06865	1405637	1405894	-1 hypothetical protein
1318413	1431755	113342 OXZ37408.1	B9N56_06870	1405912	1406775	-1 hypothetical protein
1318413	1431755	113342 OXZ37409.1	B9N56_06875	1406777	1406992	-1 conjugal transfer protein
1318413	1431755	113342 OXZ37410.1	B9N56_06880	1406993	1407316	-1 single-stranded DNA-binding protein
1318413	1431755	113342 OXZ37411.1	B9N56_06885	1407507	1408370	-1 CAAX protease
1318413	1431755	113342	B9N56_06890	1408522	1409337	-1 conjugal transfer protein TraG
1318413	1431755	113342 OXZ37412.1	B9N56_06895	1409349	1409534	-1 hypothetical protein
1318413	1431755	113342 OXZ37413.1	B9N56_06900	1409693	1410406	-1 replisome organizer
1318413	1431755	113342 OXZ37414.1	B9N56_06905	1410478	1411551	-1 hypothetical protein
1318413	1431755	113342 OXZ37415.1	B9N56_06910	1411701	1412180	-1 replication protein
1318413	1431755	113342 OXZ36991.1	B9N56_06915	1413247	1413577	-1 nickase
1318413	1431755	113342 OXZ36992.1	B9N56_06920	1413911	1414201	-1 hypothetical protein
1318413	1431755	113342 OXZ36993.1	B9N56_06925	1414300	1414521	-1 hypothetical protein
1318413	1431755	113342 OXZ36994.1	B9N56_06930	1414542	1415051	-1 RDD family protein
1318413	1431755	113342 OXZ36995.1	B9N56_06935	1415221	1416297	-1 two-component sensor histidine kinase
1318413	1431755	113342 OXZ36996.1	B9N56_06940	1416287	1416967	-1 DNA-binding response regulator
1318413	1431755	113342 OXZ36997.1	B9N56_06945	1416979	1417746	-1 hypothetical protein
1318413	1431755	113342 OXZ36998.1	B9N56_06950	1417755	1418480	-1 hypothetical protein
1318413	1431755	113342 OXZ36999.1	B9N56_06955	1418461	1419204	-1 ABC transporter ATP-binding protein
1318413	1431755	113342 OXZ37000.1	B9N56_06960	1419437	1419736	-1 hypothetical protein
1318413	1431755	113342 OXZ37001.1	B9N56_06965	1419839	1420276	-1 hypothetical protein
1318413	1431755	113342 OXZ37002.1	B9N56_06970	1420397	1420729	-1 hypothetical protein
1318413	1431755	113342 OXZ37003.1	B9N56_06975	1421029	1422471	-1 histidine kinase
1318413	1431755	113342 OXZ37004.1	B9N56_06980	1422462	1423124	-1 DNA-binding response regulator
1318413	1431755	113342 OXZ37005.1	B9N56_06985	1423249	1423989	-1 lantibiotic ABC transporter permease
1318413	1431755	113342 OXZ37006.1	B9N56_06990	1423995	1424744	-1 lantibiotic ABC transporter permease
1318413	1431755	113342 OXZ37007.1	B9N56_06995	1424737	1425447	-1 lantibiotic ABC transporter ATP-binding protein
1318413	1431755	113342	B9N56_07000	1425648	1427437	-1 recombinase TnpX
1318413	1431755	113342 OXZ37008.1	B9N56_07005	1427477	1428535	-1 conjugal transfer protein TraG
1318413	1431755	113342 OXZ37009.1	B9N56_07010	1428580	1428786	-1 hypothetical protein
1318413	1431755	113342 OXZ37010.1	B9N56_07015	1428984	1429475	-1 hypothetical protein
1318413	1431755	113342 OXZ37011.1	B9N56_07020	1429490	1430347	-1 DNA replication protein
1318413	1431755	113342 OXZ37012.1	B9N56_07025	1430362	1431339	-1 replication initiator RepA
1318413	1431755	113342 OXZ37013.1	B9N56_07030	1431465	1431755	-1 hypothetical protein
1323478	1372292	48814 OXZ37348.1	B9N56_06555	1323478	1323645	-1 aminoacyl-tRNA hydrolase
1323478	1372292	48814 OXZ37349.1	B9N56_06560	1324114	1324521	-1 RNA polymerase subunit sigma
1323478	1372292	48814 OXZ37350.1	B9N56_06565	1325321	1326664	-1 MATE family efflux transporter
1323478	1372292	48814 OXZ37351.1	B9N56_06570	1326676	1328424	-1 ABC transporter ATP-binding protein
1323478	1372292	48814 OXZ37352.1	B9N56_06575	1328378	1330132	-1 ABC transporter ATP-binding protein
1323478	1372292	48814 OXZ37353.1	B9N56_06580	1330281	1331240	1 AraC family transcriptional regulator
1323478	1372292	48814 OXZ37354.1	B9N56_06585	1331302	1332690	-1 ABC transporter ATP-binding protein
1323478	1372292	48814 OXZ37355.1	B9N56_06590	1332701	1333357	-1 cobalt transporter
1323478	1372292	48814 OXZ37356.1	B9N56_06595	1333359	1333940	-1 hypothetical protein
1323478	1372292	48814 OXZ37357.1	B9N56_06600	1333951	1337238	-1 hypothetical protein
1323478	1372292	48814 OXZ37358.1	B9N56_06605	1337255	1338298	-1 hypothetical protein
1323478	1372292	48814 OXZ37359.1	B9N56_06610	1338295	1339740	-1 hypothetical protein
1323478	1372292	48814 OXZ37360.1	B9N56_06615	1339749	1341164	-1 hypothetical protein
1323478	1372292	48814 OXZ37361.1	B9N56_06620	1341167	1342213	-1 hypothetical protein
1323478	1372292	48814 OXZ37362.1	B9N56_06625	1342235	1345675	-1 hypothetical protein
1323478	1372292	48814 OXZ37363.1	B9N56_06630	1345688	1347274	-1 2,3-dihydroxybenzoate-AMP ligase

1323478	1372292	48814 OXZ37364.1	B9N56_06635	1347271	1347957	-1 4-phosphopantetheinyl transferase
1323478	1372292	48814 OXZ37365.1	B9N56_06640	1347959	1348699	-1 thioesterase
1323478	1372292	48814 OXZ37366.1	B9N56_06645	1348820	1349788	-1 3-deoxy-7-phosphoheptulonate synthase
1323478	1372292	48814 OXZ37367.1	B9N56_06650	1349804	1350232	-1 type II 3-dehydroquinone dehydratase
1323478	1372292	48814 OXZ37368.1	B9N56_06655	1350210	1351451	-1 shikimate dehydrogenase
1323478	1372292	48814 OXZ37369.1	B9N56_06660	1351474	1352553	-1 chorismate synthase
1323478	1372292	48814 OXZ37426.1	B9N56_06665	1352540	1353832	-1 3-phosphoshikimate 1-carboxyvinyltransferase
1323478	1372292	48814 OXZ37370.1	B9N56_06670	1353829	1354875	-1 3-dehydroquinone synthase
1323478	1372292	48814 OXZ37371.1	B9N56_06675	1354879	1356240	-1 salicylate synthase
1323478	1372292	48814 OXZ37372.1	B9N56_06680	1356436	1356828	-1 transcriptional regulator
1323478	1372292	48814 OXZ37373.1	B9N56_06685	1357265	1357633	1 plasmid mobilization relaxosome protein MobC
1323478	1372292	48814 OXZ37374.1	B9N56_06690	1357633	1359003	1 endonuclease
1323478	1372292	48814 OXZ37375.1	B9N56_06695	1359062	1359808	-1 ABC transporter permease
1323478	1372292	48814 OXZ37376.1	B9N56_06700	1359823	1360515	-1 ABC transporter permease
1323478	1372292	48814 OXZ37377.1	B9N56_06705	1360517	1361431	-1 bacitracin ABC transporter ATP-binding protein
1323478	1372292	48814 OXZ37378.1	B9N56_06710	1361446	1362603	-1 hypothetical protein
1323478	1372292	48814 OXZ37379.1	B9N56_06715	1362607	1363914	-1 hypothetical protein
1323478	1372292	48814 OXZ37380.1	B9N56_06720	1364553	1364984	-1 hypothetical protein
1323478	1372292	48814 OXZ37381.1	B9N56_06725	1364997	1365260	-1 hypothetical protein
1323478	1372292	48814 OXZ37382.1	B9N56_06730	1365254	1365823	-1 hypothetical protein
1323478	1372292	48814	B9N56_06735	1366162	1366485	1 relaxase
1323478	1372292	48814 OXZ37383.1	B9N56_06740	1366606	1366953	-1 DUF3784 domain-containing protein
1323478	1372292	48814 OXZ37384.1	B9N56_06745	1366961	1368337	-1 hypothetical protein
1323478	1372292	48814 OXZ37385.1	B9N56_06750	1368347	1369141	-1 hypothetical protein
1323478	1372292	48814 OXZ37386.1	B9N56_06755	1369131	1370177	-1 hypothetical protein
1323478	1372292	48814 OXZ37387.1	B9N56_06760	1370179	1371825	-1 hypothetical protein
1323478	1372292	48814 OXZ37388.1	B9N56_06765	1372083	1372292	-1 hypothetical protein
1374256	1401860	27604 OXZ37389.1	B9N56_06770	1372602	1374263	-1 ABC transporter permease
1374256	1401860	27604 OXZ37390.1	B9N56_06775	1374256	1374522	-1 protein
1374256	1401860	27604 OXZ37391.1	B9N56_06780	1374524	1376713	-1 radical SAM protein
1374256	1401860	27604 OXZ37392.1	B9N56_06785	1376700	1376882	-1 hypothetical protein
1374256	1401860	27604	B9N56_06790	1377012	1377617	-1 DNA-binding response regulator
1374256	1401860	27604 OXZ37393.1	B9N56_06795	1377589	1379136	-1 hypothetical protein
1374256	1401860	27604 OXZ37394.1	B9N56_06800	1379450	1380544	-1 single-stranded DNA-binding protein
1374256	1401860	27604 OXZ37395.1	B9N56_06805	1380577	1390998	-1 conjugal transfer protein
1374256	1401860	27604 OXZ37396.1	B9N56_06810	1391191	1391517	-1 terminase large subunit
1374256	1401860	27604 OXZ37397.1	B9N56_06815	1391859	1393565	-1 DNA topoisomerase III
1374256	1401860	27604 OXZ37398.1	B9N56_06820	1393635	1394474	-1 abortive phage infection protein
1374256	1401860	27604 OXZ37399.1	B9N56_06825	1394467	1395060	-1 abortive phage infection protein
1374256	1401860	27604 OXZ37400.1	B9N56_06830	1395375	1396253	-1 bacteriocin
1374256	1401860	27604 OXZ37401.1	B9N56_06835	1396269	1398623	-1 copper amine oxidase
1374256	1401860	27604 OXZ37402.1	B9N56_06840	1398620	1398877	-1 hypothetical protein
1374256	1401860	27604 OXZ37403.1	B9N56_06845	1398897	1401860	-1 hypothetical protein
1405299	1420729	15430 OXZ37405.1	B9N56_06855	1402807	1405302	-1 DUF87 domain-containing protein
1405299	1420729	15430 OXZ37406.1	B9N56_06860	1405299	1405637	-1 conjugal transfer protein
1405299	1420729	15430 OXZ37407.1	B9N56_06865	1405637	1405894	-1 hypothetical protein
1405299	1420729	15430 OXZ37408.1	B9N56_06870	1405912	1406775	-1 hypothetical protein
1405299	1420729	15430 OXZ37409.1	B9N56_06875	1406777	1406992	-1 conjugal transfer protein
1405299	1420729	15430 OXZ37410.1	B9N56_06880	1406993	1407316	-1 single-stranded DNA-binding protein
1405299	1420729	15430 OXZ37411.1	B9N56_06885	1407507	1408370	-1 CAAX protease
1405299	1420729	15430	B9N56_06890	1408522	1409337	-1 conjugal transfer protein TraG
1405299	1420729	15430 OXZ37412.1	B9N56_06895	1409349	1409534	-1 hypothetical protein
1405299	1420729	15430 OXZ37413.1	B9N56_06900	1409693	1410406	-1 replisome organizer
1405299	1420729	15430 OXZ37414.1	B9N56_06905	1410478	1411551	-1 hypothetical protein
1405299	1420729	15430 OXZ37415.1	B9N56_06910	1411701	1412180	-1 replication protein
1405299	1420729	15430 OXZ36991.1	B9N56_06915	1413247	1413577	-1 nickase
1405299	1420729	15430 OXZ36992.1	B9N56_06920	1413911	1414201	-1 hypothetical protein
1405299	1420729	15430 OXZ36993.1	B9N56_06925	1414300	1414521	-1 hypothetical protein
1405299	1420729	15430 OXZ36994.1	B9N56_06930	1414542	1415051	-1 RDD family protein
1405299	1420729	15430 OXZ36995.1	B9N56_06935	1415221	1416297	-1 two-component sensor histidine kinase
1405299	1420729	15430 OXZ36996.1	B9N56_06940	1416287	1416967	-1 DNA-binding response regulator
1405299	1420729	15430 OXZ36997.1	B9N56_06945	1416979	1417746	-1 hypothetical protein
1405299	1420729	15430 OXZ36998.1	B9N56_06950	1417755	1418480	-1 hypothetical protein
1405299	1420729	15430 OXZ36999.1	B9N56_06955	1418461	1419204	-1 ABC transporter ATP-binding protein
1405299	1420729	15430 OXZ37000.1	B9N56_06960	1419437	1419736	-1 hypothetical protein
1405299	1420729	15430 OXZ37001.1	B9N56_06965	1419839	1420276	-1 hypothetical protein
1405299	1420729	15430 OXZ37002.1	B9N56_06970	1420397	1420729	-1 hypothetical protein
1557581	1566142	8561	B9N56_07590	1557581	1558190	-1 SAM-dependent methyltransferase
1557581	1566142	8561 OXZ36941.1	B9N56_07595	1558406	1559155	-1 phosphorylase
1557581	1566142	8561 OXZ36942.1	B9N56_07600	1559285	1560886	-1 macrolide ABC transporter ATP-binding protein
1557581	1566142	8561 OXZ36943.1	B9N56_07605	1561291	1561905	-1 hypothetical protein
1557581	1566142	8561 OXZ36944.1	B9N56_07610	1562111	1563475	-1 ABC transporter ATP-binding protein
1557581	1566142	8561 OXZ36945.1	B9N56_07615	1563469	1564158	-1 cobalt ABC transporter permease
1557581	1566142	8561 OXZ36946.1	B9N56_07620	1564158	1564739	-1 hypothetical protein
1557581	1566142	8561 OXZ36960.1	B9N56_07625	1564799	1566142	-1 MATE family efflux transporter
1575901	1586348	10447	B9N56_07675	1575901	1576179	-1 AraC family transcriptional regulator

1575901	1586348	10447	B9N56_07680	1576714	1576923	-1 hypothetical protein
1575901	1586348	10447 OXZ36956.1	B9N56_07685	1577181	1577573	-1 hypothetical protein
1575901	1586348	10447 OXZ36961.1	B9N56_07690	1578112	1578495	-1 hypothetical protein
1575901	1586348	10447 OXZ36957.1	B9N56_07695	1579994	1580644	-1 hypothetical protein
1575901	1586348	10447 OXZ36958.1	B9N56_07700	1580950	1581436	-1 phosphorylase
1575901	1586348	10447 OXZ36826.1	B9N56_07705	1582716	1585109	-1 hypothetical protein
1575901	1586348	10447	B9N56_07710	1585102	1585322	-1 transcriptional regulator
1575901	1586348	10447 OXZ36827.1	B9N56_07715	1585737	1586348	-1 SAM-dependent methyltransferase
1604844	1611673	6829 OXZ36840.1	B9N56_07790	1604844	1605143	1 plasmid mobilization relaxosome protein MobC
1604844	1611673	6829	B9N56_07795	1605202	1605936	1 relaxase
1604844	1611673	6829	B9N56_07800	1606003	1606533	1 hypothetical protein
1604844	1611673	6829 OXZ36841.1	B9N56_07805	1606842	1609601	-1 hypothetical protein
1604844	1611673	6829 OXZ36842.1	B9N56_07810	1609861	1610073	-1 DNA-binding protein
1604844	1611673	6829	B9N56_07815	1610249	1611089	-1 abortive phage infection protein
1604844	1611673	6829 OXZ36843.1	B9N56_07820	1611086	1611673	-1 transcriptional regulator

Table S3C: Predicted genomic islands in the genome of *F. magna* 09T408

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
7930	14062	6132	OXZ32095.1	B9N57_00015	7930	8017	1	hypothetical protein
7930	14062	6132	OXZ32096.1	B9N57_00020	8081	8533	-1	small-multidrug export protein
7930	14062	6132	OXZ32097.1	B9N57_00025	8542	9192	-1	phosphatase
7930	14062	6132	OXZ32098.1	B9N57_00030	9354	10586	1	aminopeptidase
7930	14062	6132	OXZ32099.1	B9N57_00035	10586	12382	1	oligoendopeptidase F
7930	14062	6132	OXZ32100.1	B9N57_00040	12433	13317	1	antibiotic ABC transporter ATP-binding protein
7930	14062	6132	OXZ32101.1	B9N57_00045	13310	14062	1	antibiotic ABC transporter permease
7930	14062	6132	OXZ32102.1	B9N57_00050	14052	14723	1	antibiotic ABC transporter permease
72169	82578	10409	OXZ31830.1	B9N57_00255	72169	73038	1	hypothetical protein
72169	82578	10409	OXZ31831.1	B9N57_00260	73025	75013	1	exopolyphosphatase
72169	82578	10409	OXZ31832.1	B9N57_00265	74994	75440	1	50S ribosomal protein L9
72169	82578	10409	OXZ31833.1	B9N57_00270	75474	76811	1	replicative DNA helicase
72169	82578	10409	OXZ31834.1	B9N57_00275	76808	77371	1	N-acetyltransferase
72169	82578	10409	OXZ31835.1	B9N57_00280	77376	78134	1	DNA replication protein
72169	82578	10409	OXZ31836.1	B9N57_00285	78137	79114	1	DNA replication protein DnaC
72169	82578	10409	OXZ31837.1	B9N57_00290	79111	79755	1	NAD(P)H-hydrate epimerase
72169	82578	10409	OXZ31838.1	B9N57_00295	80595	81137	1	ECF transporter S component
72169	82578	10409	OXZ31839.1	B9N57_00300	81121	81807	1	radical SAM protein
72169	82578	10409	OXZ31840.1	B9N57_00305	81874	82578	1	hypothetical protein
182046	186690	4644	OXZ31460.1	B9N57_00845	182046	182687	-1	hemolysin III
182046	186690	4644	OXZ31461.1	B9N57_00850	182841	183344	1	acetyltransferase
182046	186690	4644	OXZ31462.1	B9N57_00855	183344	184078	1	hydrolase
182046	186690	4644	OXZ31379.1	B9N57_00860	185725	186096	1	hypothetical protein
182046	186690	4644	OXZ31450.1	B9N57_00865	186343	186690	-1	toxin MazF
315622	325971	10349		B9N57_01460	315622	315807	1	DUF4926 domain-containing protein
315622	325971	10349	OXZ31235.1	B9N57_01465	316623	319379	1	Cas3
315622	325971	10349	OXZ31236.1	B9N57_01470	319372	321093	1	hypothetical protein
315622	325971	10349	OXZ31237.1	B9N57_01475	321105	321710	1	type I-E CRISPR-associated protein Cse2/CasB
315622	325971	10349	OXZ31238.1	B9N57_01480	321694	322776	1	Cas7/Cse4/CasC
315622	325971	10349	OXZ31239.1	B9N57_01485	322786	323490	1	type I-E CRISPR-associated protein Cas5/CasD
315622	325971	10349	OXZ31240.1	B9N57_01490	323494	324147	1	Cas6/Cse3/CasE
315622	325971	10349	OXZ31241.1	B9N57_01495	324144	325082	1	Cas1
315622	325971	10349	OXZ31242.1	B9N57_01500	325084	325971	1	Cas2
750468	761175	10707	OXZ30582.1	B9N57_03715	750468	751166	1	DNA-binding response regulator
750468	761175	10707	OXZ30583.1	B9N57_03720	751207	751791	1	peptidylprolyl isomerase
750468	761175	10707	OXZ30584.1	B9N57_03725	751793	752425	1	thymidine kinase
750468	761175	10707	OXZ30585.1	B9N57_03730	752447	752917	-1	S-ribosylhomocysteine lyase
750468	761175	10707	OXZ30586.1	B9N57_03735	752926	754029	-1	rod shape-determining protein RodA
750468	761175	10707	OXZ30587.1	B9N57_03740	754104	754937	1	endonuclease IV
750468	761175	10707	OXZ30588.1	B9N57_03745	754918	755544	1	endonuclease III
750468	761175	10707	OXZ30589.1	B9N57_03750	755612	756532	1	aspartate carbamoyltransferase
750468	761175	10707	OXZ30590.1	B9N57_03755	756532	756960	1	subunit
750468	761175	10707	OXZ30591.1	B9N57_03760	756960	758156	1	dihydroorotase
750468	761175	10707	OXZ30592.1	B9N57_03765	758143	758994	1	orotidine-5'-phosphate decarboxylase
750468	761175	10707	OXZ30593.1	B9N57_03770	758987	759703	1	subunit
750468	761175	10707	OXZ30594.1	B9N57_03775	759696	760592	1	subunit
750468	761175	10707	OXZ30595.1	B9N57_03780	760603	761175	1	orotate phosphoribosyltransferase
775045	779501	4456	OXZ30608.1	B9N57_03845	775045	775842	1	hypothetical protein
775045	779501	4456	OXZ30609.1	B9N57_03850	775926	777383	1	serine/threonine protein kinase
775045	779501	4456	OXZ30610.1	B9N57_03855	777385	778059	1	protein phosphatase
775045	779501	4456	OXZ30611.1	B9N57_03860	778116	779501	1	methylthiotransferase MiaB
812488	816921	4433	OXZ30642.1	B9N57_04025	812488	812823	-1	histidine triad nucleotide-binding protein
812488	816921	4433	OXZ30643.1	B9N57_04030	812870	814162	-1	C(2)-methylthiotransferase MtaB
812488	816921	4433	OXZ30644.1	B9N57_04035	814165	814887	-1	rRNA methyltransferase
812488	816921	4433	OXZ30645.1	B9N57_04040	814880	815803	-1	50S ribosomal protein L11 methyltransferase
812488	816921	4433	OXZ30646.1	B9N57_04045	815803	816921	-1	molecular chaperone DnaJ
983705	989288	5583		B9N57_04800	983705	984169	-1	IS200/IS605 family transposase
983705	989288	5583	OXZ30387.1	B9N57_04805	984389	984676	-1	cupin
983705	989288	5583	OXZ30388.1	B9N57_04810	984743	985315	-1	uracil-DNA glycosylase
983705	989288	5583		B9N57_04815	985454	985657	-1	hypothetical protein
983705	989288	5583		B9N57_04820	985647	985930	-1	hypothetical protein
983705	989288	5583		B9N57_04825	985932	986735	-1	ABC transporter
983705	989288	5583	OXZ30389.1	B9N57_04830	987500	988258	-1	SAM-dependent methyltransferase
983705	989288	5583	OXZ30390.1	B9N57_04835	988353	988946	1	transcriptional regulator
983705	989288	5583	OXZ30391.1	B9N57_04840	989097	989288	-1	hypothetical protein
1455800	1460804	5004		B9N57_07000	1455800	1456095	-1	AraC family transcriptional regulator
1455800	1460804	5004		B9N57_07005	1456206	1456360	-1	recombinase
1455800	1460804	5004	OXZ29994.1	B9N57_07010	1456581	1457231	-1	hypothetical protein
1455800	1460804	5004	OXZ29995.1	B9N57_07015	1457537	1458286	-1	phosphorylase
1455800	1460804	5004	OXZ29996.1	B9N57_07020	1458439	1458867	-1	hypothetical protein
1455800	1460804	5004	OXZ29997.1	B9N57_07025	1459220	1460248	-1	carboxypeptidase
1455800	1460804	5004		B9N57_07030	1460566	1460804	1	hypothetical protein

1473159	1506658	33499	OXZ30007.1	B9N57_07090	1473159	1474130	1 AraC family transcriptional regulator
1473159	1506658	33499	OXZ30008.1	B9N57_07095	1474325	1474681	1 plasmid mobilization relaxosome protein MobC
1473159	1506658	33499	OXZ30009.1	B9N57_07100	1474684	1476015	1 endonuclease
1473159	1506658	33499	OXZ30010.1	B9N57_07105	1476084	1476743	-1 DNA-binding protein
1473159	1506658	33499	OXZ30011.1	B9N57_07110	1476785	1485514	-1 helicase
1473159	1506658	33499	OXZ30088.1	B9N57_07115	1485598	1487133	-1 AAA family ATPase
1473159	1506658	33499	OXZ30089.1	B9N57_07120	1487215	1488927	-1 DNA topoisomerase III
1473159	1506658	33499	OXZ30012.1	B9N57_07125	1489022	1490557	-1 cell surface protein
1473159	1506658	33499	OXZ30013.1	B9N57_07130	1490532	1490771	-1 conjugal transfer protein
1473159	1506658	33499	OXZ30014.1	B9N57_07135	1490783	1492915	-1 CHAP domain-containing protein
1473159	1506658	33499	OXZ30015.1	B9N57_07140	1492919	1495348	-1 conjugal transfer protein TraE
1473159	1506658	33499	OXZ30016.1	B9N57_07145	1495260	1495649	-1 conjugal transfer protein
1473159	1506658	33499	OXZ30017.1	B9N57_07150	1495653	1495916	-1 conjugal transfer protein
1473159	1506658	33499	OXZ30018.1	B9N57_07155	1495934	1496797	-1 hypothetical protein
1473159	1506658	33499	OXZ30019.1	B9N57_07160	1496817	1497032	-1 conjugal transfer protein
1473159	1506658	33499	OXZ30020.1	B9N57_07165	1497036	1497347	-1 single-stranded DNA-binding protein
1473159	1506658	33499		B9N57_07170	1497513	1498325	-1 conjugal transfer protein TraG
1473159	1506658	33499	OXZ30021.1	B9N57_07175	1498337	1498522	-1 hypothetical protein
1473159	1506658	33499	OXZ30022.1	B9N57_07180	1498634	1499641	-1 DNA-binding protein
1473159	1506658	33499	OXZ30023.1	B9N57_07185	1499663	1499986	-1 hypothetical protein
1473159	1506658	33499	OXZ30024.1	B9N57_07190	1500160	1500912	-1 replisome organizer
1473159	1506658	33499	OXZ30025.1	B9N57_07195	1500915	1502567	-1 MobA/MobL protein
1473159	1506658	33499	OXZ30026.1	B9N57_07200	1502814	1503143	-1 hypothetical protein
1473159	1506658	33499	OXZ30027.1	B9N57_07205	1503228	1503644	-1 RNA polymerase subunit sigma-70
1473159	1506658	33499	OXZ30028.1	B9N57_07210	1503958	1505343	-1 ABC transporter
1473159	1506658	33499	OXZ30029.1	B9N57_07215	1505340	1506068	-1 transporter
1473159	1506658	33499	OXZ30030.1	B9N57_07220	1506068	1506658	-1 hypothetical protein
1535253	1542597	7344		B9N57_07355	1535253	1535486	-1 protein CapI
1535253	1542597	7344	OXZ30056.1	B9N57_07360	1535491	1536513	-1 hypothetical protein
1535253	1542597	7344	OXZ30057.1	B9N57_07365	1536548	1538062	-1 hypothetical protein
1535253	1542597	7344	OXZ30058.1	B9N57_07370	1538077	1539279	-1 hypothetical protein
1535253	1542597	7344	OXZ30059.1	B9N57_07375	1539314	1540381	-1 glycosyl transferase family 2
1535253	1542597	7344	OXZ30060.1	B9N57_07380	1540374	1541537	-1 capsule biosynthesis protein
1535253	1542597	7344	OXZ30061.1	B9N57_07385	1541551	1542597	-1 hypothetical protein
1535253	1542597	7344	OXZ30062.1	B9N57_07390	1542594	1543589	-1 ornithine cyclodeaminase
1638880	1660212	21332	OXZ29911.1	B9N57_07815	1637061	1638896	-1 multidrug ABC transporter
1638880	1660212	21332	OXZ29912.1	B9N57_07820	1638880	1640682	-1 multidrug ABC transporter
1638880	1660212	21332	OXZ29913.1	B9N57_07825	1640762	1641427	-1 histidine kinase
1638880	1660212	21332	OXZ29914.1	B9N57_07830	1641435	1642130	-1 DNA-binding response regulator
1638880	1660212	21332	OXZ29915.1	B9N57_07835	1642213	1643076	-1 UTP--glucose-1-phosphate uridylyltransferase
1638880	1660212	21332	OXZ29916.1	B9N57_07840	1643801	1646386	-1 ATP-dependent chaperone ClpB
1638880	1660212	21332	OXZ29917.1	B9N57_07845	1646405	1647349	-1 heat-shock protein
1638880	1660212	21332	OXZ29918.1	B9N57_07850	1647523	1648188	-1 nitroreductase
1638880	1660212	21332	OXZ29919.1	B9N57_07855	1648434	1649201	-1 hypothetical protein
1638880	1660212	21332	OXZ29920.1	B9N57_07860	1650005	1650556	1 hypothetical protein
1638880	1660212	21332	OXZ29921.1	B9N57_07865	1650617	1650829	1 hypothetical protein
1638880	1660212	21332	OXZ29922.1	B9N57_07870	1650909	1652057	1 MFS transporter
1638880	1660212	21332	OXZ29923.1	B9N57_07875	1652136	1652633	-1 hypothetical protein
1638880	1660212	21332	OXZ29924.1	B9N57_07880	1652669	1653142	-1 peptidase M50
1638880	1660212	21332	OXZ29925.1	B9N57_07885	1653629	1654051	-1 hypothetical protein
1638880	1660212	21332	OXZ29926.1	B9N57_07890	1654096	1655031	-1 TIGR01212 family radical SAM protein
1638880	1660212	21332	OXZ29927.1	B9N57_07895	1655024	1655464	-1 peroxiredoxin
1638880	1660212	21332	OXZ29928.1	B9N57_07900	1655457	1656293	-1 hydrolase
1638880	1660212	21332	OXZ29929.1	B9N57_07905	1656283	1656594	-1 DUF1292 domain-containing protein
1638880	1660212	21332	OXZ29930.1	B9N57_07910	1656607	1657998	-1 aminoacyl-histidine dipeptidase
1638880	1660212	21332	OXZ29931.1	B9N57_07915	1658063	1659181	-1 hypothetical protein
1638880	1660212	21332	OXZ29932.1	B9N57_07920	1659223	1660212	-1 peptide chain release factor 2
1720515	1725038	4523	OXZ29867.1	B9N57_08165	1720515	1720637	1 hypothetical protein
1720515	1725038	4523	OXZ29771.1	B9N57_08170	1721099	1721893	-1 protein
1720515	1725038	4523	OXZ29772.1	B9N57_08175	1721905	1722924	-1 iron ABC transporter
1720515	1725038	4523	OXZ29773.1	B9N57_08180	1722926	1723972	-1 iron ABC transporter
1720515	1725038	4523	OXZ29774.1	B9N57_08185	1723989	1725038	-1 iron ABC transporter permease
1816636	1830054	13418	OXZ29865.1	B9N57_08675	1816636	1822018	1 peptidase S8
1816636	1830054	13418		B9N57_08720	1823055	1823882	-1 N-acetylmuramoyl-L-alanine amidase
1816636	1830054	13418	OXZ29745.1	B9N57_08715	1824883	1825979	1 elongation factor Tu
1816636	1830054	13418	OXZ29746.1	B9N57_08695	1826980	1827071	-1 hypothetical protein
1816636	1830054	13418	OXZ29747.1	B9N57_08700	1827266	1827805	-1 transposase
1816636	1830054	13418	OXZ29748.1	B9N57_08705	1828247	1828466	1 hypothetical protein
1816636	1830054	13418	OXZ29740.1	B9N57_08750	1829467	1830054	-1 hypothetical protein

Table S3D: Predicted genomic islands in the genome of "F. nericia" 09T494

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
4923	16807	11884	OXZ39974.1	B9N50_00015	4923	9083	-1	phage tail tape measure protein
4923	16807	11884	OXZ39975.1	B9N50_00020	9307	9636	-1	hypothetical protein
4923	16807	11884	OXZ39976.1	B9N50_00025	9646	10290	-1	hypothetical protein
4923	16807	11884	OXZ39977.1	B9N50_00030	10302	10745	-1	hypothetical protein
4923	16807	11884	OXZ39978.1	B9N50_00035	10742	11089	-1	hypothetical protein
4923	16807	11884	OXZ39979.1	B9N50_00040	11086	11427	-1	hypothetical protein
4923	16807	11884	OXZ39980.1	B9N50_00045	11427	11723	-1	hypothetical protein
4923	16807	11884	OXZ39981.1	B9N50_00050	11723	12904	-1	phage major capsid protein
4923	16807	11884	OXZ39982.1	B9N50_00055	12907	13638	-1	hypothetical protein
4923	16807	11884	OXZ39983.1	B9N50_00060	13711	14841	-1	hypothetical protein
4923	16807	11884	OXZ39984.1	B9N50_00065	14829	16514	-1	hypothetical protein
4923	16807	11884	OXZ39985.1	B9N50_00070	16511	16807	-1	hypothetical protein
4923	16807	11884	OXZ39986.1	B9N50_00075	16794	17708	-1	hypothetical protein
173877	193778	19901	OXZ40153.1	B9N50_00950	173877	174989	-1	hypothetical protein
173877	193778	19901	OXZ40154.1	B9N50_00955	175269	179723	-1	hypothetical protein
173877	193778	19901	OXZ40155.1	B9N50_00960	180154	181461	-1	hypothetical protein
173877	193778	19901	OXZ40156.1	B9N50_00965	181485	183122	-1	hypothetical protein
173877	193778	19901	OXZ40157.1	B9N50_00970	183132	185336	-1	hypothetical protein
173877	193778	19901	OXZ40158.1	B9N50_00975	185254	185979	-1	hypothetical protein
173877	193778	19901	OXZ40159.1	B9N50_00980	185960	187936	-1	hypothetical protein
173877	193778	19901	OXZ40160.1	B9N50_00985	188155	188784	1	hypothetical protein
173877	193778	19901	OXZ40161.1	B9N50_00990	189230	192190	1	restriction endonuclease
173877	193778	19901	OXZ40162.1	B9N50_00995	192183	193778	1	hypothetical protein
335804	339866	4062	OXZ39656.1	B9N50_01695	335804	336445	-1	hemolysin III
335804	339866	4062	OXZ39657.1	B9N50_01700	336598	337101	1	acetyltransferase
335804	339866	4062	OXZ39658.1	B9N50_01705	337101	337835	1	hydrolase
335804	339866	4062	OXZ39659.1	B9N50_01710	338290	338865	1	cell filamentation protein Fic
335804	339866	4062	OXZ39685.1	B9N50_01715	339519	339866	-1	toxin MazF
1341275	1417222	75947	OXZ37862.1	B9N50_06755	1341275	1342078	-1	DNA-binding protein
1341275	1417222	75947	OXZ37863.1	B9N50_06760	1342268	1343788	-1	conjugal transfer protein
1341275	1417222	75947	OXZ37864.1	B9N50_06765	1343781	1345526	-1	recombinase
1341275	1417222	75947	OXZ37865.1	B9N50_06770	1345519	1347237	-1	recombinase
1341275	1417222	75947	OXZ37866.1	B9N50_06775	1347336	1347503	-1	aminoacyl-tRNA hydrolase
1341275	1417222	75947	OXZ37867.1	B9N50_06780	1347921	1348331	-1	RNA polymerase subunit sigma
1341275	1417222	75947	OXZ37868.1	B9N50_06785	1348569	1349933	-1	MATE family efflux transporter
1341275	1417222	75947	OXZ37869.1	B9N50_06790	1350018	1351760	-1	ABC transporter ATP-binding protein
1341275	1417222	75947	OXZ37870.1	B9N50_06795	1351762	1353474	-1	ABC transporter ATP-binding protein
1341275	1417222	75947	OXZ37871.1	B9N50_06800	1353478	1354893	-1	ABC transporter ATP-binding protein
1341275	1417222	75947	OXZ37872.1	B9N50_06805	1354906	1355592	-1	cobalt transporter
1341275	1417222	75947	OXZ37873.1	B9N50_06810	1355593	1356186	-1	hypothetical protein
1341275	1417222	75947	OXZ37874.1	B9N50_06815	1356358	1356969	-1	TetR family transcriptional regulator
1341275	1417222	75947	OXZ37875.1	B9N50_06820	1357080	1357736	-1	hypothetical protein
1341275	1417222	75947	OXZ37876.1	B9N50_06825	1357760	1358518	-1	hypothetical protein
1341275	1417222	75947	OXZ37877.1	B9N50_06830	1358540	1359931	-1	hypothetical protein
1341275	1417222	75947	OXZ37878.1	B9N50_06835	1359999	1365371	-1	non-ribosomal peptide synthetase
1341275	1417222	75947	OXZ37879.1	B9N50_06840	1365391	1366440	-1	oxidoreductase
1341275	1417222	75947	OXZ37880.1	B9N50_06845	1366442	1367515	-1	hypothetical protein
1341275	1417222	75947	OXZ37881.1	B9N50_06850	1367512	1368888	-1	hypothetical protein
1341275	1417222	75947	OXZ37882.1	B9N50_06855	1368913	1370370	-1	peptide synthetase
1341275	1417222	75947	OXZ37883.1	B9N50_06860	1370367	1371431	-1	oxidoreductase
1341275	1417222	75947	OXZ37884.1	B9N50_06865	1371454	1377627	-1	non-ribosomal peptide synthetase
1341275	1417222	75947	OXZ37885.1	B9N50_06870	1377644	1379233	-1	2,3-dihydroxybenzoate-AMP ligase
1341275	1417222	75947	OXZ37886.1	B9N50_06875	1379252	1379926	-1	4'-phosphopantetheinyl transferase
1341275	1417222	75947	OXZ37887.1	B9N50_06880	1379904	1380662	-1	thioesterase
1341275	1417222	75947	OXZ37888.1	B9N50_06885	1380819	1381190	-1	transcriptional regulator
1341275	1417222	75947	OXZ37889.1	B9N50_06890	1381661	1381801	-1	diacylglycerol transferase
1341275	1417222	75947	OXZ37890.1	B9N50_06895	1381850	1382218	1	plasmid mobilization relaxosome protein MobC
1341275	1417222	75947	OXZ37891.1	B9N50_06900	1382218	1383588	1	endonuclease
1341275	1417222	75947	OXZ37892.1	B9N50_06905	1383719	1384861	-1	single-stranded DNA-binding protein
1341275	1417222	75947	OXZ37893.1	B9N50_06910	1384895	1395817	-1	conjugal transfer protein
1341275	1417222	75947	OXZ37894.1	B9N50_06915	1396011	1396337	-1	terminase large subunit
1341275	1417222	75947	OXZ37895.1	B9N50_06920	1396678	1398384	-1	DNA topoisomerase III
1341275	1417222	75947	OXZ37896.1	B9N50_06925	1398801	1399679	-1	bacteriocin
1341275	1417222	75947	OXZ37897.1	B9N50_06930	1399695	1402049	-1	copper amine oxidase
1341275	1417222	75947	OXZ37898.1	B9N50_06935	1402046	1402303	-1	hypothetical protein
1341275	1417222	75947	OXZ37899.1	B9N50_06940	1402324	1405290	-1	hypothetical protein
1341275	1417222	75947	OXZ37900.1	B9N50_06945	1405300	1406265	-1	site-specific DNA-methyltransferase
1341275	1417222	75947	OXZ37901.1	B9N50_06950	1406237	1408732	-1	conjugal transfer protein TraE
1341275	1417222	75947	OXZ37902.1	B9N50_06955	1408729	1409067	-1	conjugal transfer protein
1341275	1417222	75947	OXZ37903.1	B9N50_06960	1409067	1409324	-1	hypothetical protein
1341275	1417222	75947	OXZ37904.1	B9N50_06965	1409342	1410205	-1	hypothetical protein
1341275	1417222	75947	OXZ37905.1	B9N50_06970	1410207	1410422	-1	conjugal transfer protein
1341275	1417222	75947	OXZ37906.1	B9N50_06975	1410423	1410746	-1	single-stranded DNA-binding protein
1341275	1417222	75947	OXZ37907.1	B9N50_06980	1410937	1411803	-1	CAAX protease
1341275	1417222	75947	OXZ37908.1	B9N50_06985	1411955	1413757	-1	conjugal transfer protein TraG
1341275	1417222	75947	OXZ37909.1	B9N50_06990	1413802	1414008	-1	hypothetical protein
1341275	1417222	75947	OXZ37910.1	B9N50_06995	1414207	1414698	-1	hypothetical protein
1341275	1417222	75947	OXZ38105.1	B9N50_07000	1414713	1415570	-1	DNA replication protein
1341275	1417222	75947	OXZ37911.1	B9N50_07005	1415585	1416562	-1	replication initiator RepA
1341275	1417222	75947	OXZ37912.1	B9N50_07010	1416649	1416939	-1	hypothetical protein
1341275	1417222	75947	OXZ38106.1	B9N50_07015	1416983	1417222	-1	hypothetical protein
1382218	1406265	24047	OXZ37891.1	B9N50_06900	1382218	1383588	1	endonuclease
1382218	1406265	24047	OXZ37892.1	B9N50_06905	1383719	1384861	-1	single-stranded DNA-binding protein

1382218	1406265	24047 OXZ37893.1	B9N50_06910	1384895	1395817	-1 conjugal transfer protein
1382218	1406265	24047 OXZ37894.1	B9N50_06915	1396011	1396337	-1 terminase large subunit
1382218	1406265	24047 OXZ37895.1	B9N50_06920	1396678	1398384	-1 DNA topoisomerase III
1382218	1406265	24047 OXZ37896.1	B9N50_06925	1398801	1399679	-1 bacteriocin
1382218	1406265	24047 OXZ37897.1	B9N50_06930	1399695	1402049	-1 copper amine oxidase
1382218	1406265	24047 OXZ37898.1	B9N50_06935	1402046	1402303	-1 hypothetical protein
1382218	1406265	24047 OXZ37899.1	B9N50_06940	1402324	1405290	-1 hypothetical protein
1382218	1406265	24047 OXZ37900.1	B9N50_06945	1405300	1406265	-1 site-specific DNA-methyltransferase
1382218	1406265	24047 OXZ37901.1	B9N50_06950	1406237	1408732	-1 conjugal transfer protein TraE
1408729	1416562	7833 OXZ37901.1	B9N50_06950	1406237	1408732	-1 conjugal transfer protein TraE
1408729	1416562	7833 OXZ37902.1	B9N50_06955	1408729	1409067	-1 conjugal transfer protein
1408729	1416562	7833 OXZ37903.1	B9N50_06960	1409067	1409324	-1 hypothetical protein
1408729	1416562	7833 OXZ37904.1	B9N50_06965	1409342	1410205	-1 hypothetical protein
1408729	1416562	7833 OXZ37905.1	B9N50_06970	1410207	1410422	-1 conjugal transfer protein
1408729	1416562	7833 OXZ37906.1	B9N50_06975	1410423	1410746	-1 single-stranded DNA-binding protein
1408729	1416562	7833 OXZ37907.1	B9N50_06980	1410937	1411803	-1 CAAX protease
1408729	1416562	7833 OXZ37908.1	B9N50_06985	1411955	1413757	-1 conjugal transfer protein TraG
1408729	1416562	7833 OXZ37909.1	B9N50_06990	1413802	1414008	-1 hypothetical protein
1408729	1416562	7833 OXZ37910.1	B9N50_06995	1414207	1414698	-1 hypothetical protein
1408729	1416562	7833 OXZ38105.1	B9N50_07000	1414713	1415570	-1 DNA replication protein
1408729	1416562	7833 OXZ37911.1	B9N50_07005	1415585	1416562	-1 replication initiator RepA
1551711	1651998	100287 OXZ38035.1	B9N50_07665	1551711	1553102	-1 ABC transporter
1551711	1651998	100287 OXZ38036.1	B9N50_07670	1553099	1553827	-1 transporter
1551711	1651998	100287 OXZ38037.1	B9N50_07675	1553827	1554417	-1 hypothetical protein
1551711	1651998	100287 OXZ38038.1	B9N50_07680	1554448	1556169	-1 ABC transporter permease
1551711	1651998	100287 OXZ38039.1	B9N50_07685	1556169	1557935	-1 ABC transporter permease
1551711	1651998	100287 OXZ38040.1	B9N50_07690	1558046	1558660	-1 TetR family transcriptional regulator
1551711	1651998	100287 OXZ38041.1	B9N50_07695	1558956	1559576	-1 phosphomethylpyrimidine kinase
1551711	1651998	100287	B9N50_07700	1559626	1560121	-1 terminase
1551711	1651998	100287	B9N50_07705	1560312	1561474	1 IS110 family transposase
1551711	1651998	100287 OXZ38042.1	B9N50_07710	1562235	1563971	-1 multidrug ABC transporter ATP-binding protein
1551711	1651998	100287 OXZ38043.1	B9N50_07715	1563971	1565686	-1 ABC transporter ATP-binding protein
1551711	1651998	100287 OXZ38044.1	B9N50_07720	1565690	1567171	-1 ABC transporter
1551711	1651998	100287 OXZ38111.1	B9N50_07725	1567156	1567836	-1 ABC transporter permease
1551711	1651998	100287 OXZ38045.1	B9N50_07730	1567851	1568480	-1 hypothetical protein
1551711	1651998	100287 OXZ38046.1	B9N50_07735	1568470	1569051	-1 TetR family transcriptional regulator
1551711	1651998	100287 OXZ38047.1	B9N50_07740	1569738	1570094	1 plasmid mobilization relaxosome protein MobC
1551711	1651998	100287 OXZ38048.1	B9N50_07745	1570283	1570792	-1 hypothetical protein
1551711	1651998	100287	B9N50_07750	1570932	1571213	-1 hypothetical protein
1551711	1651998	100287 OXZ38049.1	B9N50_07755	1571216	1571587	-1 transcriptional regulator
1551711	1651998	100287 OXZ38050.1	B9N50_07760	1571877	1572338	-1 flavodoxin
1551711	1651998	100287 OXZ38112.1	B9N50_07765	1572742	1573860	-1 alpha/beta hydrolase
1551711	1651998	100287 OXZ38051.1	B9N50_07770	1573866	1574123	-1 AbrB family transcriptional regulator
1551711	1651998	100287 OXZ38052.1	B9N50_07775	1574772	1575140	-1 EXLDI protein
1551711	1651998	100287	B9N50_07780	1575327	1575736	-1 recombinase family protein
1551711	1651998	100287 OXZ38113.1	B9N50_07785	1575991	1576698	-1 hypothetical protein
1551711	1651998	100287 OXZ38053.1	B9N50_07790	1577036	1577653	-1 hypothetical protein
1551711	1651998	100287	B9N50_07795	1577792	1578732	-1 recombinase family protein
1551711	1651998	100287 OXZ38114.1	B9N50_07800	1579119	1579574	-1 hypothetical protein
1551711	1651998	100287	B9N50_07805	1579830	1580329	-1 hypothetical protein
1551711	1651998	100287 OXZ38054.1	B9N50_07810	1580757	1582511	-1 recombinase family protein
1551711	1651998	100287 OXZ38055.1	B9N50_07815	1583242	1583652	-1 RNA polymerase subunit sigma
1551711	1651998	100287 OXZ38115.1	B9N50_07820	1583922	1584329	-1 hypothetical protein
1551711	1651998	100287 OXZ38056.1	B9N50_07825	1584632	1585033	1 transcriptional regulator
1551711	1651998	100287 OXZ38057.1	B9N50_07830	1585042	1585590	1 toxin
1551711	1651998	100287 OXZ38058.1	B9N50_07835	1585599	1586081	1 hypothetical protein
1551711	1651998	100287 OXZ38059.1	B9N50_07840	1586074	1587147	1 cell filamentation protein Fic
1551711	1651998	100287 OXZ38060.1	B9N50_07845	1587318	1587674	1 plasmid mobilization relaxosome protein MobC
1551711	1651998	100287 OXZ38061.1	B9N50_07850	1587676	1589007	1 endonuclease
1551711	1651998	100287	B9N50_07855	1589224	1590455	-1 IS256 family transposase
1551711	1651998	100287	B9N50_07860	1590580	1591127	-1 hypothetical protein
1551711	1651998	100287 OXZ38062.1	B9N50_07865	1591257	1591448	-1 hypothetical protein
1551711	1651998	100287 OXZ38063.1	B9N50_07870	1591634	1592872	-1 hypothetical protein
1551711	1651998	100287 OXZ38064.1	B9N50_07875	1592885	1593934	-1 hypothetical protein
1551711	1651998	100287 OXZ38065.1	B9N50_07880	1593943	1594962	-1 hypothetical protein
1551711	1651998	100287 OXZ38066.1	B9N50_07885	1594946	1596610	-1 hypothetical protein
1551711	1651998	100287 OXZ38067.1	B9N50_07890	1596603	1597754	-1 hypothetical protein
1551711	1651998	100287 OXZ38068.1	B9N50_07895	1597757	1600087	-1 ABC transporter permease
1551711	1651998	100287 OXZ38069.1	B9N50_07900	1600087	1600767	-1 ABC transporter ATP-binding protein
1551711	1651998	100287 OXZ38070.1	B9N50_07905	1601124	1601330	1 hypothetical protein
1551711	1651998	100287 OXZ38071.1	B9N50_07910	1601736	1602029	-1 hypothetical protein
1551711	1651998	100287 OXZ38072.1	B9N50_07915	1602246	1602566	-1 hypothetical protein
1551711	1651998	100287 OXZ38073.1	B9N50_07920	1602697	1603128	-1 hypothetical protein
1551711	1651998	100287 OXZ38074.1	B9N50_07925	1603141	1603407	-1 hypothetical protein
1551711	1651998	100287 OXZ38075.1	B9N50_07930	1603401	1603970	-1 hypothetical protein
1551711	1651998	100287	B9N50_07935	1604957	1605466	1 transposase
1551711	1651998	100287 OXZ38076.1	B9N50_07940	1605602	1605955	1 hypothetical protein
1551711	1651998	100287 OXZ38077.1	B9N50_07945	1606029	1606667	-1 hypothetical protein
1551711	1651998	100287 OXZ38078.1	B9N50_07950	1606664	1607827	-1 hypothetical protein
1551711	1651998	100287 OXZ38079.1	B9N50_07955	1607838	1608710	-1 hypothetical protein
1551711	1651998	100287 OXZ38080.1	B9N50_07960	1608697	1610373	-1 hypothetical protein
1551711	1651998	100287 OXZ38081.1	B9N50_07965	1610357	1611238	-1 hypothetical protein
1551711	1651998	100287 OXZ38082.1	B9N50_07970	1611328	1611522	-1 hypothetical protein
1551711	1651998	100287 OXZ38083.1	B9N50_07975	1611561	1612568	-1 hypothetical protein
1551711	1651998	100287 OXZ38084.1	B9N50_07980	1612572	1613831	-1 hypothetical protein
1551711	1651998	100287 OXZ38085.1	B9N50_07985	1614036	1615673	-1 ABC transporter permease

						CXXX repeat peptide modification system
1551711	1651998	100287 OXZ38086.1	B9N50_07990	1615666	1615932	-1 protein
1551711	1651998	100287 OXZ38087.1	B9N50_07995	1615934	1618120	-1 radical SAM protein
1551711	1651998	100287 OXZ38088.1	B9N50_08000	1618402	1619007	-1 DNA-binding response regulator
1551711	1651998	100287 OXZ38089.1	B9N50_08005	1618979	1620526	-1 hypothetical protein
1551711	1651998	100287 OXZ38090.1	B9N50_08010	1620826	1621482	-1 DNA-binding protein
1551711	1651998	100287 OXZ38091.1	B9N50_08015	1621526	1629169	-1 DNA helicase
1551711	1651998	100287 OXZ38092.1	B9N50_08020	1629156	1630121	-1 DNA (cytosine-5-)-methyltransferase
1551711	1651998	100287 OXZ38093.1	B9N50_08025	1630114	1631835	-1 DNA topoisomerase III
1551711	1651998	100287 OXZ38094.1	B9N50_08030	1631928	1632911	-1 hypothetical protein
1551711	1651998	100287 OXZ38095.1	B9N50_08035	1632904	1633515	-1 hypothetical protein
1551711	1651998	100287 OXZ38096.1	B9N50_08040	1633589	1634446	-1 bacteriocin
1551711	1651998	100287 OXZ38097.1	B9N50_08045	1634461	1635746	-1 copper amine oxidase
1551711	1651998	100287 OXZ38297.1	B9N50_05400	1636747	1637171	-1 copper amine oxidase
1551711	1651998	100287 OXZ38298.1	B9N50_05405	1637158	1637397	-1 hypothetical protein
1551711	1651998	100287 OXZ38299.1	B9N50_05410	1637412	1639991	-1 hypothetical protein
1551711	1651998	100287 OXZ38300.1	B9N50_05415	1639999	1642422	-1 conjugal transfer protein TraE
1551711	1651998	100287 OXZ38301.1	B9N50_05420	1642313	1642723	-1 conjugal transfer protein
1551711	1651998	100287 OXZ38302.1	B9N50_05425	1642725	1643015	-1 hypothetical protein
1551711	1651998	100287 OXZ38303.1	B9N50_05430	1643025	1643888	-1 hypothetical protein
1551711	1651998	100287 OXZ38304.1	B9N50_05435	1643899	1644114	-1 conjugal transfer protein
1551711	1651998	100287 OXZ38305.1	B9N50_05440	1644116	1644427	-1 single-stranded DNA-binding protein
1551711	1651998	100287 OXZ38306.1	B9N50_05445	1644616	1645071	-1 hypothetical protein
						bacteriocin ABC transporter ATP-binding
1551711	1651998	100287 OXZ38307.1	B9N50_05450	1645068	1645676	-1 protein
1551711	1651998	100287 OXZ38308.1	B9N50_05455	1645673	1647649	-1 hypothetical protein
1551711	1651998	100287 OXZ38309.1	B9N50_05460	1647814	1648152	-1 hypothetical protein
1551711	1651998	100287	B9N50_05465	1648403	1648661	-1 conjugal transfer protein TraG
1551711	1651998	100287 OXZ38310.1	B9N50_05470	1648699	1648974	-1 hypothetical protein
1551711	1651998	100287 OXZ38311.1	B9N50_05475	1648993	1650789	-1 conjugal transfer protein TraG
1551711	1651998	100287 OXZ38312.1	B9N50_05480	1650782	1651516	-1 phage antirepressor Ant
1551711	1651998	100287 OXZ38313.1	B9N50_05485	1651513	1651998	-1 conjugal transfer protein
1551711	1651998	100287 OXZ38314.1	B9N50_05490	1651991	1652818	-1 nucleoside triphosphate hydrolase
1591257	1596610	5353 OXZ38062.1	B9N50_07865	1591257	1591448	-1 hypothetical protein
1591257	1596610	5353 OXZ38063.1	B9N50_07870	1591634	1592872	-1 hypothetical protein
1591257	1596610	5353 OXZ38064.1	B9N50_07875	1592885	1593934	-1 hypothetical protein
1591257	1596610	5353 OXZ38065.1	B9N50_07880	1593943	1594962	-1 hypothetical protein
1591257	1596610	5353 OXZ38066.1	B9N50_07885	1594946	1596610	-1 hypothetical protein
1591257	1596610	5353 OXZ38067.1	B9N50_07890	1596603	1597754	-1 hypothetical protein
1611561	1619007	7446 OXZ38083.1	B9N50_07975	1611561	1612568	-1 hypothetical protein
1611561	1619007	7446 OXZ38084.1	B9N50_07980	1612572	1613831	-1 hypothetical protein
1611561	1619007	7446 OXZ38085.1	B9N50_07985	1614036	1615673	-1 ABC transporter permease
						CXXX repeat peptide modification system
1611561	1619007	7446 OXZ38086.1	B9N50_07990	1615666	1615932	-1 protein
1611561	1619007	7446 OXZ38087.1	B9N50_07995	1615934	1618120	-1 radical SAM protein
1611561	1619007	7446 OXZ38088.1	B9N50_08000	1618402	1619007	-1 DNA-binding response regulator
1611561	1619007	7446 OXZ38089.1	B9N50_08005	1618979	1620526	-1 hypothetical protein
1644116	1651998	7882 OXZ38305.1	B9N50_05440	1644116	1644427	-1 single-stranded DNA-binding protein
1644116	1651998	7882 OXZ38306.1	B9N50_05445	1644616	1645071	-1 hypothetical protein
						bacteriocin ABC transporter ATP-binding
1644116	1651998	7882 OXZ38307.1	B9N50_05450	1645068	1645676	-1 protein
1644116	1651998	7882 OXZ38308.1	B9N50_05455	1645673	1647649	-1 hypothetical protein
1644116	1651998	7882 OXZ38309.1	B9N50_05460	1647814	1648152	-1 hypothetical protein
1644116	1651998	7882	B9N50_05465	1648403	1648661	-1 conjugal transfer protein TraG
1644116	1651998	7882 OXZ38310.1	B9N50_05470	1648699	1648974	-1 hypothetical protein
1644116	1651998	7882 OXZ38311.1	B9N50_05475	1648993	1650789	-1 conjugal transfer protein TraG
1644116	1651998	7882 OXZ38312.1	B9N50_05480	1650782	1651516	-1 phage antirepressor Ant
1644116	1651998	7882 OXZ38313.1	B9N50_05485	1651513	1651998	-1 conjugal transfer protein
1644116	1651998	7882 OXZ38314.1	B9N50_05490	1651991	1652818	-1 nucleoside triphosphate hydrolase
1771690	1776504	4814 OXZ37464.1	B9N50_08530	1770150	1771697	-1 hypothetical protein
1771690	1776504	4814 OXZ37465.1	B9N50_08535	1771690	1772916	-1 hypothetical protein
1771690	1776504	4814 OXZ37466.1	B9N50_08540	1772947	1774119	-1 hypothetical protein
1771690	1776504	4814 OXZ37467.1	B9N50_08545	1774194	1775369	-1 hypothetical protein
1771690	1776504	4814 OXZ37468.1	B9N50_08550	1775362	1776504	-1 hypothetical protein

Table S3E: Predicted genomic islands in the genome of "F. nericia" 12T272

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
34527	44047	9520	OXZ36018.1	B9N53_00160	34527	35396	1	hypothetical protein
34527	44047	9520	OXZ36019.1	B9N53_00165	35383	37371	1	exopolyphosphatase
34527	44047	9520	OXZ36020.1	B9N53_00170	37352	37798	1	50S ribosomal protein L9
34527	44047	9520	OXZ36021.1	B9N53_00175	37832	39169	1	replicative DNA helicase
34527	44047	9520	OXZ36022.1	B9N53_00180	39166	39729	1	GNAT family N-acetyltransferase
34527	44047	9520	OXZ36023.1	B9N53_00185	39734	40492	1	DNA replication protein
34527	44047	9520	OXZ36024.1	B9N53_00190	40495	41472	1	DNA replication protein DnaC
34527	44047	9520	OXZ36025.1	B9N53_00195	41469	42113	1	NAD(P)H-hydrate epimerase
34527	44047	9520	OXZ36026.1	B9N53_00200	42835	43377	1	ECF transporter S component
34527	44047	9520	OXZ36027.1	B9N53_00205	43361	44047	1	radical SAM protein
604530	616700	12170	OXZ35396.1	B9N53_03100	604530	605510	-1	recombinase XerC
604530	616700	12170	OXZ35397.1	B9N53_03105	605613	606788	-1	aspartate aminotransferase
604530	616700	12170	OXZ35398.1	B9N53_03110	606769	607596	-1	metal-dependent phosphoesterase
604530	616700	12170	OXZ35399.1	B9N53_03115	607665	609206	-1	ribonuclease Y
604530	616700	12170	OXZ35400.1	B9N53_03120	609325	609987	-1	chromosome partitioning protein ParA
604530	616700	12170	OXZ35401.1	B9N53_03125	609974	610213	-1	hypothetical protein
604530	616700	12170	OXZ35402.1	B9N53_03130	610213	611796	-1	exonuclease SbcC
604530	616700	12170	OXZ35420.1	B9N53_03135	611796	612746	-1	phosphoesterase
604530	616700	12170	OXZ35403.1	B9N53_03140	612777	613868	-1	recombinase RecA
604530	616700	12170	OXZ35404.1	B9N53_03145	613937	614473	-1	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
604530	616700	12170	OXZ35405.1	B9N53_03150	614475	616700	-1	cell division protein FtsK
1277699	1282020	4321		B9N53_06220	1277699	1278187	-1	terminase
1277699	1282020	4321		B9N53_06225	1278379	1279523	1	IS110 family transposase
1277699	1282020	4321	OXZ34114.1	B9N53_06230	1280284	1282020	-1	multidrug ABC transporter ATP-binding protein
1294955	1300767	5812	OXZ34125.1	B9N53_06305	1293840	1294958	-1	alpha/beta hydrolase
1294955	1300767	5812	OXZ34126.1	B9N53_06310	1294955	1295212	-1	AbrB family transcriptional regulator
1294955	1300767	5812	OXZ34127.1	B9N53_06315	1295862	1296230	-1	EXLDI protein
1294955	1300767	5812		B9N53_06320	1296417	1296826	-1	recombinase family protein
1294955	1300767	5812	OXZ34201.1	B9N53_06325	1297080	1297787	-1	hypothetical protein
1294955	1300767	5812	OXZ34128.1	B9N53_06330	1298153	1298761	-1	hypothetical protein
1294955	1300767	5812		B9N53_06335	1298777	1299649	-1	recombinase family protein
1294955	1300767	5812	OXZ34129.1	B9N53_06340	1300150	1300767	-1	hypothetical protein
1359973	1364035	4062	OXZ34202.1	B9N53_06615	1359973	1360320	1	toxin MazF
1359973	1364035	4062	OXZ34181.1	B9N53_06620	1360974	1361549	-1	cell filamentation protein Fic
1359973	1364035	4062	OXZ34182.1	B9N53_06625	1362004	1362738	-1	hydrolase
1359973	1364035	4062	OXZ34183.1	B9N53_06630	1362738	1363241	-1	acetyltransferase
1359973	1364035	4062	OXZ34184.1	B9N53_06635	1363394	1364035	1	hemolysin III
1496002	1504337	8335	OXZ33200.1	B9N53_07260	1496002	1496184	-1	hypothetical protein
1496002	1504337	8335	OXZ33201.1	B9N53_07265	1496240	1497262	-1	hypothetical protein
1496002	1504337	8335	OXZ33202.1	B9N53_07270	1497300	1498811	-1	hypothetical protein
1496002	1504337	8335	OXZ33203.1	B9N53_07275	1498825	1500027	-1	hypothetical protein
1496002	1504337	8335	OXZ33204.1	B9N53_07280	1500062	1501129	-1	glycosyl transferase family 2
1496002	1504337	8335	OXZ33205.1	B9N53_07285	1501122	1502285	-1	capsule biosynthesis protein
1496002	1504337	8335	OXZ33206.1	B9N53_07290	1502299	1503345	-1	hypothetical protein
1496002	1504337	8335	OXZ33207.1	B9N53_07295	1503342	1504337	-1	hypothetical protein
1736754	1830377	93623	OXZ32959.1	B9N53_08375	1736754	1737218	-1	hypothetical protein
1736754	1830377	93623	OXZ32960.1	B9N53_08380	1737303	1738106	-1	DNA-binding protein
1736754	1830377	93623	OXZ32961.1	B9N53_08385	1738296	1739816	-1	conjugal transfer protein
1736754	1830377	93623	OXZ32962.1	B9N53_08390	1739809	1741551	-1	recombinase
1736754	1830377	93623	OXZ32963.1	B9N53_08395	1741544	1743262	-1	recombinase
1736754	1830377	93623	OXZ32964.1	B9N53_08400	1743361	1743528	-1	aminoacyl-tRNA hydrolase
1736754	1830377	93623	OXZ32965.1	B9N53_08405	1743945	1744355	-1	RNA polymerase subunit sigma
1736754	1830377	93623	OXZ32966.1	B9N53_08410	1744638	1746374	-1	multidrug ABC transporter ATP-binding protein
1736754	1830377	93623	OXZ32967.1	B9N53_08415	1746367	1748088	-1	ABC transporter ATP-binding protein
1736754	1830377	93623	OXZ32968.1	B9N53_08420	1748126	1749478	-1	MATE family efflux transporter
1736754	1830377	93623	OXZ32969.1	B9N53_08425	1749491	1750939	-1	ABC transporter
1736754	1830377	93623	OXZ32970.1	B9N53_08430	1750936	1751616	-1	ABC transporter permease
1736754	1830377	93623	OXZ32971.1	B9N53_08435	1751616	1752194	-1	hypothetical protein
1736754	1830377	93623	OXZ32972.1	B9N53_08440	1752246	1752812	-1	TetR family transcriptional regulator
1736754	1830377	93623	OXZ32973.1	B9N53_08445	1752898	1753650	-1	hypothetical protein
1736754	1830377	93623	OXZ32974.1	B9N53_08450	1753651	1754706	-1	saccharopine dehydrogenase
1736754	1830377	93623	OXZ32975.1	B9N53_08455	1754796	1760315	-1	non-ribosomal peptide synthetase
1736754	1830377	93623	OXZ32976.1	B9N53_08460	1760336	1762276	-1	condensation protein
1736754	1830377	93623	OXZ32977.1	B9N53_08465	1762289	1763875	-1	2,3-dihydroxybenzoate-AMP ligase
1736754	1830377	93623	OXZ32978.1	B9N53_08470	1763875	1764567	-1	4-phosphopantetheinyl transferase
1736754	1830377	93623	OXZ32979.1	B9N53_08475	1764557	1765309	-1	thioesterase
1736754	1830377	93623	OXZ32980.1	B9N53_08480	1765470	1765841	-1	transcriptional regulator
1736754	1830377	93623	OXZ32981.1	B9N53_08485	1766366	1766734	1	plasmid mobilization relaxosome protein MobC
1736754	1830377	93623	OXZ32982.1	B9N53_08490	1766734	1768104	1	endonuclease
1736754	1830377	93623		B9N53_08495	1768445	1769660	-1	IS256 family transposase
1736754	1830377	93623	OXZ32983.1	B9N53_08500	1769853	1770317	-1	hypothetical protein
1736754	1830377	93623	OXZ32984.1	B9N53_08505	1770441	1772564	-1	bacteriocin/lantibiotic ABC transporter ATP-binding protein
1736754	1830377	93623	OXZ32985.1	B9N53_08510	1772654	1775869	-1	type 2 lantipeptide synthetase LanM
1736754	1830377	93623	OXZ32986.1	B9N53_08515	1775957	1776184	-1	type 2 lantibiotic, mersacidin/lichenicidin family protein
1736754	1830377	93623	OXZ32987.1	B9N53_08520	1776259	1776981	-1	ABC transporter permease
1736754	1830377	93623	OXZ32988.1	B9N53_08525	1777001	1777735	-1	hypothetical protein
1736754	1830377	93623	OXZ32989.1	B9N53_08530	1777728	1778645	-1	ABC transporter ATP-binding protein
1736754	1830377	93623		B9N53_08535	1778911	1779289	-1	hypothetical protein

1736754	1830377	93623 OXZ32990.1	B9N53_08540	1779302	1779568	-1 hypothetical protein
1736754	1830377	93623 OXZ32991.1	B9N53_08545	1779562	1780131	-1 hypothetical protein
1736754	1830377	93623	B9N53_08550	1780470	1780774	1 relaxase
1736754	1830377	93623 OXZ32992.1	B9N53_08555	1780793	1781224	-1 hypothetical protein
1736754	1830377	93623	B9N53_08560	1781178	1782119	1 endonuclease
1736754	1830377	93623 OXZ32993.1	B9N53_08565	1782137	1782883	-1 ABC transporter permease
1736754	1830377	93623 OXZ32994.1	B9N53_08570	1782898	1783590	-1 ABC transporter permease
1736754	1830377	93623 OXZ32995.1	B9N53_08575	1783592	1784506	-1 bacitracin ABC transporter ATP-binding protein
1736754	1830377	93623 OXZ32996.1	B9N53_08580	1784521	1785678	-1 hypothetical protein
1736754	1830377	93623 OXZ32997.1	B9N53_08585	1785682	1786989	-1 hypothetical protein
1736754	1830377	93623 OXZ32998.1	B9N53_08590	1787575	1789212	-1 ABC transporter permease CXXX repeat peptide modification system
1736754	1830377	93623 OXZ32999.1	B9N53_08595	1789205	1789471	-1 protein
1736754	1830377	93623 OXZ33000.1	B9N53_08600	1789473	1791662	-1 radical SAM protein
1736754	1830377	93623 OXZ33001.1	B9N53_08605	1791649	1791831	-1 hypothetical protein
1736754	1830377	93623 OXZ33002.1	B9N53_08610	1791961	1792566	-1 DNA-binding response regulator
1736754	1830377	93623 OXZ33003.1	B9N53_08615	1792538	1794085	-1 hypothetical protein
1736754	1830377	93623 OXZ33004.1	B9N53_08620	1794400	1795494	-1 single-stranded DNA-binding protein
1736754	1830377	93623 OXZ33005.1	B9N53_08625	1795527	1805945	-1 conjugal transfer protein
1736754	1830377	93623 OXZ33006.1	B9N53_08630	1806140	1806466	-1 terminase large subunit
1736754	1830377	93623 OXZ33007.1	B9N53_08635	1806808	1808514	-1 DNA topoisomerase III
1736754	1830377	93623 OXZ33008.1	B9N53_08640	1808931	1809809	-1 bacteriocin
1736754	1830377	93623 OXZ33009.1	B9N53_08645	1809825	1812134	-1 copper amine oxidase
1736754	1830377	93623 OXZ33010.1	B9N53_08650	1812131	1812388	-1 hypothetical protein
1736754	1830377	93623 OXZ33011.1	B9N53_08655	1812408	1815371	-1 hypothetical protein
1736754	1830377	93623 OXZ33012.1	B9N53_08660	1815381	1816346	-1 site-specific DNA-methyltransferase
1736754	1830377	93623 OXZ33013.1	B9N53_08665	1816318	1818813	-1 conjugal transfer protein TraE
1736754	1830377	93623 OXZ33014.1	B9N53_08670	1818810	1819148	-1 conjugal transfer protein
1736754	1830377	93623 OXZ33015.1	B9N53_08675	1819148	1819405	-1 hypothetical protein
1736754	1830377	93623 OXZ33016.1	B9N53_08680	1819423	1820286	-1 hypothetical protein
1736754	1830377	93623 OXZ33017.1	B9N53_08685	1820288	1820503	-1 conjugal transfer protein
1736754	1830377	93623 OXZ33018.1	B9N53_08690	1820504	1820827	-1 single-stranded DNA-binding protein
1736754	1830377	93623 OXZ33019.1	B9N53_08695	1821017	1821880	-1 CAAX protease
1736754	1830377	93623 OXZ33020.1	B9N53_08700	1822032	1823834	-1 conjugal transfer protein TraG
1736754	1830377	93623 OXZ33021.1	B9N53_08705	1823879	1824085	-1 hypothetical protein
1736754	1830377	93623 OXZ33022.1	B9N53_08710	1824282	1824773	-1 DUF3801 domain-containing protein
1736754	1830377	93623 OXZ33083.1	B9N53_08715	1824788	1825645	-1 DNA replication protein
1736754	1830377	93623 OXZ33023.1	B9N53_08720	1825660	1826637	-1 replication initiator RepA
1736754	1830377	93623 OXZ33024.1	B9N53_08725	1826724	1827014	-1 hypothetical protein
1736754	1830377	93623	B9N53_08730	1827163	1828239	-1 ABC transporter ATP-binding protein
1736754	1830377	93623 OXZ33025.1	B9N53_08735	1828498	1829421	-1 RNA-binding protein
1736754	1830377	93623 OXZ33026.1	B9N53_08740	1829418	1830149	-1 insertase membrane protein insertion efficiency factor
1736754	1830377	93623 OXZ33027.1	B9N53_08745	1830165	1830377	-1 YidD
1736754	1830377	93623 OXZ33028.1	B9N53_08750	1830365	1830706	-1 ribonuclease P protein component
1736754	1741551	4797 OXZ32959.1	B9N53_08375	1736754	1737218	-1 hypothetical protein
1736754	1741551	4797 OXZ32960.1	B9N53_08380	1737303	1738106	-1 DNA-binding protein
1736754	1741551	4797 OXZ32961.1	B9N53_08385	1738296	1739816	-1 conjugal transfer protein
1736754	1741551	4797 OXZ32962.1	B9N53_08390	1739809	1741551	-1 recombinase
1736754	1741551	4797 OXZ32963.1	B9N53_08395	1741544	1743262	-1 recombinase
1743361	1754706	11345 OXZ32964.1	B9N53_08400	1743361	1743528	-1 aminoacyl-tRNA hydrolase
1743361	1754706	11345 OXZ32965.1	B9N53_08405	1743945	1744355	-1 RNA polymerase subunit sigma
1743361	1754706	11345 OXZ32966.1	B9N53_08410	1744638	1746374	-1 multidrug ABC transporter ATP-binding protein
1743361	1754706	11345 OXZ32967.1	B9N53_08415	1746367	1748088	-1 ABC transporter ATP-binding protein
1743361	1754706	11345 OXZ32968.1	B9N53_08420	1748126	1749478	-1 MATE family efflux transporter
1743361	1754706	11345 OXZ32969.1	B9N53_08425	1749491	1750939	-1 ABC transporter
1743361	1754706	11345 OXZ32970.1	B9N53_08430	1750936	1751616	-1 ABC transporter permease
1743361	1754706	11345 OXZ32971.1	B9N53_08435	1751616	1752194	-1 hypothetical protein
1743361	1754706	11345 OXZ32972.1	B9N53_08440	1752246	1752812	-1 TetR family transcriptional regulator
1743361	1754706	11345 OXZ32973.1	B9N53_08445	1752898	1753650	-1 hypothetical protein
1743361	1754706	11345 OXZ32974.1	B9N53_08450	1753651	1754706	-1 saccharopine dehydrogenase
1760336	1776981	16645 OXZ32976.1	B9N53_08460	1760336	1762276	-1 condensation protein
1760336	1776981	16645 OXZ32977.1	B9N53_08465	1762289	1763875	-1 2,3-dihydroxybenzoate-AMP ligase
1760336	1776981	16645 OXZ32978.1	B9N53_08470	1763875	1764567	-1 4-phosphopantetheinyl transferase
1760336	1776981	16645 OXZ32979.1	B9N53_08475	1764557	1765309	-1 thioesterase
1760336	1776981	16645 OXZ32980.1	B9N53_08480	1765470	1765841	-1 transcriptional regulator
1760336	1776981	16645 OXZ32981.1	B9N53_08485	1766366	1766734	1 plasmid mobilization relaxosome protein MobC
1760336	1776981	16645 OXZ32982.1	B9N53_08490	1766734	1768104	1 endonuclease
1760336	1776981	16645	B9N53_08495	1768445	1769660	-1 IS256 family transposase
1760336	1776981	16645 OXZ32983.1	B9N53_08500	1769853	1770317	-1 hypothetical protein bacteriocin/lantibiotic ABC transporter ATP-
1760336	1776981	16645 OXZ32984.1	B9N53_08505	1770441	1772564	-1 binding protein
1760336	1776981	16645 OXZ32985.1	B9N53_08510	1772654	1775869	-1 type 2 lantipeptide synthetase LanM type 2 lantibiotic, mersacidin/lichenicidin family
1760336	1776981	16645 OXZ32986.1	B9N53_08515	1775957	1776184	-1 protein
1760336	1776981	16645 OXZ32987.1	B9N53_08520	1776259	1776981	-1 ABC transporter permease
1778911	1816346	37435	B9N53_08535	1778911	1779289	-1 hypothetical protein
1778911	1816346	37435 OXZ32990.1	B9N53_08540	1779302	1779568	-1 hypothetical protein
1778911	1816346	37435 OXZ32991.1	B9N53_08545	1779562	1780131	-1 hypothetical protein
1778911	1816346	37435	B9N53_08550	1780470	1780774	1 relaxase
1778911	1816346	37435 OXZ32992.1	B9N53_08555	1780793	1781224	-1 hypothetical protein
1778911	1816346	37435	B9N53_08560	1781178	1782119	1 endonuclease
1778911	1816346	37435 OXZ32993.1	B9N53_08565	1782137	1782883	-1 ABC transporter permease
1778911	1816346	37435 OXZ32994.1	B9N53_08570	1782898	1783590	-1 ABC transporter permease

1778911	1816346	37435 OXZ32995.1	B9N53_08575	1783592	1784506	-1 bacitracin ABC transporter ATP-binding protein
1778911	1816346	37435 OXZ32996.1	B9N53_08580	1784521	1785678	-1 hypothetical protein
1778911	1816346	37435 OXZ32997.1	B9N53_08585	1785682	1786989	-1 hypothetical protein
1778911	1816346	37435 OXZ32998.1	B9N53_08590	1787575	1789212	-1 ABC transporter permease CXXX repeat peptide modification system
1778911	1816346	37435 OXZ32999.1	B9N53_08595	1789205	1789471	-1 protein
1778911	1816346	37435 OXZ33000.1	B9N53_08600	1789473	1791662	-1 radical SAM protein
1778911	1816346	37435 OXZ33001.1	B9N53_08605	1791649	1791831	-1 hypothetical protein
1778911	1816346	37435 OXZ33002.1	B9N53_08610	1791961	1792566	-1 DNA-binding response regulator
1778911	1816346	37435 OXZ33003.1	B9N53_08615	1792538	1794085	-1 hypothetical protein
1778911	1816346	37435 OXZ33004.1	B9N53_08620	1794400	1795494	-1 single-stranded DNA-binding protein
1778911	1816346	37435 OXZ33005.1	B9N53_08625	1795527	1805945	-1 conjugal transfer protein
1778911	1816346	37435 OXZ33006.1	B9N53_08630	1806140	1806466	-1 terminase large subunit
1778911	1816346	37435 OXZ33007.1	B9N53_08635	1806808	1808514	-1 DNA topoisomerase III
1778911	1816346	37435 OXZ33008.1	B9N53_08640	1808931	1809809	-1 bacteriocin
1778911	1816346	37435 OXZ33009.1	B9N53_08645	1809825	1812134	-1 copper amine oxidase
1778911	1816346	37435 OXZ33010.1	B9N53_08650	1812131	1812388	-1 hypothetical protein
1778911	1816346	37435 OXZ33011.1	B9N53_08655	1812408	1815371	-1 hypothetical protein
1778911	1816346	37435 OXZ33012.1	B9N53_08660	1815381	1816346	-1 site-specific DNA-methyltransferase
1778911	1816346	37435 OXZ33013.1	B9N53_08665	1816318	1818813	-1 conjugal transfer protein TraE
1818810	1827014	8204 OXZ33013.1	B9N53_08665	1816318	1818813	-1 conjugal transfer protein TraE
1818810	1827014	8204 OXZ33014.1	B9N53_08670	1818810	1819148	-1 conjugal transfer protein
1818810	1827014	8204 OXZ33015.1	B9N53_08675	1819148	1819405	-1 hypothetical protein
1818810	1827014	8204 OXZ33016.1	B9N53_08680	1819423	1820286	-1 hypothetical protein
1818810	1827014	8204 OXZ33017.1	B9N53_08685	1820288	1820503	-1 conjugal transfer protein
1818810	1827014	8204 OXZ33018.1	B9N53_08690	1820504	1820827	-1 single-stranded DNA-binding protein
1818810	1827014	8204 OXZ33019.1	B9N53_08695	1821017	1821880	-1 CAAX protease
1818810	1827014	8204 OXZ33020.1	B9N53_08700	1822032	1823834	-1 conjugal transfer protein TraG
1818810	1827014	8204 OXZ33021.1	B9N53_08705	1823879	1824085	-1 hypothetical protein
1818810	1827014	8204 OXZ33022.1	B9N53_08710	1824282	1824773	-1 DUF3801 domain-containing protein
1818810	1827014	8204 OXZ33083.1	B9N53_08715	1824788	1825645	-1 DNA replication protein
1818810	1827014	8204 OXZ33023.1	B9N53_08720	1825660	1826637	-1 replication initiator RepA
1818810	1827014	8204 OXZ33024.1	B9N53_08725	1826724	1827014	-1 hypothetical protein
1885694	1892257	6563 OXZ32597.1	B9N53_09040	1885694	1886158	1 IS200/IS605 family transposase
1885694	1892257	6563 OXZ32598.1	B9N53_09035	1891243	1892257	1 elongation factor Tu

Table S3F: Predicted genomic islands in the genome of "F. nericia" 12T273

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
97479	122315	24836	OXZ35127.1	B9N55_00530	97479	97877	-1	hypothetical protein
97479	122315	24836	OXZ35128.1	B9N55_00535	97946	98398	-1	small-multidrug export protein
97479	122315	24836	OXZ35129.1	B9N55_00540	98407	99057	-1	phosphatase
97479	122315	24836	OXZ35130.1	B9N55_00545	99219	100451	1	aminopeptidase
97479	122315	24836	OXZ35131.1	B9N55_00550	100451	102247	1	oligoendopeptidase F
97479	122315	24836	OXZ35132.1	B9N55_00555	102300	103184	1	antibiotic ABC transporter ATP-binding protein
97479	122315	24836	OXZ35133.1	B9N55_00560	103177	103929	1	antibiotic ABC transporter permease
97479	122315	24836	OXZ35134.1	B9N55_00565	103919	104590	1	antibiotic ABC transporter permease
97479	122315	24836	OXZ35135.1	B9N55_00570	104590	105891	1	MFS transporter
97479	122315	24836	OXZ35136.1	B9N55_00575	105948	106307	1	superoxide reductase
97479	122315	24836	OXZ35137.1	B9N55_00580	106460	107821	1	hypothetical protein
97479	122315	24836	OXZ35138.1	B9N55_00585	107859	108398	1	transposase
97479	122315	24836	OXZ35172.1	B9N55_00590	108593	109255	1	transposase
97479	122315	24836	OXZ35139.1	B9N55_00595	109420	109656	1	hypothetical protein
97479	122315	24836	OXZ35140.1	B9N55_00600	109674	110216	1	LemA family protein
97479	122315	24836	OXZ35141.1	B9N55_00605	110340	111248	1	coproporphyrinogen III oxidase
97479	122315	24836	OXZ35142.1	B9N55_00610	111248	111976	1	biotin--[acetyl-CoA-carboxylase] ligase
97479	122315	24836	OXZ35143.1	B9N55_00615	111989	112216	-1	hypothetical protein
97479	122315	24836	OXZ35144.1	B9N55_00620	112308	112709	1	transcriptional regulator
97479	122315	24836	OXZ35145.1	B9N55_00625	112747	112962	1	heavy metal transporter
97479	122315	24836	OXZ35146.1	B9N55_00630	112962	114773	1	cadmium-translocating P-type ATPase
97479	122315	24836	OXZ35147.1	B9N55_00635	114820	115131	1	hypothetical protein
97479	122315	24836	OXZ35148.1	B9N55_00640	115179	115445	-1	cytotoxin
97479	122315	24836	OXZ35149.1	B9N55_00645	115445	115702	-1	AbrB family transcriptional regulator
97479	122315	24836	OXZ35150.1	B9N55_00650	115806	116378	-1	riboflavin transporter
97479	122315	24836	OXZ35151.1	B9N55_00655	116449	117591	-1	2-iminoacetate synthase ThiH
97479	122315	24836	OXZ35152.1	B9N55_00660	117599	118363	-1	thiazole synthase
97479	122315	24836	OXZ35153.1	B9N55_00665	118353	118949	-1	thiamine biosynthesis protein ThiF
97479	122315	24836	OXZ35154.1	B9N55_00670	118951	119148	-1	thiamine biosynthesis protein ThiS
97479	122315	24836	OXZ35155.1	B9N55_00675	119369	119980	1	glutathione S-transferase
97479	122315	24836	OXZ35156.1	B9N55_00680	120077	120778	1	SAM-dependent methyltransferase
97479	122315	24836	OXZ35157.1	B9N55_00685	120795	122315	1	magnesium chelatase
138212	146541	8329	OXZ34581.1	B9N55_00760	138212	138409	1	transcriptional regulator
138212	146541	8329	OXZ34582.1	B9N55_00765	138461	139141	1	hypothetical protein
138212	146541	8329	OXZ34583.1	B9N55_00770	139134	140561	1	hypothetical protein
138212	146541	8329	OXZ34584.1	B9N55_00775	141104	142303	1	hypothetical protein
138212	146541	8329	OXZ34585.1	B9N55_00780	142319	143197	1	hypothetical protein
138212	146541	8329	OXZ34586.1	B9N55_00785	143175	143927	1	hypothetical protein
138212	146541	8329	OXZ34587.1	B9N55_00790	143928	144536	1	hypothetical protein
138212	146541	8329	OXZ34588.1	B9N55_00795	144536	144958	1	hypothetical protein
138212	146541	8329	OXZ34589.1	B9N55_00800	144961	146541	1	hypothetical protein
138461	157045	18584	OXZ34582.1	B9N55_00765	138461	139141	1	hypothetical protein
138461	157045	18584	OXZ34583.1	B9N55_00770	139134	140561	1	hypothetical protein
138461	157045	18584	OXZ34584.1	B9N55_00775	141104	142303	1	hypothetical protein
138461	157045	18584	OXZ34585.1	B9N55_00780	142319	143197	1	hypothetical protein
138461	157045	18584	OXZ34586.1	B9N55_00785	143175	143927	1	hypothetical protein
138461	157045	18584	OXZ34587.1	B9N55_00790	143928	144536	1	hypothetical protein
138461	157045	18584	OXZ34588.1	B9N55_00795	144536	144958	1	hypothetical protein
138461	157045	18584	OXZ34589.1	B9N55_00800	144961	146541	1	hypothetical protein
138461	157045	18584	OXZ34590.1	B9N55_00805	146635	147177	1	hypothetical protein
138461	157045	18584	OXZ34591.1	B9N55_00810	147277	148146	1	hypothetical protein
138461	157045	18584	OXZ34592.1	B9N55_00815	148133	150121	1	exopolyphosphatase
138461	157045	18584	OXZ34593.1	B9N55_00820	150102	150548	1	50S ribosomal protein L9
138461	157045	18584	OXZ34594.1	B9N55_00825	150582	151919	1	replicative DNA helicase
138461	157045	18584	OXZ34595.1	B9N55_00830	151916	152479	1	GNAT family N-acetyltransferase
138461	157045	18584	OXZ34596.1	B9N55_00835	152484	153242	1	DNA replication protein
138461	157045	18584	OXZ34597.1	B9N55_00840	153245	154222	1	DNA replication protein DnaC
138461	157045	18584	OXZ34598.1	B9N55_00845	154219	154863	1	NAD(P)H-hydrate epimerase
138461	157045	18584	OXZ34599.1	B9N55_00850	155059	155238	1	hypothetical protein
138461	157045	18584	OXZ34600.1	B9N55_00855	155833	156375	1	ECF transporter S component
138461	157045	18584	OXZ34601.1	B9N55_00860	156359	157045	1	radical SAM protein
253324	260267	6943	OXZ34217.1	B9N55_01390	253324	254190	1	class C sortase
253324	260267	6943	OXZ34218.1	B9N55_01395	254177	255016	1	class C sortase
253324	260267	6943	OXZ34219.1	B9N55_01400	255003	255857	1	class C sortase
253324	260267	6943	OXZ34220.1	B9N55_01405	255917	256558	-1	hemolysin III
253324	260267	6943	OXZ34221.1	B9N55_01410	256712	257215	1	acetyltransferase
253324	260267	6943	OXZ34222.1	B9N55_01415	257215	257952	1	hydrolase
253324	260267	6943		B9N55_01420	259693	260267	1	cell filamentation protein Fic
310452	354643	44191	OXZ34265.1	B9N55_01640	310452	310676	1	hypothetical protein
310452	354643	44191	OXZ34266.1	B9N55_01645	310938	311525	1	RNA polymerase subunit sigma-24
310452	354643	44191	OXZ34267.1	B9N55_01650	311611	311862	1	hypothetical protein
310452	354643	44191	OXZ34268.1	B9N55_01655	311804	312103	1	hypothetical protein
310452	354643	44191	OXZ34269.1	B9N55_01660	312103	313215	1	nuclease
310452	354643	44191	OXZ34270.1	B9N55_01665	313181	313768	1	hypothetical protein
310452	354643	44191	OXZ34271.1	B9N55_01670	313778	313978	1	hypothetical protein
310452	354643	44191	OXZ34272.1	B9N55_01675	313953	316811	1	hypothetical protein
310452	354643	44191	OXZ34273.1	B9N55_01680	316824	317024	1	hypothetical protein
310452	354643	44191	OXZ34274.1	B9N55_01685	317017	317403	1	DUF4406 domain-containing protein
310452	354643	44191	OXZ34275.1	B9N55_01690	317404	319605	1	DNA primase
310452	354643	44191	OXZ34276.1	B9N55_01695	319870	320127	1	hypothetical protein
310452	354643	44191	OXZ34277.1	B9N55_01700	320085	320366	1	nuclease
310452	354643	44191	OXZ34278.1	B9N55_01705	320367	321713	1	DEAD/DEAH box helicase

310452	354643	44191	OXZ34279.1	B9N55_01710	321806	322234	1 hypothetical protein
310452	354643	44191	OXZ34280.1	B9N55_01715	322334	322699	1 HNH endonuclease
310452	354643	44191	OXZ34281.1	B9N55_01720	322922	323389	1 terminase
310452	354643	44191	OXZ34282.1	B9N55_01725	323395	324177	1 S-adenosylmethionine synthetase
310452	354643	44191	OXZ34344.1	B9N55_01730	324177	325427	1 DNA methylase
310452	354643	44191	OXZ34283.1	B9N55_01735	325420	326016	1 endonuclease
310452	354643	44191	OXZ34284.1	B9N55_01740	326018	327460	1 DNA (cytosine-5-)-methyltransferase
310452	354643	44191	OXZ34285.1	B9N55_01745	327504	327728	1 DUF4314 domain-containing protein
310452	354643	44191	OXZ34286.1	B9N55_01750	327814	328146	1 hypothetical protein
310452	354643	44191	OXZ34287.1	B9N55_01755	328147	328377	1 hypothetical protein
310452	354643	44191	OXZ34288.1	B9N55_01760	328470	330059	1 terminase
310452	354643	44191	OXZ34289.1	B9N55_01765	330104	330523	1 conjugal transfer protein
310452	354643	44191	OXZ34290.1	B9N55_01770	330563	331837	1 phage portal protein
310452	354643	44191	OXZ34291.1	B9N55_01775	331827	332513	1 peptidase
310452	354643	44191	OXZ34292.1	B9N55_01780	332518	333708	1 phage major capsid protein
310452	354643	44191	OXZ34293.1	B9N55_01785	333719	333991	1 AraC family transcriptional regulator
310452	354643	44191	OXZ34294.1	B9N55_01790	333991	334323	1 phage head-tail adapter protein
310452	354643	44191	OXZ34295.1	B9N55_01795	334320	334700	1 hypothetical protein
310452	354643	44191	OXZ34296.1	B9N55_01800	334693	335019	1 hypothetical protein
310452	354643	44191	OXZ34297.1	B9N55_01805	335012	335191	1 hypothetical protein
310452	354643	44191	OXZ34298.1	B9N55_01810	335181	335777	1 phage tail protein
310452	354643	44191	OXZ34299.1	B9N55_01815	335780	336136	1 hypothetical protein
310452	354643	44191	OXZ34300.1	B9N55_01820	336315	336644	-1 addiction module toxin RelE
310452	354643	44191	OXZ34301.1	B9N55_01825	336641	336964	-1 prevent-host-death protein
310452	354643	44191	OXZ34302.1	B9N55_01830	337054	340119	1 phage tail tape measure protein
310452	354643	44191	OXZ34303.1	B9N55_01835	340122	340484	1 hypothetical protein
310452	354643	44191	OXZ34304.1	B9N55_01840	340484	342355	1 hypothetical protein
310452	354643	44191	OXZ34305.1	B9N55_01845	342342	343721	1 hypothetical protein
310452	354643	44191	OXZ34306.1	B9N55_01850	343723	344124	1 holin
310452	354643	44191	OXZ34307.1	B9N55_01855	344125	344934	1 lysozyme
310452	354643	44191	OXZ34308.1	B9N55_01860	345111	345701	1 TetR family transcriptional regulator
310452	354643	44191	OXZ34309.1	B9N55_01865	345706	347424	1 ABC transporter ATP-binding protein
310452	354643	44191	OXZ34310.1	B9N55_01870	347417	349153	1 multidrug ABC transporter ATP-binding protein
310452	354643	44191	OXZ34311.1	B9N55_01875	349418	349627	1 hypothetical protein
310452	354643	44191	OXZ34312.1	B9N55_01880	349687	351249	1 recombinase family protein
310452	354643	44191	OXZ34313.1	B9N55_01885	351242	351658	1 integrase
310452	354643	44191	OXZ34314.1	B9N55_01890	351651	353213	1 recombinase family protein
310452	354643	44191	OXZ34345.1	B9N55_01895	353285	353923	1 TetR family transcriptional regulator
310452	354643	44191	OXZ34315.1	B9N55_01900	354047	354643	1 hypothetical protein
310452	354643	44191	OXZ34316.1	B9N55_01905	354633	355346	1 ABC transporter permease
322334	331837	9503	OXZ34280.1	B9N55_01715	322334	322699	1 HNH endonuclease
322334	331837	9503	OXZ34281.1	B9N55_01720	322922	323389	1 terminase
322334	331837	9503	OXZ34282.1	B9N55_01725	323395	324177	1 S-adenosylmethionine synthetase
322334	331837	9503	OXZ34344.1	B9N55_01730	324177	325427	1 DNA methylase
322334	331837	9503	OXZ34283.1	B9N55_01735	325420	326016	1 endonuclease
322334	331837	9503	OXZ34284.1	B9N55_01740	326018	327460	1 DNA (cytosine-5-)-methyltransferase
322334	331837	9503	OXZ34285.1	B9N55_01745	327504	327728	1 DUF4314 domain-containing protein
322334	331837	9503	OXZ34286.1	B9N55_01750	327814	328146	1 hypothetical protein
322334	331837	9503	OXZ34287.1	B9N55_01755	328147	328377	1 hypothetical protein
322334	331837	9503	OXZ34288.1	B9N55_01760	328470	330059	1 terminase
322334	331837	9503	OXZ34289.1	B9N55_01765	330104	330523	1 conjugal transfer protein
322334	331837	9503	OXZ34290.1	B9N55_01770	330563	331837	1 phage portal protein
322334	331837	9503	OXZ34291.1	B9N55_01775	331827	332513	1 peptidase
340122	345701	5579	OXZ34303.1	B9N55_01835	340122	340484	1 hypothetical protein
340122	345701	5579	OXZ34304.1	B9N55_01840	340484	342355	1 hypothetical protein
340122	345701	5579	OXZ34305.1	B9N55_01845	342342	343721	1 hypothetical protein
340122	345701	5579	OXZ34306.1	B9N55_01850	343723	344124	1 holin
340122	345701	5579	OXZ34307.1	B9N55_01855	344125	344934	1 lysozyme
340122	345701	5579	OXZ34308.1	B9N55_01860	345111	345701	1 TetR family transcriptional regulator
365736	388679	22943	OXZ34323.1	B9N55_01945	365736	366485	1 phosphorylase
365736	388679	22943	OXZ34324.1	B9N55_01950	366790	367440	1 hypothetical protein
365736	388679	22943	OXZ34325.1	B9N55_01955	368197	369045	1 AraC family transcriptional regulator
365736	388679	22943	OXZ34346.1	B9N55_01960	369129	369554	1 abortive infection protein
365736	388679	22943		B9N55_01965	369808	370324	1 FRG domain-containing protein
365736	388679	22943	OXZ34326.1	B9N55_01970	370372	370926	1 hypothetical protein
365736	388679	22943		B9N55_01975	370978	371348	1 hypothetical protein
365736	388679	22943		B9N55_01980	371494	371690	1 transcriptional regulator
365736	388679	22943	OXZ34327.1	B9N55_01985	371742	372425	1 hypothetical protein
365736	388679	22943	OXZ34328.1	B9N55_01990	372418	373839	1 hypothetical protein
365736	388679	22943	OXZ34329.1	B9N55_01995	373991	374878	1 hypothetical protein
365736	388679	22943	OXZ34330.1	B9N55_02000	374862	375614	1 hypothetical protein
365736	388679	22943		B9N55_02005	375964	376360	1 hypothetical protein
365736	388679	22943	OXZ34331.1	B9N55_02010	376681	376884	1 hypothetical protein
365736	388679	22943	OXZ34332.1	B9N55_02015	376884	377798	1 ABC transporter ATP-binding protein
365736	388679	22943	OXZ34333.1	B9N55_02020	377795	378562	1 hypothetical protein
365736	388679	22943	OXZ34334.1	B9N55_02025	378576	379679	1 transcriptional regulator
365736	388679	22943	OXZ34335.1	B9N55_02030	379851	380051	1 transcriptional regulator
365736	388679	22943	OXZ34336.1	B9N55_02035	380210	380791	1 hypothetical protein
365736	388679	22943	OXZ34337.1	B9N55_02040	381213	382211	-1 AraC family transcriptional regulator
365736	388679	22943	OXZ34338.1	B9N55_02045	382372	384126	1 ABC transporter ATP-binding protein
365736	388679	22943	OXZ34339.1	B9N55_02050	384110	385831	1 ABC transporter ATP-binding protein
365736	388679	22943	OXZ34340.1	B9N55_02055	385843	387186	1 MATE family efflux transporter
365736	388679	22943	OXZ34341.1	B9N55_02060	387338	387591	-1 IS110 family transposase
365736	388679	22943	OXZ33675.1	B9N55_02065	388592	388679	1 hypothetical protein
365736	376884	11148	OXZ34323.1	B9N55_01945	365736	366485	1 phosphorylase
365736	376884	11148	OXZ34324.1	B9N55_01950	366790	367440	1 hypothetical protein

365736	376884	11148 OXZ34325.1	B9N55_01955	368197	369045	1 AraC family transcriptional regulator
365736	376884	11148 OXZ34346.1	B9N55_01960	369129	369554	1 abortive infection protein
365736	376884	11148	B9N55_01965	369808	370324	1 FRG domain-containing protein
365736	376884	11148 OXZ34326.1	B9N55_01970	370372	370926	1 hypothetical protein
365736	376884	11148	B9N55_01975	370978	371348	1 hypothetical protein
365736	376884	11148	B9N55_01980	371494	371690	1 transcriptional regulator
365736	376884	11148 OXZ34327.1	B9N55_01985	371742	372425	1 hypothetical protein
365736	376884	11148 OXZ34328.1	B9N55_01990	372418	373839	1 hypothetical protein
365736	376884	11148 OXZ34329.1	B9N55_01995	373991	374878	1 hypothetical protein
365736	376884	11148 OXZ34330.1	B9N55_02000	374862	375614	1 hypothetical protein
365736	376884	11148	B9N55_02005	375964	376360	1 hypothetical protein
365736	376884	11148 OXZ34331.1	B9N55_02010	376681	376884	1 hypothetical protein
379851	384126	4275 OXZ34335.1	B9N55_02030	379851	380051	1 transcriptional regulator
379851	384126	4275 OXZ34336.1	B9N55_02035	380210	380791	1 hypothetical protein
379851	384126	4275 OXZ34337.1	B9N55_02040	381213	382211	-1 AraC family transcriptional regulator
379851	384126	4275 OXZ34338.1	B9N55_02045	382372	384126	1 ABC transporter ATP-binding protein
379851	384126	4275 OXZ34339.1	B9N55_02050	384110	385831	1 ABC transporter ATP-binding protein
569426	590255	20829 OXZ33831.1	B9N55_02880	568056	569435	-1 two-component sensor histidine kinase
569426	590255	20829 OXZ33832.1	B9N55_02885	569426	570085	-1 DNA-binding response regulator
569426	590255	20829 OXZ33833.1	B9N55_02890	570118	570858	-1 mutacin I biosynthesis protein MutG
569426	590255	20829 OXZ33834.1	B9N55_02895	570858	571598	-1 antibiotic ABC transporter permease
569426	590255	20829 OXZ33835.1	B9N55_02900	571602	572303	-1 lantibiotic ABC transporter ATP-binding protein
569426	590255	20829 OXZ33836.1	B9N55_02905	572915	574204	1 hypothetical protein
569426	590255	20829 OXZ33837.1	B9N55_02910	574703	575230	1 transcriptional regulator
569426	590255	20829	B9N55_02915	575250	575632	1 conjugal transfer protein TraA
569426	590255	20829 OXZ33838.1	B9N55_02920	575768	576340	1 uracil-DNA glycosylase
569426	590255	20829 OXZ33839.1	B9N55_02925	576408	576695	1 cupin
569426	590255	20829 OXZ33840.1	B9N55_02930	577333	579390	1 elongation factor G
569426	590255	20829 OXZ33841.1	B9N55_02935	579752	580417	-1 hypothetical protein
569426	590255	20829 OXZ33842.1	B9N55_02940	580526	581422	1 cysteine synthase A
569426	590255	20829 OXZ33843.1	B9N55_02945	581409	581933	1 serine O-acetyltransferase
569426	590255	20829 OXZ33844.1	B9N55_02950	582150	583034	-1 hypothetical protein
569426	590255	20829	B9N55_02955	583083	583187	-1 hypothetical protein
569426	590255	20829 OXZ33845.1	B9N55_02960	583681	584769	1 iron ABC transporter permease
569426	590255	20829 OXZ33846.1	B9N55_02965	584759	585766	1 iron ABC transporter
569426	590255	20829 OXZ33847.1	B9N55_02970	585766	586773	1 iron ABC transporter
569426	590255	20829 OXZ33848.1	B9N55_02975	586773	587567	1 iron ABC transporter ATP-binding protein
569426	590255	20829 OXZ33849.1	B9N55_02980	587970	588371	1 hypothetical protein
569426	590255	20829	B9N55_02985	588429	589043	1 hypothetical protein
569426	590255	20829 OXZ33850.1	B9N55_02990	589164	590255	1 glycerol dehydrogenase
1088002	1095275	7273 OXZ32287.1	B9N55_05575	1088002	1088982	-1 recombinase XerC
1088002	1095275	7273 OXZ32288.1	B9N55_05580	1089092	1090267	-1 aspartate aminotransferase
1088002	1095275	7273 OXZ32289.1	B9N55_05585	1090254	1091075	-1 metal-dependent phosphoesterase
1088002	1095275	7273 OXZ32290.1	B9N55_05590	1091144	1092685	-1 ribonuclease Y
1088002	1095275	7273 OXZ32291.1	B9N55_05595	1092804	1093466	-1 chromosome partitioning protein ParA
1088002	1095275	7273 OXZ32292.1	B9N55_05600	1093453	1093692	-1 hypothetical protein
1088002	1095275	7273 OXZ32293.1	B9N55_05605	1093692	1095275	-1 exonuclease SbcC
1293167	1324490	31323 OXZ32025.1	B9N55_06545	1293167	1294498	1 endonuclease
1293167	1324490	31323 OXZ32026.1	B9N55_06550	1294609	1295265	-1 DNA-binding protein
1293167	1324490	31323 OXZ32027.1	B9N55_06555	1295309	1296637	-1 helicase
1293167	1324490	31323 OXZ32028.1	B9N55_06560	1296771	1298441	-1 group II intron reverse transcriptase/maturase
1293167	1324490	31323 OXZ32029.1	B9N55_06565	1298997	1305293	-1 DNA helicase
1293167	1324490	31323 OXZ32030.1	B9N55_06570	1305377	1306879	-1 SIR2 family protein
1293167	1324490	31323 OXZ32031.1	B9N55_06575	1306936	1307874	-1 DNA (cytosine-5-)-methyltransferase
1293167	1324490	31323 OXZ32032.1	B9N55_06580	1307867	1309588	-1 DNA topoisomerase III
1293167	1324490	31323 OXZ32033.1	B9N55_06585	1309678	1310661	-1 hypothetical protein
1293167	1324490	31323 OXZ32034.1	B9N55_06590	1310654	1311265	-1 hypothetical protein
1293167	1324490	31323 OXZ32035.1	B9N55_06595	1311384	1312199	-1 bacteriocin
1293167	1324490	31323 OXZ32036.1	B9N55_06600	1312214	1313797	-1 copper amine oxidase
1293167	1324490	31323	B9N55_06605	1313787	1314023	-1 hypothetical protein
1293167	1324490	31323 OXZ32037.1	B9N55_06610	1314038	1316617	-1 hypothetical protein
1293167	1324490	31323 OXZ32038.1	B9N55_06615	1316625	1319048	-1 conjugal transfer protein TraE
1293167	1324490	31323 OXZ32039.1	B9N55_06620	1318939	1319349	-1 conjugal transfer protein
1293167	1324490	31323 OXZ32040.1	B9N55_06625	1319351	1319641	-1 hypothetical protein
1293167	1324490	31323 OXZ32041.1	B9N55_06630	1319651	1320514	-1 hypothetical protein
1293167	1324490	31323 OXZ32042.1	B9N55_06635	1320525	1320740	-1 conjugal transfer protein
1293167	1324490	31323 OXZ32043.1	B9N55_06640	1320742	1321053	-1 single-stranded DNA-binding protein
1293167	1324490	31323 OXZ32093.1	B9N55_06645	1321276	1321893	-1 hypothetical protein
1293167	1324490	31323 OXZ32044.1	B9N55_06650	1321961	1322383	-1 polyketide cyclase
1293167	1324490	31323 OXZ32045.1	B9N55_06655	1322421	1322939	-1 cytoplasmic protein
1293167	1324490	31323	B9N55_06660	1323001	1323468	-1 conjugal transfer protein TraG
1293167	1324490	31323 OXZ32046.1	B9N55_06665	1323506	1323781	-1 hypothetical protein
1293167	1324490	31323 OXZ32047.1	B9N55_06670	1324050	1324490	-1 GNAT family N-acetyltransferase
1305377	1312199	6822 OXZ32030.1	B9N55_06570	1305377	1306879	-1 SIR2 family protein
1305377	1312199	6822 OXZ32031.1	B9N55_06575	1306936	1307874	-1 DNA (cytosine-5-)-methyltransferase
1305377	1312199	6822 OXZ32032.1	B9N55_06580	1307867	1309588	-1 DNA topoisomerase III
1305377	1312199	6822 OXZ32033.1	B9N55_06585	1309678	1310661	-1 hypothetical protein
1305377	1312199	6822 OXZ32034.1	B9N55_06590	1310654	1311265	-1 hypothetical protein
1305377	1312199	6822 OXZ32035.1	B9N55_06595	1311384	1312199	-1 bacteriocin
1320742	1325827	5085 OXZ32043.1	B9N55_06640	1320742	1321053	-1 single-stranded DNA-binding protein
1320742	1325827	5085 OXZ32093.1	B9N55_06645	1321276	1321893	-1 hypothetical protein
1320742	1325827	5085 OXZ32044.1	B9N55_06650	1321961	1322383	-1 polyketide cyclase
1320742	1325827	5085 OXZ32045.1	B9N55_06655	1322421	1322939	-1 cytoplasmic protein
1320742	1325827	5085	B9N55_06660	1323001	1323468	-1 conjugal transfer protein TraG
1320742	1325827	5085 OXZ32046.1	B9N55_06665	1323506	1323781	-1 hypothetical protein
1320742	1325827	5085 OXZ32047.1	B9N55_06670	1324050	1324490	-1 GNAT family N-acetyltransferase

1320742	1325827	5085 OXZ32048.1	B9N55_06675	1324550	1324753	-1 hypothetical protein
1320742	1325827	5085 OXZ32049.1	B9N55_06680	1324815	1325600	-1 conjugal transfer protein TraG
1320742	1325827	5085 OXZ32050.1	B9N55_06685	1325642	1325827	-1 hypothetical protein
1331207	1344342	13135 OXZ32057.1	B9N55_06720	1331207	1332949	-1 ABC transporter ATP-binding protein
1331207	1344342	13135 OXZ32058.1	B9N55_06725	1332951	1334663	-1 ABC transporter ATP-binding protein
1331207	1344342	13135 OXZ32059.1	B9N55_06730	1334667	1336082	-1 ABC transporter ATP-binding protein
1331207	1344342	13135 OXZ32060.1	B9N55_06735	1336095	1336781	-1 cobalt transporter
1331207	1344342	13135 OXZ32061.1	B9N55_06740	1336782	1337375	-1 hypothetical protein
1331207	1344342	13135 OXZ32062.1	B9N55_06745	1337547	1338158	-1 TetR family transcriptional regulator
1331207	1344342	13135 OXZ32063.1	B9N55_06750	1338259	1340085	-1 recombinase TnpX
1331207	1344342	13135 OXZ32064.1	B9N55_06755	1340125	1341177	-1 conjugal transfer protein TraG
1331207	1344342	13135 OXZ32065.1	B9N55_06760	1341170	1341904	-1 phage antirepressor Ant
1331207	1344342	13135 OXZ32066.1	B9N55_06765	1341901	1342386	-1 conjugal transfer protein
1331207	1344342	13135 OXZ32067.1	B9N55_06770	1342379	1343206	-1 nucleoside triphosphate hydrolase
1331207	1344342	13135 OXZ32068.1	B9N55_06775	1343203	1343976	-1 replication initiator protein A
1331207	1344342	13135 OXZ32069.1	B9N55_06780	1344061	1344342	-1 hypothetical protein
1684263	1728424	44161 OXZ31633.1	B9N55_08365	1684263	1685537	-1 hypothetical protein
1684263	1728424	44161 OXZ31634.1	B9N55_08370	1685632	1687314	-1 hypothetical protein
1684263	1728424	44161 OXZ31344.1	B9N55_08375	1688746	1690407	-1 ABC transporter permease CXXX repeat peptide modification system
1684263	1728424	44161 OXZ31345.1	B9N55_08380	1690400	1690666	-1 protein
1684263	1728424	44161 OXZ31346.1	B9N55_08385	1690668	1692857	-1 radical SAM protein
1684263	1728424	44161 OXZ31347.1	B9N55_08390	1692844	1693026	-1 hypothetical protein
1684263	1728424	44161 OXZ31348.1	B9N55_08395	1693156	1693761	-1 DNA-binding response regulator
1684263	1728424	44161 OXZ31349.1	B9N55_08400	1693733	1695280	-1 hypothetical protein
1684263	1728424	44161 OXZ31350.1	B9N55_08405	1695594	1696688	-1 single-stranded DNA-binding protein
1684263	1728424	44161 OXZ31351.1	B9N55_08410	1696721	1707151	-1 conjugal transfer protein
1684263	1728424	44161	B9N55_08415	1707346	1707905	-1 antibiotic ABC transporter
1684263	1728424	44161 OXZ31352.1	B9N55_08420	1708184	1709890	-1 DNA topoisomerase III
1684263	1728424	44161 OXZ31353.1	B9N55_08425	1710307	1711185	-1 bacteriocin
1684263	1728424	44161 OXZ31354.1	B9N55_08430	1711201	1713555	-1 copper amine oxidase
1684263	1728424	44161 OXZ31355.1	B9N55_08435	1713552	1713809	-1 hypothetical protein
1684263	1728424	44161 OXZ31356.1	B9N55_08440	1713829	1716792	-1 hypothetical protein
1684263	1728424	44161 OXZ31357.1	B9N55_08445	1716802	1717767	-1 site-specific DNA-methyltransferase
1684263	1728424	44161 OXZ31358.1	B9N55_08450	1717739	1720234	-1 conjugal transfer protein TraE
1684263	1728424	44161 OXZ31359.1	B9N55_08455	1720231	1720569	-1 conjugal transfer protein
1684263	1728424	44161 OXZ31360.1	B9N55_08460	1720569	1720826	-1 hypothetical protein
1684263	1728424	44161 OXZ31361.1	B9N55_08465	1720844	1721707	-1 hypothetical protein
1684263	1728424	44161 OXZ31362.1	B9N55_08470	1721709	1721924	-1 conjugal transfer protein
1684263	1728424	44161 OXZ31363.1	B9N55_08475	1721925	1722248	-1 single-stranded DNA-binding protein
1684263	1728424	44161 OXZ31364.1	B9N55_08480	1722438	1723301	-1 CAAX protease
1684263	1728424	44161 OXZ31365.1	B9N55_08485	1723453	1725255	-1 conjugal transfer protein TraG
1684263	1728424	44161 OXZ31366.1	B9N55_08490	1725300	1725503	-1 hypothetical protein
1684263	1728424	44161 OXZ31367.1	B9N55_08495	1725692	1726183	-1 hypothetical protein
1684263	1728424	44161 OXZ31368.1	B9N55_08500	1726198	1727055	-1 DNA replication protein
1684263	1728424	44161 OXZ31369.1	B9N55_08505	1727070	1728047	-1 replication initiator RepA
1684263	1728424	44161 OXZ31370.1	B9N55_08510	1728134	1728424	-1 hypothetical protein
1690400	1716792	26392 OXZ31344.1	B9N55_08375	1688746	1690407	-1 ABC transporter permease CXXX repeat peptide modification system
1690400	1716792	26392 OXZ31345.1	B9N55_08380	1690400	1690666	-1 protein
1690400	1716792	26392 OXZ31346.1	B9N55_08385	1690668	1692857	-1 radical SAM protein
1690400	1716792	26392 OXZ31347.1	B9N55_08390	1692844	1693026	-1 hypothetical protein
1690400	1716792	26392 OXZ31348.1	B9N55_08395	1693156	1693761	-1 DNA-binding response regulator
1690400	1716792	26392 OXZ31349.1	B9N55_08400	1693733	1695280	-1 hypothetical protein
1690400	1716792	26392 OXZ31350.1	B9N55_08405	1695594	1696688	-1 single-stranded DNA-binding protein
1690400	1716792	26392 OXZ31351.1	B9N55_08410	1696721	1707151	-1 conjugal transfer protein
1690400	1716792	26392	B9N55_08415	1707346	1707905	-1 antibiotic ABC transporter
1690400	1716792	26392 OXZ31352.1	B9N55_08420	1708184	1709890	-1 DNA topoisomerase III
1690400	1716792	26392 OXZ31353.1	B9N55_08425	1710307	1711185	-1 bacteriocin
1690400	1716792	26392 OXZ31354.1	B9N55_08430	1711201	1713555	-1 copper amine oxidase
1690400	1716792	26392 OXZ31355.1	B9N55_08435	1713552	1713809	-1 hypothetical protein
1690400	1716792	26392 OXZ31356.1	B9N55_08440	1713829	1716792	-1 hypothetical protein
1720231	1728424	8193 OXZ31358.1	B9N55_08450	1717739	1720234	-1 conjugal transfer protein TraE
1720231	1728424	8193 OXZ31359.1	B9N55_08455	1720231	1720569	-1 conjugal transfer protein
1720231	1728424	8193 OXZ31360.1	B9N55_08460	1720569	1720826	-1 hypothetical protein
1720231	1728424	8193 OXZ31361.1	B9N55_08465	1720844	1721707	-1 hypothetical protein
1720231	1728424	8193 OXZ31362.1	B9N55_08470	1721709	1721924	-1 conjugal transfer protein
1720231	1728424	8193 OXZ31363.1	B9N55_08475	1721925	1722248	-1 single-stranded DNA-binding protein
1720231	1728424	8193 OXZ31364.1	B9N55_08480	1722438	1723301	-1 CAAX protease
1720231	1728424	8193 OXZ31365.1	B9N55_08485	1723453	1725255	-1 conjugal transfer protein TraG
1720231	1728424	8193 OXZ31366.1	B9N55_08490	1725300	1725503	-1 hypothetical protein
1720231	1728424	8193 OXZ31367.1	B9N55_08495	1725692	1726183	-1 hypothetical protein
1720231	1728424	8193 OXZ31368.1	B9N55_08500	1726198	1727055	-1 DNA replication protein
1720231	1728424	8193 OXZ31369.1	B9N55_08505	1727070	1728047	-1 replication initiator RepA
1720231	1728424	8193 OXZ31370.1	B9N55_08510	1728134	1728424	-1 hypothetical protein
1799490	1811368	11878 OXZ31185.1	B9N55_08875	1799490	1800239	-1 phosphorylase
1799490	1811368	11878	B9N55_08880	1800273	1800602	-1 hypothetical protein
1799490	1811368	11878 OXZ31186.1	B9N55_08885	1800703	1801284	-1 hypothetical protein
1799490	1811368	11878 OXZ31187.1	B9N55_08890	1801737	1802165	-1 hypothetical protein
1799490	1811368	11878 OXZ31188.1	B9N55_08895	1802314	1803678	-1 ABC transporter ATP-binding protein
1799490	1811368	11878 OXZ31189.1	B9N55_08900	1803672	1804361	-1 cobalt ABC transporter permease
1799490	1811368	11878 OXZ31190.1	B9N55_08905	1804361	1804942	-1 hypothetical protein
1799490	1811368	11878 OXZ31024.1	B9N55_09060	1806353	1808938	-1 ATP-dependent chaperone ClpB
1799490	1811368	11878 OXZ31025.1	B9N55_09065	1808957	1809901	-1 heat-shock protein
1799490	1811368	11878 OXZ31026.1	B9N55_09070	1810010	1810675	-1 nitroreductase
1799490	1811368	11878 OXZ31027.1	B9N55_09075	1810829	1811368	-1 RNA polymerase subunit sigma
1897911	1902891	4980 OXZ30960.1	B9N55_09420	1897911	1897998	-1 hypothetical protein

1897911	1902891	4980 OXZ30822.1	B9N55_09480	1901495	1902157	-1 hypothetical protein
1897911	1902891	4980 OXZ30823.1	B9N55_09485	1902352	1902891	-1 transposase
1914240	1959903	45663 OXZ30881.1	B9N55_09450	1914240	1914451	-1 translation elongation factor Tu
1914240	1959903	45663 OXZ31113.1	B9N55_08910	1915452	1917072	-1 hypothetical protein
1914240	1959903	45663 OXZ31114.1	B9N55_08915	1917069	1918730	-1 hypothetical protein
1914240	1959903	45663 OXZ31115.1	B9N55_08920	1918731	1920428	-1 hypothetical protein
1914240	1959903	45663 OXZ31116.1	B9N55_08925	1920448	1921431	-1 3-deoxy-7-phosphoheptulonate synthase
1914240	1959903	45663 OXZ31117.1	B9N55_08930	1921436	1921774	-1 dehydroquinase class II
1914240	1959903	45663	B9N55_08935	1921773	1922009	-1 chorismate synthase
1914240	1959903	45663	B9N55_08940	1921996	1923290	-1 3-phosphoshikimate 1-carboxyvinyltransferase
1914240	1959903	45663 OXZ31118.1	B9N55_08945	1923287	1924333	-1 3-dehydroquinase synthase
1914240	1959903	45663 OXZ31119.1	B9N55_08950	1924337	1924723	-1 salicylate synthase
1914240	1959903	45663 OXZ31120.1	B9N55_08955	1924888	1925148	-1 hypothetical protein
1914240	1959903	45663 OXZ31121.1	B9N55_08960	1925141	1925569	-1 hypothetical protein
1914240	1959903	45663 OXZ31122.1	B9N55_08965	1925892	1926284	-1 transcriptional regulator
1914240	1959903	45663 OXZ31123.1	B9N55_08970	1926721	1927089	1 plasmid mobilization relaxosome protein MobC
1914240	1959903	45663 OXZ31124.1	B9N55_08975	1927089	1928459	1 endonuclease
1914240	1959903	45663 OXZ31125.1	B9N55_08980	1928518	1929264	-1 ABC transporter permease
1914240	1959903	45663 OXZ31126.1	B9N55_08985	1929279	1929971	-1 ABC transporter permease
1914240	1959903	45663 OXZ31127.1	B9N55_08990	1929973	1930887	-1 bacitracin ABC transporter ATP-binding protein
1914240	1959903	45663 OXZ31128.1	B9N55_08995	1930902	1932059	-1 hypothetical protein
1914240	1959903	45663 OXZ31129.1	B9N55_09000	1932063	1933370	-1 hypothetical protein
1914240	1959903	45663 OXZ31130.1	B9N55_09005	1934009	1934440	-1 hypothetical protein
1914240	1959903	45663 OXZ31131.1	B9N55_09010	1934453	1934716	-1 hypothetical protein
1914240	1959903	45663 OXZ31132.1	B9N55_09015	1934710	1935279	-1 hypothetical protein
1914240	1959903	45663	B9N55_09020	1935618	1935941	1 relaxase
1914240	1959903	45663 OXZ31133.1	B9N55_09025	1936062	1936409	-1 DUF3784 domain-containing protein
1914240	1959903	45663 OXZ31134.1	B9N55_09030	1936417	1937793	-1 hypothetical protein
1914240	1959903	45663 OXZ31135.1	B9N55_09035	1937803	1938597	-1 hypothetical protein
1914240	1959903	45663 OXZ31136.1	B9N55_09040	1938587	1939453	-1 hypothetical protein
1914240	1959903	45663 OXZ31137.1	B9N55_09045	1939635	1940819	-1 hypothetical protein
1914240	1959903	45663 OXZ31138.1	B9N55_09050	1940947	1941279	-1 hypothetical protein
1914240	1959903	45663 OXZ31139.1	B9N55_09055	1941537	1941746	-1 hypothetical protein
1914240	1959903	45663 OXZ30824.1	B9N55_09470	1948165	1948863	-1 hypothetical protein
1914240	1959903	45663 OXZ30825.1	B9N55_09475	1949022	1949561	-1 transposase
1914240	1959903	45663 OXZ30779.1	B9N55_09500	1950607	1951809	-1 hypothetical protein
1914240	1959903	45663 OXZ30778.1	B9N55_09505	1952810	1953858	-1 IS110 family transposase
1914240	1959903	45663 OXZ30943.1	B9N55_09440	1955001	1959903	-1 hypothetical protein
1915452	1948863	33411 OXZ31113.1	B9N55_08910	1915452	1917072	-1 hypothetical protein
1915452	1948863	33411 OXZ31114.1	B9N55_08915	1917069	1918730	-1 hypothetical protein
1915452	1948863	33411 OXZ31115.1	B9N55_08920	1918731	1920428	-1 hypothetical protein
1915452	1948863	33411 OXZ31116.1	B9N55_08925	1920448	1921431	-1 3-deoxy-7-phosphoheptulonate synthase
1915452	1948863	33411 OXZ31117.1	B9N55_08930	1921436	1921774	-1 dehydroquinase class II
1915452	1948863	33411	B9N55_08935	1921773	1922009	-1 chorismate synthase
1915452	1948863	33411	B9N55_08940	1921996	1923290	-1 3-phosphoshikimate 1-carboxyvinyltransferase
1915452	1948863	33411 OXZ31118.1	B9N55_08945	1923287	1924333	-1 3-dehydroquinase synthase
1915452	1948863	33411 OXZ31119.1	B9N55_08950	1924337	1924723	-1 salicylate synthase
1915452	1948863	33411 OXZ31120.1	B9N55_08955	1924888	1925148	-1 hypothetical protein
1915452	1948863	33411 OXZ31121.1	B9N55_08960	1925141	1925569	-1 hypothetical protein
1915452	1948863	33411 OXZ31122.1	B9N55_08965	1925892	1926284	-1 transcriptional regulator
1915452	1948863	33411 OXZ31123.1	B9N55_08970	1926721	1927089	1 plasmid mobilization relaxosome protein MobC
1915452	1948863	33411 OXZ31124.1	B9N55_08975	1927089	1928459	1 endonuclease
1915452	1948863	33411 OXZ31125.1	B9N55_08980	1928518	1929264	-1 ABC transporter permease
1915452	1948863	33411 OXZ31126.1	B9N55_08985	1929279	1929971	-1 ABC transporter permease
1915452	1948863	33411 OXZ31127.1	B9N55_08990	1929973	1930887	-1 bacitracin ABC transporter ATP-binding protein
1915452	1948863	33411 OXZ31128.1	B9N55_08995	1930902	1932059	-1 hypothetical protein
1915452	1948863	33411 OXZ31129.1	B9N55_09000	1932063	1933370	-1 hypothetical protein
1915452	1948863	33411 OXZ31130.1	B9N55_09005	1934009	1934440	-1 hypothetical protein
1915452	1948863	33411 OXZ31131.1	B9N55_09010	1934453	1934716	-1 hypothetical protein
1915452	1948863	33411 OXZ31132.1	B9N55_09015	1934710	1935279	-1 hypothetical protein
1915452	1948863	33411	B9N55_09020	1935618	1935941	1 relaxase
1915452	1948863	33411 OXZ31133.1	B9N55_09025	1936062	1936409	-1 DUF3784 domain-containing protein
1915452	1948863	33411 OXZ31134.1	B9N55_09030	1936417	1937793	-1 hypothetical protein
1915452	1948863	33411 OXZ31135.1	B9N55_09035	1937803	1938597	-1 hypothetical protein
1915452	1948863	33411 OXZ31136.1	B9N55_09040	1938587	1939453	-1 hypothetical protein
1915452	1948863	33411 OXZ31137.1	B9N55_09045	1939635	1940819	-1 hypothetical protein
1915452	1948863	33411 OXZ31138.1	B9N55_09050	1940947	1941279	-1 hypothetical protein
1915452	1948863	33411 OXZ31139.1	B9N55_09055	1941537	1941746	-1 hypothetical protein
1915452	1948863	33411 OXZ30824.1	B9N55_09470	1948165	1948863	-1 hypothetical protein

Table S3G: Predicted genomic islands in the genome of "F. nericia" 12T306

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
125213	131694	6481	OXZ36396.1	B9N54_00540	125213	126550	1	replicative DNA helicase
125213	131694	6481	OXZ36397.1	B9N54_00545	126547	127110	1	GNAT family N-acetyltransferase
125213	131694	6481	OXZ36398.1	B9N54_00550	127115	127873	1	DNA replication protein
125213	131694	6481	OXZ36399.1	B9N54_00555	127876	128853	1	DNA replication protein DnaC
125213	131694	6481	OXZ36400.1	B9N54_00560	128850	129494	1	NAD(P)H-hydrate epimerase
125213	131694	6481	OXZ36401.1	B9N54_00565	130482	131024	1	ECF transporter S component
125213	131694	6481	OXZ36402.1	B9N54_00570	131008	131694	1	radical SAM protein
229146	236132	6986	OXZ36325.1	B9N54_01130	229146	229787	-1	hemolysin III
229146	236132	6986	OXZ36326.1	B9N54_01135	229940	230443	1	acetyltransferase
229146	236132	6986	OXZ36327.1	B9N54_01140	230443	231177	1	hydrolase
229146	236132	6986	OXZ36328.1	B9N54_01145	232657	233232	1	cell filamentation protein Fic
229146	236132	6986	OXZ36329.1	B9N54_01150	234109	234351	-1	prevent-host-death protein
229146	236132	6986	OXZ36330.1	B9N54_01155	234514	235122	-1	hypothetical protein
229146	236132	6986	OXZ36331.1	B9N54_01160	235206	236132	-1	hypothetical protein
280334	298282	17948	OXZ36371.1	B9N54_01370	280334	281362	1	carboxypeptidase
280334	298282	17948	OXZ36372.1	B9N54_01375	281715	282143	1	hypothetical protein
280334	298282	17948	OXZ36373.1	B9N54_01380	282297	283046	1	phosphorylase
280334	298282	17948	OXZ36374.1	B9N54_01385	283352	284002	1	hypothetical protein
280334	298282	17948	OXZ36375.1	B9N54_01390	284842	285633	1	CPBP family intramembrane metalloprotease
280334	298282	17948	OXZ36376.1	B9N54_01395	285695	286162	1	abortive infection protein
280334	298282	17948		B9N54_01400	286395	286911	1	FRG domain-containing protein
280334	298282	17948	OXZ36377.1	B9N54_01405	286959	287513	1	hypothetical protein
280334	298282	17948		B9N54_01410	287548	287942	1	hypothetical protein
280334	298282	17948	OXZ36378.1	B9N54_01415	288232	289779	1	hypothetical protein
280334	298282	17948	OXZ36379.1	B9N54_01420	289751	290356	1	DNA-binding response regulator
280334	298282	17948	OXZ36380.1	B9N54_01425	290535	290939	1	hypothetical protein
280334	298282	17948	OXZ36381.1	B9N54_01430	290994	291878	1	multidrug ABC transporter ATP-binding protein
280334	298282	17948	OXZ36382.1	B9N54_01435	291862	292587	1	hypothetical protein
280334	298282	17948		B9N54_01440	292680	292882	1	hypothetical protein
280334	298282	17948	OXZ36383.1	B9N54_01445	293661	294560	1	bacitracin ABC transporter ATP-binding protein
280334	298282	17948	OXZ36384.1	B9N54_01450	294557	295399	1	ABC transporter permease
280334	298282	17948		B9N54_01455	295465	295956	1	ABC transporter permease
280334	298282	17948	OXZ36385.1	B9N54_01460	295970	296236	1	hypothetical protein
280334	298282	17948	OXZ36386.1	B9N54_01465	296310	296704	-1	relaxase
280334	298282	17948	OXZ36136.1	B9N54_01470	297705	297829	-1	transposase
280334	298282	17948	OXZ36137.1	B9N54_01475	297893	298282	-1	hypothetical protein
281715	298282	16567	OXZ36372.1	B9N54_01375	281715	282143	1	hypothetical protein
281715	298282	16567	OXZ36373.1	B9N54_01380	282297	283046	1	phosphorylase
281715	298282	16567	OXZ36374.1	B9N54_01385	283352	284002	1	hypothetical protein
281715	298282	16567	OXZ36375.1	B9N54_01390	284842	285633	1	CPBP family intramembrane metalloprotease
281715	298282	16567	OXZ36376.1	B9N54_01395	285695	286162	1	abortive infection protein
281715	298282	16567		B9N54_01400	286395	286911	1	FRG domain-containing protein
281715	298282	16567	OXZ36377.1	B9N54_01405	286959	287513	1	hypothetical protein
281715	298282	16567		B9N54_01410	287548	287942	1	hypothetical protein
281715	298282	16567	OXZ36378.1	B9N54_01415	288232	289779	1	hypothetical protein
281715	298282	16567	OXZ36379.1	B9N54_01420	289751	290356	1	DNA-binding response regulator
281715	298282	16567	OXZ36380.1	B9N54_01425	290535	290939	1	hypothetical protein
281715	298282	16567	OXZ36381.1	B9N54_01430	290994	291878	1	multidrug ABC transporter ATP-binding protein
281715	298282	16567	OXZ36382.1	B9N54_01435	291862	292587	1	hypothetical protein
281715	298282	16567		B9N54_01440	292680	292882	1	hypothetical protein
281715	298282	16567	OXZ36383.1	B9N54_01445	293661	294560	1	bacitracin ABC transporter ATP-binding protein
281715	298282	16567	OXZ36384.1	B9N54_01450	294557	295399	1	ABC transporter permease
281715	298282	16567		B9N54_01455	295465	295956	1	ABC transporter permease
281715	298282	16567	OXZ36385.1	B9N54_01460	295970	296236	1	hypothetical protein
281715	298282	16567	OXZ36386.1	B9N54_01465	296310	296704	-1	relaxase
281715	298282	16567	OXZ36136.1	B9N54_01470	297705	297829	-1	transposase
281715	298282	16567	OXZ36137.1	B9N54_01475	297893	298282	-1	hypothetical protein
454821	459306	4485	OXZ36294.1	B9N54_02190	454821	455048	1	mobilization protein
454821	459306	4485	OXZ36273.1	B9N54_02195	455377	455802	-1	MarR family transcriptional regulator
454821	459306	4485	OXZ36274.1	B9N54_02200	455804	456178	-1	hypothetical protein
454821	459306	4485		B9N54_02205	456629	456724	-1	glutamyl-tRNA amidotransferase
454821	459306	4485	OXZ36275.1	B9N54_02210	456938	457369	-1	transcriptional regulator
454821	459306	4485	OXZ36276.1	B9N54_02215	457631	457825	1	hypothetical protein
454821	459306	4485	OXZ36277.1	B9N54_02220	457827	458951	1	site-specific integrase
454821	459306	4485	OXZ36278.1	B9N54_02225	458944	459306	1	hypothetical protein
455377	468722	13345	OXZ36273.1	B9N54_02195	455377	455802	-1	MarR family transcriptional regulator
455377	468722	13345	OXZ36274.1	B9N54_02200	455804	456178	-1	hypothetical protein
455377	468722	13345		B9N54_02205	456629	456724	-1	glutamyl-tRNA amidotransferase
455377	468722	13345	OXZ36275.1	B9N54_02210	456938	457369	-1	transcriptional regulator
455377	468722	13345	OXZ36276.1	B9N54_02215	457631	457825	1	hypothetical protein
455377	468722	13345	OXZ36277.1	B9N54_02220	457827	458951	1	site-specific integrase
455377	468722	13345	OXZ36278.1	B9N54_02225	458944	459306	1	hypothetical protein
455377	468722	13345	OXZ36279.1	B9N54_02230	459424	460914	1	virulence-associated protein E
455377	468722	13345	OXZ36280.1	B9N54_02235	461243	461605	1	plasmid mobilization relaxosome protein MobC
455377	468722	13345	OXZ36281.1	B9N54_02240	461612	461860	1	hypothetical protein
455377	468722	13345	OXZ36295.1	B9N54_02245	461947	462342	1	hypothetical protein
455377	468722	13345	OXZ36282.1	B9N54_02250	462352	463794	1	hypothetical protein
455377	468722	13345	OXZ36283.1	B9N54_02255	463886	464056	1	XRE family transcriptional regulator
455377	468722	13345	OXZ36284.1	B9N54_02260	464147	464470	1	mobilization protein

455377	468722	13345 OXZ36285.1	B9N54_02265	464472	464711	1 hypothetical protein
455377	468722	13345 OXZ36286.1	B9N54_02270	464735	467233	-1 ABC transporter permease
455377	468722	13345 OXZ36287.1	B9N54_02275	467220	467909	-1 peptide ABC transporter ATP-binding protein
455377	468722	13345 OXZ36288.1	B9N54_02280	468185	468722	1 IS110 family transposase
461243	468722	7479 OXZ36280.1	B9N54_02235	461243	461605	1 plasmid mobilization relaxosome protein MobC
461243	468722	7479 OXZ36281.1	B9N54_02240	461612	461860	1 hypothetical protein
461243	468722	7479 OXZ36295.1	B9N54_02245	461947	462342	1 hypothetical protein
461243	468722	7479 OXZ36282.1	B9N54_02250	462352	463794	1 hypothetical protein
461243	468722	7479 OXZ36283.1	B9N54_02255	463886	464056	1 XRE family transcriptional regulator
461243	468722	7479 OXZ36284.1	B9N54_02260	464147	464470	1 mobilization protein
461243	468722	7479 OXZ36285.1	B9N54_02265	464472	464711	1 hypothetical protein
461243	468722	7479 OXZ36286.1	B9N54_02270	464735	467233	-1 ABC transporter permease
461243	468722	7479 OXZ36287.1	B9N54_02275	467220	467909	-1 peptide ABC transporter ATP-binding protein
461243	468722	7479 OXZ36288.1	B9N54_02280	468185	468722	1 IS110 family transposase
872345	880377	8032 OXZ35246.1	B9N54_04320	872345	873178	1 hypothetical protein
872345	880377	8032 OXZ35247.1	B9N54_04325	873299	873718	-1 flavodoxin
872345	880377	8032 OXZ35248.1	B9N54_04330	873722	874267	-1 hypothetical protein
872345	880377	8032 OXZ35249.1	B9N54_04335	874473	874697	1 preprotein translocase subunit SecG
872345	880377	8032 OXZ35250.1	B9N54_04340	874722	876734	1 sodium-translocating pyrophosphatase
872345	880377	8032 OXZ35251.1	B9N54_04345	876871	876995	1 transposase
872345	880377	8032 OXZ34999.1	B9N54_04350	877996	878159	1 hypothetical protein
872345	880377	8032 OXZ35000.1	B9N54_04355	878282	879610	1 hemolysin
872345	880377	8032 OXZ35001.1	B9N54_04360	879622	880377	1 type I methionyl aminopeptidase
895090	901022	5932 OXZ35013.1	B9N54_04435	895090	895281	1 50S ribosomal protein L35
895090	901022	5932 OXZ35014.1	B9N54_04440	895300	895653	1 50S ribosomal protein L20
895090	901022	5932 OXZ35015.1	B9N54_04445	895685	895960	-1 hypothetical protein
895090	901022	5932 OXZ35016.1	B9N54_04450	895960	896577	-1 recombinase RecX
895090	901022	5932 OXZ35017.1	B9N54_04455	896766	897005	1 hypothetical protein
895090	901022	5932 OXZ35018.1	B9N54_04460	897014	898090	1 phosphoesterase
895090	901022	5932 OXZ35019.1	B9N54_04465	898087	900339	1 DNA repair protein Rad50
895090	901022	5932 OXZ35020.1	B9N54_04470	900342	901022	1 serine/threonine protein phosphatase
949309	953561	4252 OXZ34685.1	B9N54_04705	949309	949935	-1 LexA repressor
949309	953561	4252 OXZ34686.1	B9N54_04710	950110	950421	1 peptidoglycan-binding protein LysM
949309	953561	4252 OXZ34687.1	B9N54_04715	950497	951477	-1 recombinase XerC
949309	953561	4252 OXZ34688.1	B9N54_04720	951587	952753	-1 aspartate aminotransferase
949309	953561	4252 OXZ34689.1	B9N54_04725	952740	953561	-1 metal-dependent phosphoesterase
1135201	1177204	42003 OXZ33900.1	B9N54_05575	1135201	1136436	-1 site-specific integrase
1135201	1177204	42003 OXZ33901.1	B9N54_05580	1136514	1136723	-1 excisionase
1135201	1177204	42003 OXZ33902.1	B9N54_05585	1137159	1137569	-1 RNA polymerase subunit sigma
1135201	1177204	42003 OXZ33903.1	B9N54_05590	1137791	1139212	-1 ABC transporter
1135201	1177204	42003 OXZ33910.1	B9N54_05595	1139200	1139889	-1 ABC transporter permease
1135201	1177204	42003 OXZ33904.1	B9N54_05600	1139882	1140472	-1 hypothetical protein
1135201	1177204	42003 OXZ33905.1	B9N54_05605	1140483	1142216	-1 multidrug ABC transporter ATP-binding protein
1135201	1177204	42003 OXZ33906.1	B9N54_05610	1142218	1143948	-1 ABC transporter ATP-binding protein
1135201	1177204	42003 OXZ33907.1	B9N54_05615	1144006	1144641	-1 TetR family transcriptional regulator
1135201	1177204	42003 OXZ33673.1	B9N54_05620	1146067	1146423	1 plasmid mobilization relaxosome protein MobC
1135201	1177204	42003 OXZ33674.1	B9N54_05625	1146425	1147488	1 endonuclease
1135201	1177204	42003 OXZ33647.1	B9N54_05630	1148554	1148883	1 relaxase
1135201	1177204	42003 OXZ33581.1	B9N54_05635	1148928	1149680	-1 ABC transporter permease
1135201	1177204	42003 OXZ33582.1	B9N54_05640	1149681	1150412	-1 ABC transporter permease
1135201	1177204	42003 OXZ33583.1	B9N54_05645	1150405	1151328	-1 bacitracin ABC transporter ATP-binding protein
1135201	1177204	42003 OXZ33584.1	B9N54_05650	1151343	1152110	-1 ABC transporter permease
1135201	1177204	42003 OXZ33585.1	B9N54_05655	1152230	1153138	-1 two-component sensor histidine kinase
1135201	1177204	42003 OXZ33586.1	B9N54_05660	1153142	1153840	-1 DNA-binding response regulator
1135201	1177204	42003 OXZ33587.1	B9N54_05665	1153861	1154073	-1 transcriptional regulator
1135201	1177204	42003 OXZ33588.1	B9N54_05670	1154397	1155056	-1 DNA-binding protein
1135201	1177204	42003 OXZ33589.1	B9N54_05675	1155100	1162743	-1 DNA helicase
1135201	1177204	42003 OXZ33590.1	B9N54_05680	1162730	1163695	-1 DNA (cytosine-5-)-methyltransferase
1135201	1177204	42003 OXZ33591.1	B9N54_05685	1163688	1165409	-1 DNA topoisomerase III
1135201	1177204	42003 OXZ33592.1	B9N54_05690	1165516	1166934	-1 AAA family ATPase
1135201	1177204	42003 OXZ33593.1	B9N54_05695	1167015	1167884	-1 bacteriocin
1135201	1177204	42003 OXZ33594.1	B9N54_05700	1167899	1169482	-1 copper amine oxidase
1135201	1177204	42003 OXZ33595.1	B9N54_05705	1169469	1169708	-1 hypothetical protein
1135201	1177204	42003 OXZ33596.1	B9N54_05710	1169723	1172302	-1 hypothetical protein
1135201	1177204	42003 OXZ33648.1	B9N54_05715	1172310	1174553	-1 conjugal transfer protein TraE
1135201	1177204	42003 OXZ33597.1	B9N54_05720	1174624	1175034	-1 conjugal transfer protein
1135201	1177204	42003 OXZ33598.1	B9N54_05725	1175036	1175326	-1 hypothetical protein
1135201	1177204	42003 OXZ33599.1	B9N54_05730	1175336	1176199	-1 hypothetical protein
1135201	1177204	42003 OXZ33600.1	B9N54_05735	1176210	1176425	-1 conjugal transfer protein
1135201	1177204	42003 OXZ33601.1	B9N54_05740	1176427	1176738	-1 single-stranded DNA-binding protein
1135201	1177204	42003 OXZ33602.1	B9N54_05745	1176929	1177204	-1 hypothetical protein
1136514	1146423	9909 OXZ33901.1	B9N54_05580	1136514	1136723	-1 excisionase
1136514	1146423	9909 OXZ33902.1	B9N54_05585	1137159	1137569	-1 RNA polymerase subunit sigma
1136514	1146423	9909 OXZ33903.1	B9N54_05590	1137791	1139212	-1 ABC transporter
1136514	1146423	9909 OXZ33910.1	B9N54_05595	1139200	1139889	-1 ABC transporter permease
1136514	1146423	9909 OXZ33904.1	B9N54_05600	1139882	1140472	-1 hypothetical protein
1136514	1146423	9909 OXZ33905.1	B9N54_05605	1140483	1142216	-1 multidrug ABC transporter ATP-binding protein
1136514	1146423	9909 OXZ33906.1	B9N54_05610	1142218	1143948	-1 ABC transporter ATP-binding protein
1136514	1146423	9909 OXZ33907.1	B9N54_05615	1144006	1144641	-1 TetR family transcriptional regulator
1136514	1146423	9909 OXZ33673.1	B9N54_05620	1146067	1146423	1 plasmid mobilization relaxosome protein MobC
1162730	1167884	5154 OXZ33589.1	B9N54_05675	1155100	1162743	-1 DNA helicase
1162730	1167884	5154 OXZ33590.1	B9N54_05680	1162730	1163695	-1 DNA (cytosine-5-)-methyltransferase
1162730	1167884	5154 OXZ33591.1	B9N54_05685	1163688	1165409	-1 DNA topoisomerase III
1162730	1167884	5154 OXZ33592.1	B9N54_05690	1165516	1166934	-1 AAA family ATPase

1162730	1167884	5154 OXZ33593.1	B9N54_05695	1167015	1167884	-1 bacteriocin
1185429	1198486	13057 OXZ33611.1	B9N54_05795	1185429	1187150	-1 ABC transporter ATP-binding protein
1185429	1198486	13057 OXZ33612.1	B9N54_05800	1187140	1188897	-1 ABC transporter ATP-binding protein
1185429	1198486	13057 OXZ33613.1	B9N54_05805	1188915	1190297	-1 ABC transporter ATP-binding protein
1185429	1198486	13057 OXZ33614.1	B9N54_05810	1190290	1191003	-1 cobalt transporter
1185429	1198486	13057 OXZ33615.1	B9N54_05815	1191003	1191599	-1 hypothetical protein
1185429	1198486	13057 OXZ33616.1	B9N54_05820	1191680	1192285	-1 TetR family transcriptional regulator
1185429	1198486	13057 OXZ33617.1	B9N54_05825	1192402	1194231	-1 recombinase TnpX
1185429	1198486	13057 OXZ33618.1	B9N54_05830	1194271	1195323	-1 conjugal transfer protein TraG
1185429	1198486	13057 OXZ33619.1	B9N54_05835	1195316	1196050	-1 phage antirepressor Ant
1185429	1198486	13057 OXZ33620.1	B9N54_05840	1196047	1196532	-1 conjugal transfer protein
1185429	1198486	13057 OXZ33621.1	B9N54_05845	1196525	1197352	-1 nucleoside triphosphate hydrolase
1185429	1198486	13057 OXZ33622.1	B9N54_05850	1197349	1198122	-1 replication initiator protein A
1185429	1198486	13057 OXZ33623.1	B9N54_05855	1198205	1198486	-1 hypothetical protein
1631909	1691704	59795 OXZ32456.1	B9N54_07905	1631909	1632202	-1 hypothetical protein
1631909	1691704	59795 OXZ32457.1	B9N54_07910	1632337	1632645	-1 exosortase
1631909	1691704	59795	B9N54_07915	1632651	1633321	-1 ATPase
1631909	1691704	59795 OXZ32458.1	B9N54_07920	1633701	1634243	-1 hypothetical protein
1631909	1691704	59795 OXZ32459.1	B9N54_07925	1634540	1636144	-1 macrolide ABC transporter ATP-binding protein
1631909	1691704	59795	B9N54_07930	1636624	1637011	-1 hypothetical protein
1631909	1691704	59795 OXZ32460.1	B9N54_07935	1637071	1637562	-1 protein-S-isoprenylcysteine methyltransferase
1631909	1691704	59795 OXZ32461.1	B9N54_07940	1637576	1638514	-1 esterase
1631909	1691704	59795 OXZ32462.1	B9N54_07945	1638583	1639209	-1 hypothetical protein
1631909	1691704	59795 OXZ32463.1	B9N54_07950	1639237	1639845	-1 SAM-dependent methyltransferase
1631909	1691704	59795 OXZ32464.1	B9N54_07955	1640060	1640809	-1 phosphorylase
1631909	1691704	59795 OXZ32465.1	B9N54_07960	1640944	1641558	-1 hypothetical protein
1631909	1691704	59795 OXZ32466.1	B9N54_07965	1641767	1643131	-1 ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32467.1	B9N54_07970	1643125	1643814	-1 cobalt ABC transporter permease
1631909	1691704	59795 OXZ32468.1	B9N54_07975	1643814	1644398	-1 hypothetical protein
1631909	1691704	59795 OXZ32469.1	B9N54_07980	1644458	1645801	-1 MATE family efflux transporter
1631909	1691704	59795 OXZ32470.1	B9N54_07985	1645813	1647534	-1 ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32471.1	B9N54_07990	1647518	1649272	-1 ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32472.1	B9N54_07995	1649433	1650425	1 AraC family transcriptional regulator
1631909	1691704	59795	B9N54_08000	1650854	1651616	-1 hypothetical protein
1631909	1691704	59795 OXZ32473.1	B9N54_08005	1651609	1653345	-1 multidrug ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32474.1	B9N54_08010	1653338	1655059	-1 ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32475.1	B9N54_08015	1655059	1656522	-1 ABC transporter
1631909	1691704	59795 OXZ32476.1	B9N54_08020	1656524	1657195	-1 cobalt transporter
1631909	1691704	59795 OXZ32477.1	B9N54_08025	1657192	1657782	-1 hypothetical protein
1631909	1691704	59795 OXZ32478.1	B9N54_08030	1657849	1658826	-1 AraC family transcriptional regulator
1631909	1691704	59795 OXZ32479.1	B9N54_08035	1658836	1659420	-1 TetR family transcriptional regulator
1631909	1691704	59795 OXZ32480.1	B9N54_08040	1659858	1660199	1 plasmid mobilization relaxosome protein MobC
1631909	1691704	59795 OXZ32481.1	B9N54_08045	1660574	1662907	-1 peptidase S8
1631909	1691704	59795 OXZ32482.1	B9N54_08050	1662910	1664007	-1 ATPase
1631909	1691704	59795 OXZ32483.1	B9N54_08055	1664488	1664934	-1 abortive infection protein
1631909	1691704	59795 OXZ32484.1	B9N54_08060	1665018	1665866	-1 AraC family transcriptional regulator 23S rRNA (uracil(1939)-C(5))-methyltransferase
1631909	1691704	59795	B9N54_08065	1666434	1667498	-1 RlmD
1631909	1691704	59795 OXZ32485.1	B9N54_08070	1667999	1669765	-1 hypothetical protein
1631909	1691704	59795 OXZ32493.1	B9N54_08075	1669780	1670097	-1 nucleotide pyrophosphohydrolase
1631909	1691704	59795 OXZ32486.1	B9N54_08080	1670110	1671900	-1 hypothetical protein
1631909	1691704	59795	B9N54_08085	1672610	1673406	-1 lysophospholipase
1631909	1691704	59795 OXZ32487.1	B9N54_08090	1673763	1674020	-1 hypothetical protein
1631909	1691704	59795 OXZ32488.1	B9N54_08095	1674041	1676476	-1 ABC transporter permease
1631909	1691704	59795 OXZ32489.1	B9N54_08100	1676469	1677149	-1 peptide ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32490.1	B9N54_08105	1677202	1678062	-1 two-component sensor histidine kinase
1631909	1691704	59795 OXZ32491.1	B9N54_08110	1678063	1678713	-1 DNA-binding response regulator
1631909	1691704	59795 OXZ32492.1	B9N54_08115	1678899	1679023	1 transposase
1631909	1691704	59795 OXZ32171.1	B9N54_08120	1680024	1680187	1 hypothetical protein
1631909	1691704	59795 OXZ32172.1	B9N54_08125	1680267	1682039	-1 recombinase family protein
1631909	1691704	59795 OXZ32173.1	B9N54_08130	1682620	1684011	-1 ABC transporter
1631909	1691704	59795 OXZ32174.1	B9N54_08135	1684008	1684736	-1 transporter
1631909	1691704	59795 OXZ32175.1	B9N54_08140	1684736	1685326	-1 hypothetical protein
1631909	1691704	59795 OXZ32176.1	B9N54_08145	1685352	1687076	-1 ABC transporter permease
1631909	1691704	59795 OXZ32177.1	B9N54_08150	1687073	1688842	-1 ABC transporter permease
1631909	1691704	59795 OXZ32178.1	B9N54_08155	1688950	1689564	-1 TetR family transcriptional regulator
1631909	1691704	59795 OXZ32179.1	B9N54_08160	1689968	1691704	-1 multidrug ABC transporter ATP-binding protein
1631909	1691704	59795 OXZ32180.1	B9N54_08165	1691697	1693415	-1 ABC transporter ATP-binding protein
1653338	1665866	12528 OXZ32473.1	B9N54_08005	1651609	1653345	-1 multidrug ABC transporter ATP-binding protein
1653338	1665866	12528 OXZ32474.1	B9N54_08010	1653338	1655059	-1 ABC transporter ATP-binding protein
1653338	1665866	12528 OXZ32475.1	B9N54_08015	1655059	1656522	-1 ABC transporter
1653338	1665866	12528 OXZ32476.1	B9N54_08020	1656524	1657195	-1 cobalt transporter
1653338	1665866	12528 OXZ32477.1	B9N54_08025	1657192	1657782	-1 hypothetical protein
1653338	1665866	12528 OXZ32478.1	B9N54_08030	1657849	1658826	-1 AraC family transcriptional regulator
1653338	1665866	12528 OXZ32479.1	B9N54_08035	1658836	1659420	-1 TetR family transcriptional regulator
1653338	1665866	12528 OXZ32480.1	B9N54_08040	1659858	1660199	1 plasmid mobilization relaxosome protein MobC
1653338	1665866	12528 OXZ32481.1	B9N54_08045	1660574	1662907	-1 peptidase S8
1653338	1665866	12528 OXZ32482.1	B9N54_08050	1662910	1664007	-1 ATPase
1653338	1665866	12528 OXZ32483.1	B9N54_08055	1664488	1664934	-1 abortive infection protein
1653338	1665866	12528 OXZ32484.1	B9N54_08060	1665018	1665866	-1 AraC family transcriptional regulator
1722538	1824911	102373 OXZ32116.1	B9N54_08255	1720719	1722554	-1 multidrug ABC transporter
1722538	1824911	102373 OXZ32117.1	B9N54_08260	1722538	1724340	-1 multidrug ABC transporter
1722538	1824911	102373 OXZ32118.1	B9N54_08265	1724420	1725085	-1 histidine kinase

1722538	1824911	102373	OXZ32119.1	B9N54_08270	1725093	1725788	-1 DNA-binding response regulator
1722538	1824911	102373	OXZ32120.1	B9N54_08275	1725872	1726735	-1 UTP--glucose-1-phosphate uridylyltransferase
1722538	1824911	102373	OXZ32121.1	B9N54_08280	1727463	1730048	-1 ATP-dependent chaperone ClpB
1722538	1824911	102373	OXZ32122.1	B9N54_08285	1730067	1731011	-1 heat-shock protein
1722538	1824911	102373	OXZ32123.1	B9N54_08290	1731172	1731837	-1 nitroreductase
1722538	1824911	102373	OXZ32124.1	B9N54_08295	1731989	1732528	-1 RNA polymerase subunit sigma
1722538	1824911	102373	OXZ32125.1	B9N54_08300	1732767	1733222	1 hypothetical protein
1722538	1824911	102373	OXZ32126.1	B9N54_08305	1733323	1737573	-1 hypothetical protein
1722538	1824911	102373		B9N54_08310	1738533	1738844	-1 hypothetical protein
1722538	1824911	102373	OXZ32127.1	B9N54_08315	1738878	1739078	-1 hypothetical protein
1722538	1824911	102373	OXZ32128.1	B9N54_08320	1739665	1740216	1 hypothetical protein
1722538	1824911	102373	OXZ32129.1	B9N54_08325	1740277	1740489	1 hypothetical protein
1722538	1824911	102373	OXZ32130.1	B9N54_08330	1740569	1741717	1 MFS transporter
1722538	1824911	102373	OXZ32131.1	B9N54_08335	1741802	1742299	-1 hypothetical protein
1722538	1824911	102373	OXZ32132.1	B9N54_08340	1742333	1742806	-1 peptidase M50
1722538	1824911	102373	OXZ32133.1	B9N54_08345	1743311	1744294	-1 albumin-binding protein
1722538	1824911	102373	OXZ32134.1	B9N54_08350	1744957	1745379	-1 hypothetical protein
1722538	1824911	102373	OXZ32135.1	B9N54_08355	1745424	1746359	-1 TIGR01212 family radical SAM protein
1722538	1824911	102373	OXZ32136.1	B9N54_08360	1746352	1746792	-1 peroxiredoxin
1722538	1824911	102373	OXZ32137.1	B9N54_08365	1746785	1747621	-1 hydrolase
1722538	1824911	102373	OXZ32138.1	B9N54_08370	1747611	1747934	-1 DUF1292 domain-containing protein
1722538	1824911	102373	OXZ32139.1	B9N54_08375	1747949	1749340	-1 aminoacyl-histidine dipeptidase
1722538	1824911	102373	OXZ32140.1	B9N54_08380	1749405	1750523	-1 hypothetical protein
1722538	1824911	102373	OXZ32141.1	B9N54_08385	1750577	1751566	-1 peptide chain release factor 2
1722538	1824911	102373	OXZ32142.1	B9N54_08390	1751598	1751777	-1 hypothetical protein
1722538	1824911	102373	OXZ32143.1	B9N54_08395	1752103	1754832	-1 preprotein translocase subunit SecA
1722538	1824911	102373	OXZ32144.1	B9N54_08400	1755433	1756143	-1 transaldolase
1722538	1824911	102373	OXZ32145.1	B9N54_08405	1756171	1757529	-1 PTS ascorbate transporter subunit IIC
1722538	1824911	102373	OXZ32146.1	B9N54_08410	1757547	1757822	-1 PTS maltose transporter subunit IIBC
1722538	1824911	102373	OXZ32147.1	B9N54_08415	1757815	1758285	-1 PTS sugar transporter subunit IIA
1722538	1824911	102373	OXZ32148.1	B9N54_08420	1758393	1759310	-1 malate transporter
1722538	1824911	102373	OXZ32149.1	B9N54_08425	1759819	1761279	-1 peptide-binding protein
1722538	1824911	102373	OXZ32150.1	B9N54_08430	1761468	1762613	-1 hypothetical protein UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--
1722538	1824911	102373	OXZ32151.1	B9N54_08435	1763296	1764732	-1 2, 6-diaminopimelate ligase
1722538	1824911	102373	OXZ32152.1	B9N54_08440	1764988	1765842	-1 beta-carotene 15,15'-monooxygenase
1722538	1824911	102373	OXZ32153.1	B9N54_08445	1765862	1766728	-1 polyphosphate--nucleotide phosphotransferase
1722538	1824911	102373	OXZ32154.1	B9N54_08450	1766927	1767913	1 alkane 1-monooxygenase
1722538	1824911	102373	OXZ32155.1	B9N54_08455	1768168	1769046	-1 ribokinase
1722538	1824911	102373	OXZ32156.1	B9N54_08460	1769195	1773166	-1 hypothetical protein
1722538	1824911	102373	OXZ32157.1	B9N54_08465	1773446	1779070	-1 hypothetical protein
1722538	1824911	102373	OXZ32158.1	B9N54_08470	1779344	1780198	1 hypothetical protein
1722538	1824911	102373	OXZ32159.1	B9N54_08475	1780318	1788978	-1 hypothetical protein
1722538	1824911	102373	OXZ32106.1	B9N54_08480	1790559	1791107	1 hypothetical protein
1722538	1824911	102373	OXZ32107.1	B9N54_08485	1791143	1792447	1 N-acetylmuramoyl-L-alanine amidase
1722538	1824911	102373	OXZ32108.1	B9N54_08490	1792594	1792701	1 transposase
1722538	1824911	102373	OXZ31954.1	B9N54_08495	1793975	1794298	-1 hypothetical protein
1722538	1824911	102373	OXZ31955.1	B9N54_08500	1794364	1794858	-1 hypothetical protein
1722538	1824911	102373	OXZ31956.1	B9N54_08505	1794926	1795753	-1 hypothetical protein
1722538	1824911	102373	OXZ31957.1	B9N54_08510	1795918	1796565	1 sugar ABC transporter ATP-binding protein
1722538	1824911	102373	OXZ31958.1	B9N54_08515	1796549	1797193	1 sugar ABC transporter permease
1722538	1824911	102373	OXZ31959.1	B9N54_08520	1797194	1797712	1 hypothetical protein
1722538	1824911	102373	OXZ31857.1	B9N54_08525	1799044	1799571	1 hypothetical protein calcium-translocating P-type ATPase, SERCA-
1722538	1824911	102373	OXZ31919.1	B9N54_08530	1800427	1803114	-1 type
1722538	1824911	102373	OXZ31858.1	B9N54_08535	1803284	1804042	-1 metal-dependent hydrolase
1722538	1824911	102373	OXZ31859.1	B9N54_08540	1804168	1804638	1 aminoacyl-tRNA deacylase
1722538	1824911	102373	OXZ31860.1	B9N54_08545	1804641	1805945	1 glutamate--cysteine ligase
1722538	1824911	102373	OXZ31861.1	B9N54_08550	1805938	1807248	1 glutathionylspermidine synthase
1722538	1824911	102373	OXZ31862.1	B9N54_08555	1807345	1807614	-1 Txe/YoeB family addiction module toxin
1722538	1824911	102373	OXZ31863.1	B9N54_08560	1807608	1807856	-1 prevent-host-death protein
1722538	1824911	102373	OXZ31864.1	B9N54_08565	1808039	1808458	1 CMP deaminase
1722538	1824911	102373	OXZ31865.1	B9N54_08570	1808470	1811889	1 pyruvate carboxylase
1722538	1824911	102373	OXZ31866.1	B9N54_08575	1811926	1812330	-1 DUF3139 domain-containing protein
1722538	1824911	102373	OXZ31867.1	B9N54_08580	1812461	1812703	1 cell division protein FtsW
1722538	1824911	102373	OXZ31868.1	B9N54_08585	1812806	1813213	1 hypothetical protein
1722538	1824911	102373	OXZ31869.1	B9N54_08590	1813229	1813735	-1 thiol reductase thioredoxin
1722538	1824911	102373	OXZ31870.1	B9N54_08595	1813840	1814184	-1 hypothetical protein
1722538	1824911	102373	OXZ31871.1	B9N54_08600	1814249	1814938	-1 hypothetical protein
1722538	1824911	102373	OXZ31872.1	B9N54_08605	1814935	1819629	-1 FMN-binding domain-containing protein
1722538	1824911	102373	OXZ31920.1	B9N54_08610	1819874	1820827	-1 2-dehydropantoate 2-reductase
1722538	1824911	102373	OXZ31873.1	B9N54_08615	1820847	1822496	-1 inorganic pyrophosphatase
1722538	1824911	102373	OXZ31874.1	B9N54_08620	1822661	1823182	1 N-carbamoylsarcosine amidohydrolase
1722538	1824911	102373		B9N54_08625	1823405	1823742	-1 RNA helicase
1722538	1824911	102373	OXZ31875.1	B9N54_08630	1824068	1824496	-1 hypothetical protein
1722538	1824911	102373	OXZ31876.1	B9N54_08635	1824555	1824911	-1 hypothetical protein
1867992	1874956	6964	OXZ31643.1	B9N54_08875	1867992	1868531	1 transposase
1867992	1874956	6964	OXZ31644.1	B9N54_08880	1868726	1869351	1 IS3 family transposase
1867992	1874956	6964	OXZ31452.1	B9N54_08900	1872118	1872655	-1 IS110 family transposase
1867992	1874956	6964	OXZ31645.1	B9N54_08870	1873742	1874956	1 IS256 family transposase

Table S3H: Predicted genomic islands in the genome of "F. nericia" CCUG54800

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
68253	77535	9282	OXZ29102.1	B9N49_00325	68253	69122	1	hypothetical protein
68253	77535	9282	OXZ29103.1	B9N49_00330	69109	71097	1	exopolyphosphatase
68253	77535	9282	OXZ29104.1	B9N49_00335	71078	71524	1	50S ribosomal protein L9
68253	77535	9282	OXZ29105.1	B9N49_00340	71558	72895	1	replicative DNA helicase
68253	77535	9282	OXZ29106.1	B9N49_00345	72892	73455	1	GNAT family N-acetyltransferase
68253	77535	9282	OXZ29107.1	B9N49_00350	73460	74218	1	DNA replication protein
68253	77535	9282	OXZ29108.1	B9N49_00355	74221	75198	1	DNA replication protein DnaC
68253	77535	9282	OXZ29109.1	B9N49_00360	75195	75839	1	NAD(P)H-hydrate epimerase
68253	77535	9282	OXZ29110.1	B9N49_00365	76323	76865	1	ECF transporter S component
68253	77535	9282	OXZ29111.1	B9N49_00370	76849	77535	1	radical SAM protein
1015853	1107796	91943	OXZ27717.1	B9N49_05145	1015853	1016062	-1	excisionase
1015853	1107796	91943	OXZ27718.1	B9N49_05150	1016498	1016908	-1	RNA polymerase subunit sigma
1015853	1107796	91943	OXZ27361.1	B9N49_05155	1018276	1018815	1	transposase
1015853	1107796	91943	OXZ27362.1	B9N49_05160	1018803	1019684	1	hypothetical protein
1015853	1107796	91943	OXZ27348.1	B9N49_05165	1020784	1021207	-1	MATE family efflux transporter
1015853	1107796	91943	OXZ27349.1	B9N49_05170	1021249	1022712	-1	ABC transporter
1015853	1107796	91943	OXZ27350.1	B9N49_05175	1022715	1023449	-1	transporter
1015853	1107796	91943	OXZ27351.1	B9N49_05180	1023449	1024030	-1	hypothetical protein
1015853	1107796	91943	OXZ27352.1	B9N49_05185	1024111	1025844	-1	multidrug ABC transporter ATP-binding protein
1015853	1107796	91943	OXZ27353.1	B9N49_05190	1025838	1027583	-1	ABC transporter ATP-binding protein
1015853	1107796	91943	OXZ27354.1	B9N49_05195	1027677	1028300	-1	TetR family transcriptional regulator
1015853	1107796	91943	OXZ27355.1	B9N49_05200	1028609	1028965	1	plasmid mobilization relaxosome protein MobC
1015853	1107796	91943	OXZ27356.1	B9N49_05205	1028967	1030298	1	endonuclease
1015853	1107796	91943	OXZ27357.1	B9N49_05210	1030454	1031110	-1	DNA-binding protein
1015853	1107796	91943		B9N49_05215	1031154	1038797	-1	DNA helicase
1015853	1107796	91943	OXZ27360.1	B9N49_05220	1038882	1040384	-1	SIR2 family protein
1015853	1107796	91943	OXZ27358.1	B9N49_05225	1040441	1041379	-1	DNA (cytosine-5-)-methyltransferase
1015853	1107796	91943	OXZ27359.1	B9N49_05230	1041372	1043093	-1	DNA topoisomerase III
1015853	1107796	91943	OXZ27256.1	B9N49_05235	1044146	1044516	-1	thioesterase
1015853	1107796	91943	OXZ27257.1	B9N49_05240	1044673	1045044	-1	transcriptional regulator
1015853	1107796	91943		B9N49_05245	1045511	1045651	-1	diacylglycerol transferase
1015853	1107796	91943	OXZ27258.1	B9N49_05250	1045700	1046068	1	plasmid mobilization relaxosome protein MobC
1015853	1107796	91943	OXZ27259.1	B9N49_05255	1046068	1047438	1	endonuclease
1015853	1107796	91943	OXZ27260.1	B9N49_05260	1047599	1048474	-1	single-stranded DNA-binding protein
1015853	1107796	91943	OXZ27261.1	B9N49_05265	1048775	1059184	-1	conjugal transfer protein
1015853	1107796	91943	OXZ27262.1	B9N49_05270	1059379	1059819	-1	terminase large subunit
1015853	1107796	91943	OXZ27263.1	B9N49_05275	1060047	1061753	-1	DNA topoisomerase III
1015853	1107796	91943	OXZ27264.1	B9N49_05280	1062170	1063048	-1	bacteriocin
1015853	1107796	91943	OXZ27265.1	B9N49_05285	1063064	1065418	-1	copper amine oxidase
1015853	1107796	91943	OXZ27266.1	B9N49_05290	1065415	1065672	-1	hypothetical protein
1015853	1107796	91943	OXZ27267.1	B9N49_05295	1065692	1068655	-1	hypothetical protein
1015853	1107796	91943	OXZ27268.1	B9N49_05300	1068665	1069630	-1	site-specific DNA-methyltransferase
1015853	1107796	91943	OXZ27269.1	B9N49_05305	1069602	1072097	-1	conjugal transfer protein TraE
1015853	1107796	91943		B9N49_05310	1072094	1072288	-1	conjugal transfer protein
1015853	1107796	91943	OXZ27270.1	B9N49_05315	1072332	1072470	1	transposase
1015853	1107796	91943	OXZ27234.1	B9N49_05320	1073471	1073609	-1	transposase
1015853	1107796	91943	OXZ27235.1	B9N49_05325	1073690	1075696	-1	hypothetical protein
1015853	1107796	91943	OXZ27236.1	B9N49_05330	1075697	1076452	-1	bacitracin ABC transporter ATP-binding protein
1015853	1107796	91943	OXZ27237.1	B9N49_05335	1076436	1078589	-1	lantibiotic transporter
1015853	1107796	91943	OXZ27238.1	B9N49_05340	1078573	1080699	-1	hypothetical protein
1015853	1107796	91943	OXZ27239.1	B9N49_05345	1080671	1081477	-1	hypothetical protein
1015853	1107796	91943	OXZ27240.1	B9N49_05350	1081750	1082406	-1	DNA-binding protein
1015853	1107796	91943	OXZ27241.1	B9N49_05355	1082450	1090093	-1	DNA helicase
1015853	1107796	91943	OXZ27242.1	B9N49_05360	1090176	1092389	-1	hypothetical protein
1015853	1107796	91943	OXZ27243.1	B9N49_05365	1092425	1093387	-1	DNA (cytosine-5-)-methyltransferase
1015853	1107796	91943	OXZ27244.1	B9N49_05370	1093380	1095101	-1	DNA topoisomerase III
1015853	1107796	91943	OXZ27245.1	B9N49_05375	1095190	1096173	-1	hypothetical protein
1015853	1107796	91943	OXZ27246.1	B9N49_05380	1096166	1096777	-1	hypothetical protein
1015853	1107796	91943	OXZ27247.1	B9N49_05385	1096851	1097711	-1	bacteriocin
1015853	1107796	91943	OXZ27248.1	B9N49_05390	1097726	1099309	-1	copper amine oxidase
1015853	1107796	91943	OXZ27249.1	B9N49_05395	1099296	1099535	-1	hypothetical protein
1015853	1107796	91943	OXZ27250.1	B9N49_05400	1099550	1102129	-1	hypothetical protein
1015853	1107796	91943	OXZ27251.1	B9N49_05405	1102137	1104560	-1	conjugal transfer protein TraE
1015853	1107796	91943	OXZ27252.1	B9N49_05410	1104451	1104861	-1	conjugal transfer protein
1015853	1107796	91943	OXZ27253.1	B9N49_05415	1104863	1105153	-1	hypothetical protein
1015853	1107796	91943	OXZ27254.1	B9N49_05420	1105163	1106026	-1	hypothetical protein
1015853	1107796	91943	OXZ27255.1	B9N49_05425	1106037	1106183	-1	hypothetical protein
1015853	1107796	91943	OXZ27208.1	B9N49_05430	1107352	1107483	-1	hypothetical protein
1015853	1107796	91943	OXZ27209.1	B9N49_05435	1107485	1107796	-1	single-stranded DNA-binding protein
1038882	1068655	29773	OXZ27360.1	B9N49_05220	1038882	1040384	-1	SIR2 family protein
1038882	1068655	29773	OXZ27358.1	B9N49_05225	1040441	1041379	-1	DNA (cytosine-5-)-methyltransferase
1038882	1068655	29773	OXZ27359.1	B9N49_05230	1041372	1043093	-1	DNA topoisomerase III
1038882	1068655	29773	OXZ27256.1	B9N49_05235	1044146	1044516	-1	thioesterase
1038882	1068655	29773	OXZ27257.1	B9N49_05240	1044673	1045044	-1	transcriptional regulator
1038882	1068655	29773		B9N49_05245	1045511	1045651	-1	diacylglycerol transferase
1038882	1068655	29773	OXZ27258.1	B9N49_05250	1045700	1046068	1	plasmid mobilization relaxosome protein MobC
1038882	1068655	29773	OXZ27259.1	B9N49_05255	1046068	1047438	1	endonuclease
1038882	1068655	29773	OXZ27260.1	B9N49_05260	1047599	1048474	-1	single-stranded DNA-binding protein
1038882	1068655	29773	OXZ27261.1	B9N49_05265	1048775	1059184	-1	conjugal transfer protein
1038882	1068655	29773	OXZ27262.1	B9N49_05270	1059379	1059819	-1	terminase large subunit
1038882	1068655	29773	OXZ27263.1	B9N49_05275	1060047	1061753	-1	DNA topoisomerase III
1038882	1068655	29773	OXZ27264.1	B9N49_05280	1062170	1063048	-1	bacteriocin

1038882	1068655	29773 OXZ27265.1	B9N49_05285	1063064	1065418	-1 copper amine oxidase
1038882	1068655	29773 OXZ27266.1	B9N49_05290	1065415	1065672	-1 hypothetical protein
1038882	1068655	29773 OXZ27267.1	B9N49_05295	1065692	1068655	-1 hypothetical protein
1073690	1082406	8716 OXZ27235.1	B9N49_05325	1073690	1075696	-1 hypothetical protein
1073690	1082406	8716 OXZ27236.1	B9N49_05330	1075697	1076452	-1 bacitracin ABC transporter ATP-binding protein
1073690	1082406	8716 OXZ27237.1	B9N49_05335	1076436	1078589	-1 lantibiotic transporter
1073690	1082406	8716 OXZ27238.1	B9N49_05340	1078573	1080699	-1 hypothetical protein
1073690	1082406	8716 OXZ27239.1	B9N49_05345	1080671	1081477	-1 hypothetical protein
1073690	1082406	8716 OXZ27240.1	B9N49_05350	1081750	1082406	-1 DNA-binding protein
1090176	1097711	7535 OXZ27242.1	B9N49_05360	1090176	1092389	-1 hypothetical protein
1090176	1097711	7535 OXZ27243.1	B9N49_05365	1092425	1093387	-1 DNA (cytosine-5-)-methyltransferase
1090176	1097711	7535 OXZ27244.1	B9N49_05370	1093380	1095101	-1 DNA topoisomerase III
1090176	1097711	7535 OXZ27245.1	B9N49_05375	1095190	1096173	-1 hypothetical protein
1090176	1097711	7535 OXZ27246.1	B9N49_05380	1096166	1096777	-1 hypothetical protein
1090176	1097711	7535 OXZ27247.1	B9N49_05385	1096851	1097711	-1 bacteriocin
1107485	1112210	4725 OXZ27209.1	B9N49_05435	1107485	1107796	-1 single-stranded DNA-binding protein
1107485	1112210	4725	B9N49_05440	1107992	1109461	-1 hypothetical protein
1107485	1112210	4725 OXZ27210.1	B9N49_05445	1109479	1110015	-1 ClbS/DfsB family four-helix bundle protein
1107485	1112210	4725 OXZ27211.1	B9N49_05450	1110077	1110856	-1 conjugal transfer protein TraG
1107485	1112210	4725 OXZ27175.1	B9N49_05455	1112025	1112210	-1 hypothetical protein
1116939	1128106	11167 OXZ27181.1	B9N49_05485	1116939	1117214	-1 hypothetical protein
1116939	1128106	11167 OXZ27182.1	B9N49_05490	1117268	1118815	-1 hypothetical protein
1116939	1128106	11167 OXZ27183.1	B9N49_05495	1118812	1119522	-1 ABC transporter
1116939	1128106	11167 OXZ27184.1	B9N49_05500	1119589	1119897	-1 lysis protein
1116939	1128106	11167 OXZ27185.1	B9N49_05505	1119878	1120477	-1 hypothetical protein
1116939	1128106	11167 OXZ27186.1	B9N49_05510	1120467	1120742	-1 transcriptional regulator
1116939	1128106	11167 OXZ27187.1	B9N49_05515	1120873	1122723	-1 recombinase TnpX
1116939	1128106	11167 OXZ27034.1	B9N49_05520	1123890	1124942	-1 conjugal transfer protein TraG
1116939	1128106	11167 OXZ27035.1	B9N49_05525	1124935	1125669	-1 phage antirepressor Ant
1116939	1128106	11167 OXZ27036.1	B9N49_05530	1125666	1126151	-1 conjugal transfer protein
1116939	1128106	11167 OXZ27037.1	B9N49_05535	1126144	1126971	-1 nucleoside triphosphate hydrolase
1116939	1128106	11167 OXZ27038.1	B9N49_05540	1126968	1127741	-1 replication initiator protein A
1116939	1128106	11167 OXZ27039.1	B9N49_05545	1127825	1128106	-1 hypothetical protein
1464214	1499122	34908 OXZ26914.1	B9N49_07075	1464214	1465734	-1 conjugal transfer protein
1464214	1499122	34908 OXZ26915.1	B9N49_07080	1465727	1467469	-1 recombinase
1464214	1499122	34908 OXZ26916.1	B9N49_07085	1467462	1469180	-1 recombinase
1464214	1499122	34908 OXZ26917.1	B9N49_07090	1469279	1469446	-1 aminoacyl-tRNA hydrolase
1464214	1499122	34908 OXZ26918.1	B9N49_07095	1469899	1470372	-1 RNA polymerase subunit sigma
1464214	1499122	34908 OXZ26919.1	B9N49_07100	1471116	1472459	-1 MATE family efflux transporter
1464214	1499122	34908 OXZ26920.1	B9N49_07105	1472491	1474236	-1 ABC transporter permease
1464214	1499122	34908 OXZ26921.1	B9N49_07110	1474229	1476019	-1 ABC transporter ATP-binding protein
1464214	1499122	34908 OXZ26922.1	B9N49_07115	1476009	1477475	-1 ABC transporter
1464214	1499122	34908 OXZ26923.1	B9N49_07120	1477460	1478161	-1 ABC transporter permease
1464214	1499122	34908 OXZ26924.1	B9N49_07125	1478164	1478760	-1 hypothetical protein
1464214	1499122	34908 OXZ26925.1	B9N49_07130	1478902	1479540	-1 TetR family transcriptional regulator
1464214	1499122	34908 OXZ26926.1	B9N49_07135	1479648	1480358	-1 hypothetical protein
1464214	1499122	34908 OXZ26927.1	B9N49_07140	1480375	1481460	-1 hypothetical protein
1464214	1499122	34908 OXZ26928.1	B9N49_07145	1481471	1482445	-1 hypothetical protein
1464214	1499122	34908 OXZ26929.1	B9N49_07150	1482438	1487345	-1 hypothetical protein
1464214	1499122	34908 OXZ26930.1	B9N49_07155	1487345	1487614	-1 hypothetical protein
1464214	1499122	34908 OXZ26931.1	B9N49_07160	1487619	1488635	-1 hypothetical protein
1464214	1499122	34908 OXZ26932.1	B9N49_07165	1488653	1490071	-1 hypothetical protein
1464214	1499122	34908 OXZ26933.1	B9N49_07170	1490082	1493816	-1 hypothetical protein
1464214	1499122	34908 OXZ26780.1	B9N49_07175	1494883	1495941	-1 conjugal transfer protein TraG
1464214	1499122	34908 OXZ26781.1	B9N49_07180	1495986	1496192	-1 hypothetical protein
1464214	1499122	34908 OXZ26782.1	B9N49_07185	1496390	1496881	-1 hypothetical protein
1464214	1499122	34908 OXZ26783.1	B9N49_07190	1496896	1497753	-1 DNA replication protein
1464214	1499122	34908 OXZ26784.1	B9N49_07195	1497768	1498745	-1 replication initiator RepA
1464214	1499122	34908 OXZ26785.1	B9N49_07200	1498832	1499122	-1 hypothetical protein
1487619	1499122	11503 OXZ26931.1	B9N49_07160	1487619	1488635	-1 hypothetical protein
1487619	1499122	11503 OXZ26932.1	B9N49_07165	1488653	1490071	-1 hypothetical protein
1487619	1499122	11503 OXZ26933.1	B9N49_07170	1490082	1493816	-1 hypothetical protein
1487619	1499122	11503 OXZ26780.1	B9N49_07175	1494883	1495941	-1 conjugal transfer protein TraG
1487619	1499122	11503 OXZ26781.1	B9N49_07180	1495986	1496192	-1 hypothetical protein
1487619	1499122	11503 OXZ26782.1	B9N49_07185	1496390	1496881	-1 hypothetical protein
1487619	1499122	11503 OXZ26783.1	B9N49_07190	1496896	1497753	-1 DNA replication protein
1487619	1499122	11503 OXZ26784.1	B9N49_07195	1497768	1498745	-1 replication initiator RepA
1487619	1499122	11503 OXZ26785.1	B9N49_07200	1498832	1499122	-1 hypothetical protein
1535913	1544549	8636 OXZ26766.1	B9N49_07380	1535913	1536200	-1 cupin
1535913	1544549	8636 OXZ26767.1	B9N49_07385	1536268	1536840	-1 uracil-DNA glycosylase
1535913	1544549	8636 OXZ26768.1	B9N49_07390	1537611	1538900	-1 hypothetical protein
1535913	1544549	8636 OXZ26769.1	B9N49_07395	1539274	1540941	-1 DNA mismatch repair protein
1535913	1544549	8636 OXZ26770.1	B9N49_07400	1540951	1541985	-1 DNA (cytosine-5-)-methyltransferase
1535913	1544549	8636 OXZ26771.1	B9N49_07405	1542042	1542998	-1 restriction endonuclease
1535913	1544549	8636 OXZ26772.1	B9N49_07410	1543008	1544030	-1 DNA (cytosine-5-)-methyltransferase
1535913	1544549	8636 OXZ26773.1	B9N49_07415	1544017	1544253	-1 DNA-binding protein
1535913	1544549	8636 OXZ26774.1	B9N49_07420	1544361	1544549	-1 hypothetical protein
1612738	1655078	42340 OXZ26698.1	B9N49_07720	1612738	1613161	-1 MATE family efflux transporter
1612738	1655078	42340 OXZ26699.1	B9N49_07725	1613183	1614928	-1 ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26700.1	B9N49_07730	1614929	1616641	-1 ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26701.1	B9N49_07735	1616658	1618166	-1 ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26702.1	B9N49_07740	1618154	1618828	-1 hypothetical protein
1612738	1655078	42340 OXZ26703.1	B9N49_07745	1618846	1619448	-1 hypothetical protein
1612738	1655078	42340 OXZ26707.1	B9N49_07750	1619590	1620561	-1 AraC family transcriptional regulator
1612738	1655078	42340 OXZ26704.1	B9N49_07755	1620591	1621352	-1 alpha/beta hydrolase
1612738	1655078	42340 OXZ26705.1	B9N49_07760	1621336	1622415	-1 semialdehyde dehydrogenase
1612738	1655078	42340 OXZ26706.1	B9N49_07765	1622464	1627974	-1 non-ribosomal peptide synthetase

1612738	1655078	42340 OXZ26708.1	B9N49_07770	1627994	1629048	-1 hypothetical protein
1612738	1655078	42340 OXZ26697.1	B9N49_07775	1630103	1631170	-1 MATE family efflux transporter
1612738	1655078	42340 OXZ26589.1	B9N49_07780	1632171	1632409	1 IS30 family transposase
1612738	1655078	42340 OXZ26590.1	B9N49_07785	1632518	1633267	-1 phosphorylase
1612738	1655078	42340 OXZ26591.1	B9N49_07790	1633527	1635131	-1 macrolide ABC transporter ATP-binding protein
1612738	1655078	42340	B9N49_07795	1635454	1635747	-1 transposase
1612738	1655078	42340 OXZ26592.1	B9N49_07800	1635859	1636473	-1 hypothetical protein
1612738	1655078	42340 OXZ26593.1	B9N49_07805	1636678	1638042	-1 ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26594.1	B9N49_07810	1638030	1638725	-1 cobalt ABC transporter permease
1612738	1655078	42340 OXZ26595.1	B9N49_07815	1638725	1639309	-1 hypothetical protein
1612738	1655078	42340 OXZ26596.1	B9N49_07820	1639369	1640712	-1 MATE family efflux transporter
1612738	1655078	42340 OXZ26597.1	B9N49_07825	1640724	1642445	-1 ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26598.1	B9N49_07830	1642429	1644183	-1 ABC transporter ATP-binding protein
1612738	1655078	42340	B9N49_07835	1644344	1645335	1 AraC family transcriptional regulator
1612738	1655078	42340	B9N49_07840	1645700	1646460	-1 hypothetical protein
1612738	1655078	42340 OXZ26599.1	B9N49_07845	1646453	1648189	-1 multidrug ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26600.1	B9N49_07850	1648182	1649903	-1 ABC transporter ATP-binding protein
1612738	1655078	42340 OXZ26601.1	B9N49_07855	1649903	1651366	-1 ABC transporter
1612738	1655078	42340 OXZ26602.1	B9N49_07860	1651368	1652039	-1 cobalt transporter
1612738	1655078	42340 OXZ26603.1	B9N49_07865	1652036	1652626	-1 hypothetical protein
1612738	1655078	42340 OXZ26604.1	B9N49_07870	1652693	1653670	-1 AraC family transcriptional regulator
1612738	1655078	42340 OXZ26605.1	B9N49_07875	1653680	1654264	-1 TetR family transcriptional regulator
1612738	1655078	42340 OXZ26606.1	B9N49_07880	1654722	1655078	1 plasmid mobilization relaxosome protein MobC
1612738	1618828	6090 OXZ26698.1	B9N49_07720	1612738	1613161	-1 MATE family efflux transporter
1612738	1618828	6090 OXZ26699.1	B9N49_07725	1613183	1614928	-1 ABC transporter ATP-binding protein
1612738	1618828	6090 OXZ26700.1	B9N49_07730	1614929	1616641	-1 ABC transporter ATP-binding protein
1612738	1618828	6090 OXZ26701.1	B9N49_07735	1616658	1618166	-1 ABC transporter ATP-binding protein
1612738	1618828	6090 OXZ26702.1	B9N49_07740	1618154	1618828	-1 hypothetical protein
1635454	1640712	5258	B9N49_07795	1635454	1635747	-1 transposase
1635454	1640712	5258 OXZ26592.1	B9N49_07800	1635859	1636473	-1 hypothetical protein
1635454	1640712	5258 OXZ26593.1	B9N49_07805	1636678	1638042	-1 ABC transporter ATP-binding protein
1635454	1640712	5258 OXZ26594.1	B9N49_07810	1638030	1638725	-1 cobalt ABC transporter permease
1635454	1640712	5258 OXZ26595.1	B9N49_07815	1638725	1639309	-1 hypothetical protein
1635454	1640712	5258 OXZ26596.1	B9N49_07820	1639369	1640712	-1 MATE family efflux transporter
1663712	1668015	4303 OXZ26611.1	B9N49_07920	1663029	1663721	-1 MBL fold metallo-hydrolase
1663712	1668015	4303 OXZ26612.1	B9N49_07925	1663712	1664101	-1 cytidine deaminase
1663712	1668015	4303 OXZ26613.1	B9N49_07930	1664147	1664671	-1 hypothetical protein
1663712	1668015	4303 OXZ26614.1	B9N49_07935	1664888	1665619	23S rRNA (adenine(2058)-N(6))-
1663712	1668015	4303 OXZ26615.1	B9N49_07940	1666115	1666396	-1 methyltransferase Erm(A)
1663712	1668015	4303	B9N49_07945	1666428	1667165	-1 hypothetical protein
1663712	1668015	4303 OXZ26616.1	B9N49_07950	1667146	1668015	-1 SAM-dependent methyltransferase
1666115	1722368	56253 OXZ26615.1	B9N49_07940	1666115	1666396	-1 hypothetical protein
1666115	1722368	56253	B9N49_07945	1666428	1667165	-1 SAM-dependent methyltransferase
1666115	1722368	56253 OXZ26616.1	B9N49_07950	1667146	1668015	-1 hypothetical protein
1666115	1722368	56253 OXZ26617.1	B9N49_07955	1668719	1670290	-1 recombinase family protein
1666115	1722368	56253 OXZ26618.1	B9N49_07960	1670283	1670699	-1 integrase
1666115	1722368	56253 OXZ26619.1	B9N49_07965	1670692	1672254	-1 recombinase family protein
1666115	1722368	56253 OXZ26620.1	B9N49_07970	1672314	1672523	-1 hypothetical protein
1666115	1722368	56253 OXZ26621.1	B9N49_07975	1672887	1674623	-1 multidrug ABC transporter ATP-binding protein
1666115	1722368	56253 OXZ26622.1	B9N49_07980	1674616	1676334	-1 ABC transporter ATP-binding protein
1666115	1722368	56253 OXZ26623.1	B9N49_07985	1676339	1676929	-1 TetR family transcriptional regulator
1666115	1722368	56253 OXZ26624.1	B9N49_07990	1677106	1677915	-1 lysozyme
1666115	1722368	56253 OXZ26625.1	B9N49_07995	1677916	1678317	-1 holin
1666115	1722368	56253 OXZ26626.1	B9N49_08000	1678319	1679698	-1 hypothetical protein
1666115	1722368	56253 OXZ26627.1	B9N49_08005	1679685	1681556	-1 hypothetical protein
1666115	1722368	56253 OXZ26628.1	B9N49_08010	1681556	1681918	-1 hypothetical protein
1666115	1722368	56253 OXZ26629.1	B9N49_08015	1681918	1684983	-1 phage tail tape measure protein
1666115	1722368	56253 OXZ26630.1	B9N49_08020	1685073	1685396	1 prevent-host-death protein
1666115	1722368	56253 OXZ26631.1	B9N49_08025	1685393	1685722	1 addiction module toxin RelE
1666115	1722368	56253 OXZ26632.1	B9N49_08030	1685901	1686257	-1 hypothetical protein
1666115	1722368	56253 OXZ26633.1	B9N49_08035	1686260	1686856	-1 phage tail protein
1666115	1722368	56253 OXZ26634.1	B9N49_08040	1686846	1687025	-1 hypothetical protein
1666115	1722368	56253 OXZ26635.1	B9N49_08045	1687018	1687344	-1 hypothetical protein
1666115	1722368	56253 OXZ26636.1	B9N49_08050	1687337	1687717	-1 hypothetical protein
1666115	1722368	56253 OXZ26637.1	B9N49_08055	1687714	1688046	-1 phage head-tail adapter protein
1666115	1722368	56253 OXZ26638.1	B9N49_08060	1688046	1688318	-1 AraC family transcriptional regulator
1666115	1722368	56253 OXZ26639.1	B9N49_08065	1688329	1689519	-1 phage major capsid protein
1666115	1722368	56253 OXZ26640.1	B9N49_08070	1689522	1690208	-1 peptidase
1666115	1722368	56253 OXZ26641.1	B9N49_08075	1690198	1691472	-1 phage portal protein
1666115	1722368	56253 OXZ26642.1	B9N49_08080	1691499	1692395	-1 cell filamentation protein Fic
1666115	1722368	56253 OXZ26643.1	B9N49_08085	1692496	1694085	-1 terminase
1666115	1722368	56253 OXZ26644.1	B9N49_08090	1694178	1694408	-1 hypothetical protein
1666115	1722368	56253 OXZ26645.1	B9N49_08095	1694409	1694741	-1 hypothetical protein
1666115	1722368	56253 OXZ26646.1	B9N49_08100	1694822	1695052	-1 DUF4314 domain-containing protein
1666115	1722368	56253 OXZ26647.1	B9N49_08105	1695096	1696538	-1 DNA (cytosine-5-)-methyltransferase
1666115	1722368	56253 OXZ26648.1	B9N49_08110	1696531	1697766	-1 DNA modification methylase
1666115	1722368	56253 OXZ26649.1	B9N49_08115	1697763	1698545	-1 S-adenosylmethionine synthetase
1666115	1722368	56253 OXZ26650.1	B9N49_08120	1698551	1699198	-1 terminase
1666115	1722368	56253 OXZ26651.1	B9N49_08125	1699252	1699608	-1 HNH endonuclease
1666115	1722368	56253 OXZ26652.1	B9N49_08130	1699798	1700055	1 AbrB family transcriptional regulator
1666115	1722368	56253 OXZ26653.1	B9N49_08135	1700055	1700321	1 cytotoxin
1666115	1722368	56253 OXZ26654.1	B9N49_08140	1700398	1700799	-1 hypothetical protein
1666115	1722368	56253 OXZ26655.1	B9N49_08145	1700847	1702190	-1 DEAD/DEAH box helicase
1666115	1722368	56253 OXZ26656.1	B9N49_08150	1702191	1702472	-1 nuclease

1666115	1722368	56253 OXZ26657.1	B9N49_08155	1702430	1702687	-1 hypothetical protein
1666115	1722368	56253 OXZ26658.1	B9N49_08160	1702950	1705151	-1 DNA primase
1666115	1722368	56253 OXZ26659.1	B9N49_08165	1705152	1705538	-1 DUF4406 domain-containing protein
1666115	1722368	56253 OXZ26660.1	B9N49_08170	1705531	1705731	-1 hypothetical protein
1666115	1722368	56253 OXZ26661.1	B9N49_08175	1705745	1708603	-1 hypothetical protein
1666115	1722368	56253 OXZ26662.1	B9N49_08180	1708578	1708778	-1 hypothetical protein
1666115	1722368	56253 OXZ26663.1	B9N49_08185	1708788	1709375	-1 hypothetical protein
1666115	1722368	56253 OXZ26664.1	B9N49_08190	1709341	1710453	-1 nuclease
1666115	1722368	56253 OXZ26665.1	B9N49_08195	1710453	1710752	-1 hypothetical protein
1666115	1722368	56253 OXZ26666.1	B9N49_08200	1710694	1711065	-1 hypothetical protein
1666115	1722368	56253 OXZ26667.1	B9N49_08205	1711053	1711571	-1 RNA polymerase subunit sigma-70
1666115	1722368	56253 OXZ26668.1	B9N49_08210	1712143	1712928	-1 hypothetical protein
1666115	1722368	56253 OXZ26669.1	B9N49_08215	1712931	1713302	-1 transcriptional regulator 23S rRNA (uracil(1939)-C(5))-methyltransferase
1666115	1722368	56253 OXZ26670.1	B9N49_08220	1713553	1714767	-1 RlmD
1666115	1722368	56253 OXZ26671.1	B9N49_08225	1714860	1716656	-1 ABC transporter
1666115	1722368	56253 OXZ26672.1	B9N49_08230	1716649	1718409	-1 multidrug ABC transporter ATP-binding protein
1666115	1722368	56253 OXZ26673.1	B9N49_08235	1718384	1718860	-1 MarR family transcriptional regulator
1666115	1722368	56253 OXZ26674.1	B9N49_08240	1719023	1720324	-1 phosphomethylpyrimidine synthase cyclic pyranopterin monophosphate synthase
1666115	1722368	56253 OXZ26675.1	B9N49_08245	1720505	1721419	-1 MoaC
1666115	1722368	56253 OXZ26676.1	B9N49_08250	1721421	1722368	-1 GTP 3',8-cyclase MoaA
1904216	1927243	23027 OXZ26463.1	B9N49_09015	1904216	1904974	-1 metal-dependent hydrolase
1904216	1927243	23027 OXZ26464.1	B9N49_09020	1905100	1905570	1 aminoacyl-tRNA deacylase
1904216	1927243	23027 OXZ26465.1	B9N49_09025	1905573	1906877	1 glutamate--cysteine ligase
1904216	1927243	23027 OXZ26466.1	B9N49_09030	1906870	1908180	1 glutathionylspermidine synthase
1904216	1927243	23027 OXZ26467.1	B9N49_09035	1908279	1908548	-1 Txe/YoeB family addiction module toxin
1904216	1927243	23027 OXZ26468.1	B9N49_09040	1908542	1908790	-1 prevent-host-death protein
1904216	1927243	23027 OXZ26469.1	B9N49_09045	1908972	1909391	1 CMP deaminase
1904216	1927243	23027 OXZ26470.1	B9N49_09050	1909403	1912822	1 pyruvate carboxylase
1904216	1927243	23027 OXZ26471.1	B9N49_09055	1912883	1913277	-1 hypothetical protein
1904216	1927243	23027 OXZ26373.1	B9N49_09060	1914278	1914416	-1 transposase
1904216	1927243	23027 OXZ26374.1	B9N49_09065	1914481	1914885	-1 DUF3139 domain-containing protein
1904216	1927243	23027 OXZ26375.1	B9N49_09070	1915016	1915258	1 cell division protein FtsW
1904216	1927243	23027 OXZ26376.1	B9N49_09075	1915362	1915769	1 hypothetical protein
1904216	1927243	23027 OXZ26377.1	B9N49_09080	1915786	1916292	-1 thiol reductase thioredoxin
1904216	1927243	23027 OXZ26378.1	B9N49_09085	1916397	1916741	-1 hypothetical protein
1904216	1927243	23027 OXZ26379.1	B9N49_09090	1916809	1917498	-1 hypothetical protein
1904216	1927243	23027 OXZ26380.1	B9N49_09095	1917495	1922597	-1 FMN-binding domain-containing protein
1904216	1927243	23027 OXZ26446.1	B9N49_09100	1922842	1923795	-1 2-dehydropantoate 2-reductase
1904216	1927243	23027 OXZ26381.1	B9N49_09105	1923815	1925464	-1 inorganic pyrophosphatase
1904216	1927243	23027 OXZ26382.1	B9N49_09110	1925629	1926150	1 N-carbamoylsarcosine amidohydrolase
1904216	1927243	23027 OXZ26383.1	B9N49_09115	1926192	1926818	1 hypothetical protein
1904216	1927243	23027 OXZ26384.1	B9N49_09120	1926887	1927243	-1 hypothetical protein
1978424	2050817	72393 OXZ26444.1	B9N49_09450	1978424	1978642	1 hypothetical protein
1978424	2050817	72393 OXZ26445.1	B9N49_09455	1978652	1978798	1 YvrJ family protein
1978424	2050817	72393 OXZ26339.1	B9N49_09620	1982645	1984502	-1 hypothetical protein
1978424	2050817	72393 OXZ26340.1	B9N49_09625	1984526	1985835	-1 2,3-dihydroxybenzoate-AMP ligase
1978424	2050817	72393 OXZ26306.1	B9N49_09730	1990594	1990988	-1 IS3 family transposase
1978424	2050817	72393 OXZ26307.1	B9N49_09735	1991183	1991626	-1 transposase
1978424	2050817	72393 OXZ26272.1	B9N49_09745	1992786	1993660	1 IS30 family transposase
1978424	2050817	72393 OXZ26341.1	B9N49_09560	1994661	1995031	-1 thioesterase
1978424	2050817	72393 OXZ26342.1	B9N49_09565	1995194	1995565	-1 transcriptional regulator
1978424	2050817	72393 OXZ26343.1	B9N49_09570	1995941	1996297	1 plasmid mobilization relaxosome protein MobC
1978424	2050817	72393 OXZ26344.1	B9N49_09575	1996299	1997630	1 endonuclease
1978424	2050817	72393 OXZ26345.1	B9N49_09580	1998089	1999705	-1 ABC transporter-like protein
1978424	2050817	72393 OXZ26346.1	B9N49_09585	1999720	2001807	-1 ABC transporter permease
1978424	2050817	72393 OXZ26347.1	B9N49_09590	2001809	2002483	-1 ABC transporter ATP-binding protein
1978424	2050817	72393 OXZ26348.1	B9N49_09595	2002493	2003836	-1 radical SAM domain-containing protein
1978424	2050817	72393 OXZ26349.1	B9N49_09600	2004202	2004630	-1 hypothetical protein
1978424	2050817	72393 OXZ26350.1	B9N49_09605	2004643	2004906	-1 hypothetical protein
1978424	2050817	72393 OXZ26351.1	B9N49_09610	2004900	2005469	-1 hypothetical protein
1978424	2050817	72393 OXZ26352.1	B9N49_09615	2005823	2006014	1 hypothetical protein
1978424	2050817	72393 OXZ26328.1	B9N49_09680	2007188	2007334	1 hypothetical protein
1978424	2050817	72393 OXZ26329.1	B9N49_09685	2007336	2008199	1 hypothetical protein
1978424	2050817	72393 OXZ26330.1	B9N49_09690	2008217	2008474	1 hypothetical protein
1978424	2050817	72393	B9N49_09695	2008474	2008623	1 conjugal transfer protein
1978424	2050817	72393 OXZ26331.1	B9N49_09700	2008662	2008749	-1 hypothetical protein
1978424	2050817	72393 OXZ26178.1	B9N49_09775	2009750	2010348	1 hypothetical protein
1978424	2050817	72393 OXZ26337.1	B9N49_09630	2011349	2013215	-1 non-ribosomal peptide synthetase
1978424	2050817	72393 OXZ26338.1	B9N49_09635	2013228	2014531	-1 2,3-dihydroxybenzoate-AMP ligase
1978424	2050817	72393 OXZ26273.1	B9N49_09740	2015532	2016545	-1 elongation factor Tu
1978424	2050817	72393 OXZ26181.1	B9N49_09755	2017546	2017915	-1 phage antirepressor Ant
1978424	2050817	72393 OXZ26182.1	B9N49_09760	2017912	2018226	-1 hypothetical protein
1978424	2050817	72393 OXZ26308.1	B9N49_09720	2019290	2019847	1 transposase
1978424	2050817	72393 OXZ26309.1	B9N49_09725	2019874	2020704	1 hypothetical protein
1978424	2050817	72393 OXZ26332.1	B9N49_09670	2021838	2023118	-1 group II intron reverse transcriptase/maturase
1978424	2050817	72393	B9N49_09650	2024585	2025400	1 conjugal transfer protein TraG
1978424	2050817	72393 OXZ26333.1	B9N49_09655	2025552	2026418	1 CAAX protease
1978424	2050817	72393 OXZ26334.1	B9N49_09660	2026609	2026932	1 single-stranded DNA-binding protein
1978424	2050817	72393 OXZ26335.1	B9N49_09665	2026933	2027064	1 hypothetical protein
1978424	2050817	72393 OXZ26336.1	B9N49_09640	2028341	2030200	-1 group II intron reverse transcriptase/maturase
1978424	2050817	72393 OXZ26179.1	B9N49_09765	2031943	2032029	1 hypothetical protein
1978424	2050817	72393 OXZ26180.1	B9N49_09770	2032256	2032620	-1 hypothetical protein
1978424	2050817	72393 OXZ26353.1	B9N49_09460	2033621	2033706	1 hypothetical protein
1978424	2050817	72393 OXZ26354.1	B9N49_09465	2033784	2034179	-1 hypothetical protein
1978424	2050817	72393 OXZ26355.1	B9N49_09470	2034121	2034435	-1 hypothetical protein

1978424	2050817	72393 OXZ26356.1	B9N49_09475	2034641	2034817	-1 lantibiotic salivaricin M precursor
1978424	2050817	72393 OXZ26357.1	B9N49_09480	2034941	2035561	1 DNA-binding protein
1978424	2050817	72393 OXZ26358.1	B9N49_09485	2035862	2037409	1 hypothetical protein
1978424	2050817	72393 OXZ26359.1	B9N49_09490	2037381	2037986	1 DNA-binding response regulator
1978424	2050817	72393 OXZ26360.1	B9N49_09495	2038268	2040454	1 radical SAM protein CXXX repeat peptide modification system
1978424	2050817	72393 OXZ26361.1	B9N49_09500	2040456	2040722	1 protein
1978424	2050817	72393 OXZ26362.1	B9N49_09505	2040715	2042352	1 ABC transporter permease
1978424	2050817	72393 OXZ26363.1	B9N49_09510	2042936	2044330	1 hypothetical protein
1978424	2050817	72393 OXZ26364.1	B9N49_09515	2044333	2045364	1 hypothetical protein
1978424	2050817	72393 OXZ26365.1	B9N49_09520	2045515	2046402	1 hypothetical protein
1978424	2050817	72393 OXZ26366.1	B9N49_09525	2046419	2046700	1 hypothetical protein
1978424	2050817	72393 OXZ26367.1	B9N49_09530	2046712	2047179	1 hypothetical protein
1978424	2050817	72393 OXZ26368.1	B9N49_09535	2047188	2047391	1 hypothetical protein
1978424	2050817	72393 OXZ26369.1	B9N49_09540	2047388	2048299	1 hypothetical protein
1978424	2050817	72393 OXZ26370.1	B9N49_09545	2048325	2049098	1 hypothetical protein
1978424	2050817	72393 OXZ26371.1	B9N49_09550	2049095	2050033	1 hypothetical protein
1978424	2050817	72393 OXZ26372.1	B9N49_09555	2050026	2050817	1 hypothetical protein
1978652	1985835	7183 OXZ26445.1	B9N49_09455	1978652	1978798	1 YvrJ family protein
1978652	1985835	7183 OXZ26339.1	B9N49_09620	1982645	1984502	-1 hypothetical protein
1978652	1985835	7183 OXZ26340.1	B9N49_09625	1984526	1985835	-1 2,3-dihydroxybenzoate-AMP ligase
1991183	2004906	13723 OXZ26307.1	B9N49_09735	1991183	1991626	-1 transposase
1991183	2004906	13723 OXZ26272.1	B9N49_09745	1992786	1993660	1 IS30 family transposase
1991183	2004906	13723 OXZ26341.1	B9N49_09560	1994661	1995031	-1 thioesterase
1991183	2004906	13723 OXZ26342.1	B9N49_09565	1995194	1995565	-1 transcriptional regulator
1991183	2004906	13723 OXZ26343.1	B9N49_09570	1995941	1996297	1 plasmid mobilization relaxosome protein MobC
1991183	2004906	13723 OXZ26344.1	B9N49_09575	1996299	1997630	1 endonuclease
1991183	2004906	13723 OXZ26345.1	B9N49_09580	1998089	1999705	-1 ABC transporter-like protein
1991183	2004906	13723 OXZ26346.1	B9N49_09585	1999720	2001807	-1 ABC transporter permease
1991183	2004906	13723 OXZ26347.1	B9N49_09590	2001809	2002483	-1 ABC transporter ATP-binding protein
1991183	2004906	13723 OXZ26348.1	B9N49_09595	2002493	2003836	-1 radical SAM domain-containing protein
1991183	2004906	13723 OXZ26349.1	B9N49_09600	2004202	2004630	-1 hypothetical protein
1991183	2004906	13723 OXZ26350.1	B9N49_09605	2004643	2004906	-1 hypothetical protein
1991183	2004906	13723 OXZ26351.1	B9N49_09610	2004900	2005469	-1 hypothetical protein
2017546	2026418	8872 OXZ26181.1	B9N49_09755	2017546	2017915	-1 phage antirepressor Ant
2017546	2026418	8872 OXZ26182.1	B9N49_09760	2017912	2018226	-1 hypothetical protein
2017546	2026418	8872 OXZ26308.1	B9N49_09720	2019290	2019847	1 transposase
2017546	2026418	8872 OXZ26309.1	B9N49_09725	2019874	2020704	1 hypothetical protein
2017546	2026418	8872 OXZ26332.1	B9N49_09670	2021838	2023118	-1 group II intron reverse transcriptase/maturase
2017546	2026418	8872	B9N49_09650	2024585	2025400	1 conjugal transfer protein TraG
2017546	2026418	8872 OXZ26333.1	B9N49_09655	2025552	2026418	1 CAAX protease
2046419	2056025	9606 OXZ26366.1	B9N49_09525	2046419	2046700	1 hypothetical protein
2046419	2056025	9606 OXZ26367.1	B9N49_09530	2046712	2047179	1 hypothetical protein
2046419	2056025	9606 OXZ26368.1	B9N49_09535	2047188	2047391	1 hypothetical protein
2046419	2056025	9606 OXZ26369.1	B9N49_09540	2047388	2048299	1 hypothetical protein
2046419	2056025	9606 OXZ26370.1	B9N49_09545	2048325	2049098	1 hypothetical protein
2046419	2056025	9606 OXZ26371.1	B9N49_09550	2049095	2050033	1 hypothetical protein
2046419	2056025	9606 OXZ26372.1	B9N49_09555	2050026	2050817	1 hypothetical protein
2046419	2056025	9606 OXZ26325.1	B9N49_09705	2052644	2053152	1 thioesterase
2046419	2056025	9606 OXZ26326.1	B9N49_09710	2053142	2053834	1 4-phosphopantetheinyl transferase
2046419	2056025	9606 OXZ26327.1	B9N49_09715	2053834	2054243	1 2,3-dihydroxybenzoate-AMP ligase
2046419	2056025	9606 OXZ26271.1	B9N49_09750	2055244	2056025	-1 hypothetical protein

Table S3I: Predicted genomic islands in the genome of "F. nericia" T151023

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
81511	88758	7247	OXZ29531.1	B9N51_00605	79542	81530	1	exopolyphosphatase
81511	88758	7247	OXZ29532.1	B9N51_00610	81511	81957	1	50S ribosomal protein L9
81511	88758	7247	OXZ29533.1	B9N51_00615	81991	83328	1	replicative DNA helicase
81511	88758	7247	OXZ29534.1	B9N51_00620	83325	83888	1	GNAT family N-acetyltransferase
81511	88758	7247	OXZ29535.1	B9N51_00625	83893	84651	1	DNA replication protein
81511	88758	7247	OXZ29536.1	B9N51_00630	84654	85631	1	DNA replication protein DnaC
81511	88758	7247	OXZ29537.1	B9N51_00635	85628	86272	1	NAD(P)H-hydrate epimerase
81511	88758	7247	OXZ29538.1	B9N51_00640	86777	87319	1	ECF transporter S component
81511	88758	7247	OXZ29539.1	B9N51_00645	87303	87989	1	radical SAM protein
81511	88758	7247	OXZ29540.1	B9N51_00650	88054	88758	1	hypothetical protein
143045	188929	45884	OXZ29593.1	B9N51_00925	143045	143674	1	50S ribosomal protein L3
143045	188929	45884	OXZ29594.1	B9N51_00930	143690	144313	1	50S ribosomal protein L4
143045	188929	45884	OXZ29595.1	B9N51_00935	144313	144603	1	50S ribosomal protein L23
143045	188929	45884	OXZ29596.1	B9N51_00940	144620	145450	1	50S ribosomal protein L2
143045	188929	45884	OXZ29597.1	B9N51_00945	145463	145747	1	30S ribosomal protein S19
143045	188929	45884	OXZ29598.1	B9N51_00950	145765	146103	1	50S ribosomal protein L22
143045	188929	45884	OXZ29599.1	B9N51_00955	146115	146849	1	30S ribosomal protein S3
143045	188929	45884	OXZ29600.1	B9N51_00960	146871	147314	1	50S ribosomal protein L16
143045	188929	45884	OXZ29601.1	B9N51_00965	147304	147510	1	50S ribosomal protein L29
143045	188929	45884	OXZ29602.1	B9N51_00970	147516	147770	1	30S ribosomal protein S17
143045	188929	45884	OXZ29603.1	B9N51_00975	147795	148163	1	50S ribosomal protein L14
143045	188929	45884	OXZ29604.1	B9N51_00980	148182	148490	1	50S ribosomal protein L24
143045	188929	45884	OXZ29605.1	B9N51_00985	148509	149051	1	50S ribosomal protein L5
143045	188929	45884	OXZ29606.1	B9N51_00990	149064	149249	1	30S ribosomal protein S14 type Z
143045	188929	45884	OXZ29607.1	B9N51_00995	149271	149666	1	30S ribosomal protein S8
143045	188929	45884	OXZ29608.1	B9N51_01000	149693	150232	1	50S ribosomal protein L6
143045	188929	45884	OXZ29609.1	B9N51_01005	150247	150609	1	50S ribosomal protein L18
143045	188929	45884	OXZ29610.1	B9N51_01010	150630	151136	1	30S ribosomal protein S5
143045	188929	45884	OXZ29611.1	B9N51_01015	151150	151332	1	50S ribosomal protein L30
143045	188929	45884	OXZ29612.1	B9N51_01020	151344	151793	1	50S ribosomal protein L15
143045	188929	45884	OXZ29613.1	B9N51_01025	151795	153069	1	preprotein translocase subunit SecY
143045	188929	45884	OXZ29614.1	B9N51_01030	153080	153727	1	adenylate kinase
143045	188929	45884	OXZ29615.1	B9N51_01035	153733	154017	1	KOW domain-containing protein
143045	188929	45884	OXZ29616.1	B9N51_01040	153998	154213	1	translation initiation factor IF-1
143045	188929	45884	OXZ29617.1	B9N51_01045	154228	154341	1	50S ribosomal protein L36
143045	188929	45884	OXZ29618.1	B9N51_01050	154354	154704	1	30S ribosomal protein S13
143045	188929	45884	OXZ29619.1	B9N51_01055	154720	155127	1	30S ribosomal protein S11
143045	188929	45884	OXZ29620.1	B9N51_01060	155183	156136	1	DNA-directed RNA polymerase subunit alpha
143045	188929	45884	OXZ29621.1	B9N51_01065	156150	156545	1	50S ribosomal protein L17
143045	188929	45884	OXZ29622.1	B9N51_01070	156909	158750	1	hypothetical protein
143045	188929	45884	OXZ29623.1	B9N51_01075	159388	161361	1	N-acetylmuramoyl-L-alanine amidase
143045	188929	45884	OXZ29624.1	B9N51_01080	161458	162054	1	30S ribosomal protein S4
143045	188929	45884	OXZ29625.1	B9N51_01085	162158	163393	1	peptidoglycan-binding protein
143045	188929	45884	OXZ29524.1	B9N51_01130	167644	171711	1	hypothetical protein
143045	188929	45884	OXZ29525.1	B9N51_01135	171807	171895	-1	hypothetical protein
143045	188929	45884	OXZ29516.1	B9N51_01140	173176	182115	1	hypothetical protein
143045	188929	45884	OXZ29517.1	B9N51_01145	182248	182928	1	hypothetical protein
143045	188929	45884	OXZ29518.1	B9N51_01150	183357	185522	1	hypothetical protein
143045	188929	45884	OXZ29519.1	B9N51_01155	185644	187059	1	cell wall anchor protein
143045	188929	45884	OXZ29520.1	B9N51_01160	187237	188103	1	class C sortase
143045	188929	45884	OXZ29521.1	B9N51_01165	188090	188929	1	class C sortase
143045	188929	45884	OXZ29522.1	B9N51_01170	188916	189767	1	class C sortase
210413	218373	7960	OXZ29323.1	B9N51_01710	210413	210874	1	CtsR family transcriptional regulator
210413	218373	7960	OXZ29324.1	B9N51_01715	210885	211484	1	hypothetical protein
210413	218373	7960	OXZ29325.1	B9N51_01720	211477	212472	1	ATP--guanido phosphotransferase ATP-dependent Clp protease ATP-binding
210413	218373	7960	OXZ29326.1	B9N51_01725	212469	214889	1	protein ClpC
210413	218373	7960	OXZ29327.1	B9N51_01730	214891	216252	1	DNA repair protein RadA
210413	218373	7960	OXZ29328.1	B9N51_01735	216281	216586	-1	hypothetical protein
210413	218373	7960	OXZ29329.1	B9N51_01740	216688	218373	-1	M3 family oligoendopeptidase
598893	604825	5932	OXZ28763.1	B9N51_03760	598893	599084	1	50S ribosomal protein L35
598893	604825	5932	OXZ28764.1	B9N51_03765	599103	599456	1	50S ribosomal protein L20
598893	604825	5932	OXZ28765.1	B9N51_03770	599488	599763	-1	hypothetical protein
598893	604825	5932	OXZ28766.1	B9N51_03775	599763	600380	-1	recombinase RecX
598893	604825	5932	OXZ28767.1	B9N51_03780	600569	600808	1	hypothetical protein
598893	604825	5932	OXZ28768.1	B9N51_03785	600817	601893	1	phosphoesterase
598893	604825	5932	OXZ28769.1	B9N51_03790	601890	604142	1	DNA repair protein Rad50
598893	604825	5932	OXZ28770.1	B9N51_03795	604145	604825	1	serine/threonine protein phosphatase
614359	676348	61989	OXZ28780.1	B9N51_03845	614359	615057	1	DNA-binding response regulator
614359	676348	61989	OXZ28781.1	B9N51_03850	615099	615683	1	peptidylprolyl isomerase
614359	676348	61989	OXZ28782.1	B9N51_03855	615685	616296	1	thymidine kinase
614359	676348	61989	OXZ28783.1	B9N51_03860	616339	616809	-1	S-ribosylhomocysteine lyase
614359	676348	61989	OXZ28784.1	B9N51_03865	616818	617921	-1	rod shape-determining protein RodA
614359	676348	61989	OXZ28785.1	B9N51_03870	618006	618839	1	endonuclease IV
614359	676348	61989	OXZ28786.1	B9N51_03875	618820	619446	1	endonuclease III
614359	676348	61989	OXZ28787.1	B9N51_03880	619515	620435	1	aspartate carbamoyltransferase aspartate carbamoyltransferase regulatory
614359	676348	61989	OXZ28788.1	B9N51_03885	620435	620863	1	subunit
614359	676348	61989	OXZ28789.1	B9N51_03890	620863	622059	1	dihydroorotase
614359	676348	61989	OXZ28790.1	B9N51_03895	622046	622897	1	orotidine-5'-phosphate decarboxylase dihydroorotate dehydrogenase electron transfer
614359	676348	61989	OXZ28791.1	B9N51_03900	622890	623606	1	subunit

614359	676348	61989 OXZ28792.1	B9N51_03905	623599	624495	dihydroorotate dehydrogenase B catalytic 1 subunit
614359	676348	61989 OXZ28793.1	B9N51_03910	624506	625078	1 orotate phosphoribosyltransferase
614359	676348	61989 OXZ28794.1	B9N51_03915	625207	625911	1 isoprenyl transferase
614359	676348	61989 OXZ28795.1	B9N51_03920	625908	626687	1 phosphatidate cytidyltransferase
614359	676348	61989 OXZ28796.1	B9N51_03925	626700	627704	1 RIP metalloprotease RseP 4-hydroxy-3-methylbut-2-en-1-yl diphosphate
614359	676348	61989 OXZ28797.1	B9N51_03930	627755	628804	1 synthase
614359	676348	61989 OXZ28798.1	B9N51_03935	628805	633070	1 PolC-type DNA polymerase III
614359	676348	61989 OXZ28799.1	B9N51_03940	633103	634086	1 phosphate starvation-inducible protein PhoH
614359	676348	61989 OXZ28800.1	B9N51_03945	634067	634528	1 rRNA maturation RNase YbeY
614359	676348	61989 OXZ28801.1	B9N51_03950	634512	635255	1 diacylglycerol kinase
614359	676348	61989 OXZ28802.1	B9N51_03955	635263	635658	1 cytidine deaminase
614359	676348	61989 OXZ28803.1	B9N51_03960	635651	636535	1 GTPase Era
614359	676348	61989 OXZ28804.1	B9N51_03965	636535	637239	1 DNA repair protein RecO
614359	676348	61989 OXZ28805.1	B9N51_03970	637249	638937	1 hypothetical protein
614359	676348	61989 OXZ28806.1	B9N51_03975	638948	639739	1 hypothetical protein
614359	676348	61989 OXZ28807.1	B9N51_03980	639829	641271	1 serine/threonine protein kinase
614359	676348	61989 OXZ28808.1	B9N51_03985	641273	641947	1 protein phosphatase tRNA (N6-isopentenyl adenosine(37)-C2)-
614359	676348	61989 OXZ28809.1	B9N51_03990	642004	643389	1 methylthiotransferase MiaB
614359	676348	61989 OXZ28810.1	B9N51_03995	643391	645970	1 DNA mismatch repair protein MutS
614359	676348	61989 OXZ28811.1	B9N51_04000	645963	647846	1 DNA mismatch repair protein MutL tRNA (adenosine(37)-N6)-
614359	676348	61989 OXZ28812.1	B9N51_04005	647843	648787	1 dimethylallyltransferase MiaA
614359	676348	61989 OXZ28813.1	B9N51_04010	648774	650048	1 hypothetical protein
614359	676348	61989 OXZ28814.1	B9N51_04015	650099	650725	-1 LexA repressor
614359	676348	61989 OXZ28815.1	B9N51_04020	650900	651211	1 peptidoglycan-binding protein LysM
614359	676348	61989 OXZ28816.1	B9N51_04025	651291	652271	-1 recombinase XerC
614359	676348	61989	B9N51_04030	652377	653553	-1 aspartate aminotransferase
614359	676348	61989 OXZ28817.1	B9N51_04035	653540	654361	-1 metal-dependent phosphoesterase
614359	676348	61989 OXZ28818.1	B9N51_04040	654430	655971	-1 ribonuclease Y
614359	676348	61989 OXZ28819.1	B9N51_04045	656090	656752	-1 chromosome partitioning protein ParA
614359	676348	61989 OXZ28820.1	B9N51_04050	656739	656978	-1 hypothetical protein
614359	676348	61989 OXZ28821.1	B9N51_04055	656978	658561	-1 exonuclease SbcC
614359	676348	61989 OXZ28822.1	B9N51_04060	658561	659511	-1 phosphoesterase
614359	676348	61989 OXZ28822.1	B9N51_04065	659542	660633	-1 recombinase RecA CDP-diacylglycerol--glycerol-3-phosphate 3-
614359	676348	61989 OXZ28823.1	B9N51_04070	660702	661238	-1 phosphatidyltransferase
614359	676348	61989 OXZ28824.1	B9N51_04075	661240	663465	-1 cell division protein FtsK deoxyuridine 5'-triphosphate
614359	676348	61989 OXZ28825.1	B9N51_04080	663468	663899	-1 nucleotidohydrolase
614359	676348	61989 OXZ28826.1	B9N51_04085	663951	666095	-1 polyribonucleotide nucleotidyltransferase
614359	676348	61989 OXZ28827.1	B9N51_04090	666142	666408	-1 30S ribosomal protein S15
614359	676348	61989 OXZ28828.1	B9N51_04095	666489	667415	-1 riboflavin biosynthesis protein RibF
614359	676348	61989 OXZ28829.1	B9N51_04100	667406	668269	-1 tRNA pseudouridine(55) synthase TruB
614359	676348	61989 OXZ28830.1	B9N51_04105	668253	669221	-1 exopolyphosphatase
614359	676348	61989 OXZ28831.1	B9N51_04110	669211	669576	-1 ribosome-binding factor A
614359	676348	61989 OXZ28832.1	B9N51_04115	669584	671884	-1 translation initiation factor IF-2
614359	676348	61989 OXZ28833.1	B9N51_04120	671903	672166	-1 RNA-binding protein transcription termination/antitermination protein
614359	676348	61989 OXZ28834.1	B9N51_04125	672192	673466	-1 NusA
614359	676348	61989 OXZ28835.1	B9N51_04130	673476	673940	-1 ribosome maturation factor
614359	676348	61989 OXZ28836.1	B9N51_04135	674047	674460	-1 hypothetical protein
614359	676348	61989 OXZ28837.1	B9N51_04140	674460	675443	-1 hypothetical protein
614359	676348	61989 OXZ28838.1	B9N51_04145	675445	676062	-1 nodulation efficiency protein D
614359	676348	61989 OXZ28839.1	B9N51_04150	676169	676348	-1 30S ribosomal protein S21
858783	869107	10324 OXZ28383.1	B9N51_04985	858783	860063	1 hypothetical protein
858783	869107	10324 OXZ28384.1	B9N51_04990	860056	860400	1 hypothetical protein
858783	869107	10324 OXZ28250.1	B9N51_04995	861555	861643	1 hypothetical protein
858783	869107	10324 OXZ28251.1	B9N51_05000	861771	862706	-1 sugar ABC transporter permease
858783	869107	10324 OXZ28252.1	B9N51_05005	862706	863806	-1 ABC transporter permease
858783	869107	10324 OXZ28253.1	B9N51_05010	863796	865328	-1 heme ABC transporter ATP-binding protein BMP family ABC transporter substrate-binding
858783	869107	10324 OXZ28254.1	B9N51_05015	865394	866470	-1 protein
858783	869107	10324 OXZ28255.1	B9N51_05020	866710	867735	1 NADH dehydrogenase subunit
858783	869107	10324 OXZ28256.1	B9N51_05025	867758	869107	-1 uracil permease
1340012	1346417	6405 OXZ27371.1	B9N51_07210	1340012	1340278	-1 hypothetical protein
1340012	1346417	6405 OXZ27372.1	B9N51_07215	1340262	1340555	-1 hypothetical protein
1340012	1346417	6405 OXZ27373.1	B9N51_07220	1340686	1341210	1 DNA topology modulation protein FlaR
1340012	1346417	6405	B9N51_07225	1341893	1343837	-1 cell wall protein
1340012	1346417	6405 OXZ27374.1	B9N51_07230	1344543	1344977	-1 GNAT family N-acetyltransferase
1340012	1346417	6405 OXZ27375.1	B9N51_07235	1345000	1345698	-1 hypothetical protein
1340012	1346417	6405 OXZ27376.1	B9N51_07240	1345698	1346417	-1 peptidase S51
1378722	1422726	44004 OXZ29512.1	B9N51_01610	1378722	1379030	-1 exosortase
1378722	1422726	44004 OXZ29511.1	B9N51_01605	1379036	1379707	-1 ATPase
1378722	1422726	44004 OXZ29510.1	B9N51_01600	1379912	1381450	-1 hypothetical protein
1378722	1422726	44004 OXZ29509.1	B9N51_01595	1381626	1383134	-1 AAA family ATPase
1378722	1422726	44004 OXZ29508.1	B9N51_01590	1383877	1384767	-1 methionine sulfoxide reductase
1378722	1422726	44004 OXZ29507.1	B9N51_01585	1385002	1386354	-1 hemolysin
1378722	1422726	44004	B9N51_01580	1386767	1387560	-1 lysophospholipase
1378722	1422726	44004 OXZ29506.1	B9N51_01575	1387770	1390295	-1 hypothetical protein
1378722	1422726	44004	B9N51_01570	1390527	1390706	-1 hypothetical protein
1378722	1422726	44004	B9N51_01565	1390676	1390825	-1 protein-S-isoprenylcysteine methyltransferase
1378722	1422726	44004 OXZ29505.1	B9N51_01560	1390839	1391777	-1 esterase
1378722	1422726	44004 OXZ29504.1	B9N51_01555	1391846	1392472	-1 hypothetical protein
1378722	1422726	44004 OXZ29503.1	B9N51_01550	1392500	1393108	-1 SAM-dependent methyltransferase

1378722	1422726	44004 OXZ29502.1	B9N51_01545	1393324	1394073	-1 phosphorylase
1378722	1422726	44004 OXZ29501.1	B9N51_01540	1394196	1395803	-1 macrolide ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29500.1	B9N51_01535	1396207	1396821	-1 hypothetical protein
1378722	1422726	44004 OXZ29499.1	B9N51_01530	1397160	1398557	-1 ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29498.1	B9N51_01525	1398550	1399266	-1 cobalt transporter
1378722	1422726	44004 OXZ29497.1	B9N51_01520	1399263	1399862	-1 hypothetical protein
1378722	1422726	44004 OXZ29496.1	B9N51_01515	1399872	1401593	-1 ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29495.1	B9N51_01510	1401577	1403331	-1 ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29494.1	B9N51_01505	1403492	1404484	1 AraC family transcriptional regulator
1378722	1422726	44004 OXZ29493.1	B9N51_01500	1404669	1405148	-1 mercury transporter
1378722	1422726	44004 OXZ29492.1	B9N51_01495	1405547	1405960	-1 hypothetical protein
1378722	1422726	44004 OXZ29491.1	B9N51_01490	1406031	1406336	-1 hypothetical protein
1378722	1422726	44004	B9N51_01485	1406504	1406635	-1 adenine methylase
1378722	1422726	44004 OXZ29514.1	B9N51_01480	1406849	1407139	-1 RNA methyltransferase
1378722	1422726	44004 OXZ29490.1	B9N51_01475	1407153	1408907	-1 recombinase family protein
1378722	1422726	44004 OXZ29489.1	B9N51_01470	1409399	1410751	-1 MATE family efflux transporter
1378722	1422726	44004 OXZ29488.1	B9N51_01465	1410773	1412518	-1 ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29487.1	B9N51_01460	1412519	1414231	-1 ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29486.1	B9N51_01455	1414247	1415755	-1 ABC transporter ATP-binding protein
1378722	1422726	44004 OXZ29485.1	B9N51_01450	1415743	1416417	-1 hypothetical protein
1378722	1422726	44004 OXZ29484.1	B9N51_01445	1416435	1417037	-1 hypothetical protein
1378722	1422726	44004 OXZ29483.1	B9N51_01440	1417179	1418150	-1 AraC family transcriptional regulator
1378722	1422726	44004 OXZ29482.1	B9N51_01435	1418470	1419747	-1 IS110 family transposase
1378722	1422726	44004 OXZ29481.1	B9N51_01430	1420159	1420500	1 plasmid mobilization relaxosome protein MobC
1378722	1422726	44004 OXZ29480.1	B9N51_01425	1420822	1422726	-1 DNA helicase UvrD
1378722	1422726	44004 OXZ29479.1	B9N51_01420	1422714	1424804	-1 ATP-dependent endonuclease
1393324	1399862	6538 OXZ29502.1	B9N51_01545	1393324	1394073	-1 phosphorylase
1393324	1399862	6538 OXZ29501.1	B9N51_01540	1394196	1395803	-1 macrolide ABC transporter ATP-binding protein
1393324	1399862	6538 OXZ29500.1	B9N51_01535	1396207	1396821	-1 hypothetical protein
1393324	1399862	6538 OXZ29499.1	B9N51_01530	1397160	1398557	-1 ABC transporter ATP-binding protein
1393324	1399862	6538 OXZ29498.1	B9N51_01525	1398550	1399266	-1 cobalt transporter
1393324	1399862	6538 OXZ29497.1	B9N51_01520	1399263	1399862	-1 hypothetical protein
1405547	1418150	12603 OXZ29492.1	B9N51_01495	1405547	1405960	-1 hypothetical protein
1405547	1418150	12603 OXZ29491.1	B9N51_01490	1406031	1406336	-1 hypothetical protein
1405547	1418150	12603	B9N51_01485	1406504	1406635	-1 adenine methylase
1405547	1418150	12603 OXZ29514.1	B9N51_01480	1406849	1407139	-1 RNA methyltransferase
1405547	1418150	12603 OXZ29490.1	B9N51_01475	1407153	1408907	-1 recombinase family protein
1405547	1418150	12603 OXZ29489.1	B9N51_01470	1409399	1410751	-1 MATE family efflux transporter
1405547	1418150	12603 OXZ29488.1	B9N51_01465	1410773	1412518	-1 ABC transporter ATP-binding protein
1405547	1418150	12603 OXZ29487.1	B9N51_01460	1412519	1414231	-1 ABC transporter ATP-binding protein
1405547	1418150	12603 OXZ29486.1	B9N51_01455	1414247	1415755	-1 ABC transporter ATP-binding protein
1405547	1418150	12603 OXZ29485.1	B9N51_01450	1415743	1416417	-1 hypothetical protein
1405547	1418150	12603 OXZ29484.1	B9N51_01445	1416435	1417037	-1 hypothetical protein
1405547	1418150	12603 OXZ29483.1	B9N51_01440	1417179	1418150	-1 AraC family transcriptional regulator
1420159	1426302	6143 OXZ29481.1	B9N51_01430	1420159	1420500	1 plasmid mobilization relaxosome protein MobC
1420159	1426302	6143 OXZ29480.1	B9N51_01425	1420822	1422726	-1 DNA helicase UvrD
1420159	1426302	6143 OXZ29479.1	B9N51_01420	1422714	1424804	-1 ATP-dependent endonuclease
1420159	1426302	6143 OXZ29478.1	B9N51_01415	1424882	1425718	-1 abortive phage infection protein
1420159	1426302	6143 OXZ29477.1	B9N51_01410	1425715	1426302	-1 transcriptional regulator
1469754	1474021	4267 OXZ29513.1	B9N51_01200	1469754	1470101	1 toxin MazF
1469754	1474021	4267 OXZ29435.1	B9N51_01195	1470680	1471255	-1 cell filamentation protein Fic
1469754	1474021	4267 OXZ29434.1	B9N51_01190	1471990	1472724	-1 hydrolase
1469754	1474021	4267 OXZ29433.1	B9N51_01185	1472724	1473227	-1 acetyltransferase
1469754	1474021	4267 OXZ29432.1	B9N51_01180	1473380	1474021	1 hemolysin III
1526090	1536080	9990 OXZ27316.1	B9N51_07615	1524271	1526106	-1 multidrug ABC transporter
1526090	1536080	9990 OXZ27317.1	B9N51_07620	1526090	1527892	-1 multidrug ABC transporter
1526090	1536080	9990 OXZ27318.1	B9N51_07625	1527972	1528637	-1 histidine kinase
1526090	1536080	9990 OXZ27319.1	B9N51_07630	1528645	1529340	-1 DNA-binding response regulator
1526090	1536080	9990 OXZ27320.1	B9N51_07635	1529422	1530285	-1 UTP--glucose-1-phosphate uridylyltransferase
1526090	1536080	9990 OXZ27321.1	B9N51_07640	1531007	1533592	-1 ATP-dependent chaperone ClpB
1526090	1536080	9990 OXZ27322.1	B9N51_07645	1533611	1534555	-1 heat-shock protein
1526090	1536080	9990 OXZ27347.1	B9N51_07650	1534724	1535368	-1 nitroreductase
1526090	1536080	9990 OXZ27323.1	B9N51_07655	1535541	1536080	-1 RNA polymerase subunit sigma
1677255	1704148	26893 OXZ29725.1	B9N51_00210	1677255	1677599	1 anti-sigma factor
1677255	1704148	26893 OXZ29726.1	B9N51_00215	1677604	1678380	1 B/F/G family RNA polymerase sigma-70 factor
1677255	1704148	26893 OXZ29727.1	B9N51_00220	1678381	1678992	1 glutamine ABC transporter ATP-binding protein
1677255	1704148	26893 OXZ29728.1	B9N51_00225	1678994	1679767	1 amino acid ABC transporter permease
1677255	1704148	26893 OXZ29729.1	B9N51_00230	1679781	1681139	1 fumarate hydratase, class II
1677255	1704148	26893 OXZ29738.1	B9N51_00235	1681262	1681438	1 transaldolase
1677255	1704148	26893 OXZ29730.1	B9N51_00240	1682099	1682743	-1 hypothetical protein
1677255	1704148	26893 OXZ29731.1	B9N51_00245	1682740	1683399	-1 ABC transporter
1677255	1704148	26893 OXZ29732.1	B9N51_00250	1683562	1683996	-1 hypothetical protein
1677255	1704148	26893 OXZ29733.1	B9N51_00255	1684006	1684404	-1 hypothetical protein
1677255	1704148	26893 OXZ29734.1	B9N51_00260	1684512	1684697	-1 hypothetical protein
1677255	1704148	26893 OXZ29735.1	B9N51_00265	1684709	1684927	1 hypothetical protein
1677255	1704148	26893 OXZ29736.1	B9N51_00270	1684937	1685083	1 YvrJ family protein
1677255	1704148	26893 OXZ27007.1	B9N51_08160	1686267	1687624	-1 hypothetical protein
1677255	1704148	26893 OXZ27023.1	B9N51_08145	1688904	1690073	1 IS110 family transposase
1677255	1704148	26893 OXZ27032.1	B9N51_08100	1691294	1691947	-1 hypothetical protein
1677255	1704148	26893 OXZ27033.1	B9N51_08105	1692112	1692678	-1 transposase
1677255	1704148	26893 OXZ27008.1	B9N51_08150	1695626	1696225	-1 hypothetical protein
1677255	1704148	26893 OXZ27009.1	B9N51_08155	1696272	1696791	-1 hypothetical protein
1677255	1704148	26893	B9N51_08110	1697926	1702752	-1 hypothetical protein

1677255	1704148	26893	B9N51_08115	1703206	1703397	-1 transcriptional regulator
1677255	1704148	26893 OXZ27030.1	B9N51_08120	1703504	1704148	-1 hypothetical protein
1684937	1696791	11854 OXZ29736.1	B9N51_00270	1684937	1685083	1 YvrJ family protein
1684937	1696791	11854 OXZ27007.1	B9N51_08160	1686267	1687624	-1 hypothetical protein
1684937	1696791	11854 OXZ27023.1	B9N51_08145	1688904	1690073	1 IS110 family transposase
1684937	1696791	11854 OXZ27032.1	B9N51_08100	1691294	1691947	-1 hypothetical protein
1684937	1696791	11854 OXZ27033.1	B9N51_08105	1692112	1692678	-1 transposase
1684937	1696791	11854 OXZ27008.1	B9N51_08150	1695626	1696225	-1 hypothetical protein
1684937	1696791	11854 OXZ27009.1	B9N51_08155	1696272	1696791	-1 hypothetical protein
1703206	1716235	13029	B9N51_08115	1703206	1703397	-1 transcriptional regulator
1703206	1716235	13029 OXZ27030.1	B9N51_08120	1703504	1704148	-1 hypothetical protein
1703206	1716235	13029 OXZ27031.1	B9N51_08125	1704290	1704423	-1 hypothetical protein
1703206	1716235	13029 OXZ27029.1	B9N51_08140	1711588	1712868	1 group II intron reverse transcriptase/maturase
1703206	1716235	13029 OXZ26940.1	B9N51_08200	1715865	1716235	-1 IS200/IS605 family transposase

Table S3J: Predicted genomic islands in the genome of "F. nericia" T160124

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
507	18470	17963	OXZ26312.1	B9N52_00015	507	1049	1	LemA family protein
507	18470	17963	OXZ26313.1	B9N52_00020	1173	2081	1	coproporphyrinogen III oxidase
507	18470	17963	OXZ26314.1	B9N52_00025	2081	2809	1	biotin--[acetyl-CoA-carboxylase] ligase
507	18470	17963	OXZ26315.1	B9N52_00030	2822	3049	-1	hypothetical protein
507	18470	17963	OXZ26316.1	B9N52_00035	3142	3543	1	transcriptional regulator
507	18470	17963	OXZ26317.1	B9N52_00040	3588	3803	1	heavy metal transporter
507	18470	17963	OXZ26318.1	B9N52_00045	3803	5614	1	cadmium-translocating P-type ATPase
507	18470	17963	OXZ26319.1	B9N52_00050	5661	5972	1	hypothetical protein
507	18470	17963	OXZ26320.1	B9N52_00055	6054	6332	1	damage-inducible protein J
507	18470	17963	OXZ26321.1	B9N52_00060	6431	6688	-1	AbrB family transcriptional regulator
507	18470	17963	OXZ26322.1	B9N52_00065	6792	7367	-1	riboflavin transporter
507	18470	17963	OXZ26323.1	B9N52_00070	7458	11297	1	hypothetical protein
507	18470	17963	OXZ26324.1	B9N52_00075	11319	11442	1	transposase
507	18470	17963	OXZ26274.1	B9N52_00080	12592	13746	-1	2-iminoacetate synthase ThiH
507	18470	17963	OXZ26275.1	B9N52_00085	13754	14518	-1	thiazole synthase
507	18470	17963	OXZ26276.1	B9N52_00090	14508	15104	-1	thiamine biosynthesis protein ThiF
507	18470	17963	OXZ26277.1	B9N52_00095	15106	15303	-1	thiamine biosynthesis protein ThiS
507	18470	17963	OXZ26278.1	B9N52_00100	15524	16135	1	glutathione S-transferase
507	18470	17963	OXZ26279.1	B9N52_00105	16232	16933	1	SAM-dependent methyltransferase
507	18470	17963	OXZ26280.1	B9N52_00110	16950	18470	1	magnesium chelatase
40249	48234	7985	OXZ26299.1	B9N52_00205	38280	40268	1	exopolyphosphatase
40249	48234	7985	OXZ26300.1	B9N52_00210	40249	40695	1	50S ribosomal protein L9
40249	48234	7985	OXZ26301.1	B9N52_00215	40729	42066	1	replicative DNA helicase
40249	48234	7985	OXZ26302.1	B9N52_00220	42063	42626	1	GNAT family N-acetyltransferase
40249	48234	7985	OXZ26303.1	B9N52_00225	42631	43389	1	DNA replication protein
40249	48234	7985	OXZ26304.1	B9N52_00230	43392	44369	1	DNA replication protein DnaC
40249	48234	7985	OXZ26305.1	B9N52_00235	44366	45010	1	NAD(P)H-hydrate epimerase
40249	48234	7985	OXZ26183.1	B9N52_00240	46139	46226	1	hypothetical protein
40249	48234	7985	OXZ26184.1	B9N52_00245	46466	46645	1	hypothetical protein
40249	48234	7985	OXZ26185.1	B9N52_00250	47022	47564	1	ECF transporter S component
40249	48234	7985	OXZ26186.1	B9N52_00255	47548	48234	1	radical SAM protein
498315	512770	14455	OXZ25905.1	B9N52_02425	498315	498785	1	30S ribosomal protein S7
498315	512770	14455	OXZ25906.1	B9N52_02430	498814	500901	1	elongation factor G
498315	512770	14455	OXZ25907.1	B9N52_02435	500913	502106	1	elongation factor Tu
498315	512770	14455	OXZ25908.1	B9N52_02440	502513	505694	1	hypothetical protein
498315	512770	14455	OXZ25792.1	B9N52_02445	506695	509981	1	hypothetical protein
498315	512770	14455	OXZ25793.1	B9N52_02450	510028	510627	1	hypothetical protein
498315	512770	14455	OXZ25794.1	B9N52_02455	511021	512190	-1	IS110 family transposase
498315	512770	14455	OXZ25795.1	B9N52_02460	512477	512770	1	hypothetical protein
506695	512770	6075	OXZ25792.1	B9N52_02445	506695	509981	1	hypothetical protein
506695	512770	6075	OXZ25793.1	B9N52_02450	510028	510627	1	hypothetical protein
506695	512770	6075	OXZ25794.1	B9N52_02455	511021	512190	-1	IS110 family transposase
506695	512770	6075	OXZ25795.1	B9N52_02460	512477	512770	1	hypothetical protein
717980	723912	5932	OXZ25469.1	B9N52_03640	717980	718171	1	50S ribosomal protein L35
717980	723912	5932	OXZ25470.1	B9N52_03645	718190	718543	1	50S ribosomal protein L20
717980	723912	5932	OXZ25471.1	B9N52_03650	718575	718850	-1	hypothetical protein
717980	723912	5932	OXZ25472.1	B9N52_03655	718850	719467	-1	recombinase RecX
717980	723912	5932	OXZ25473.1	B9N52_03660	719656	719895	1	hypothetical protein
717980	723912	5932	OXZ25474.1	B9N52_03665	719904	720980	1	phosphoesterase
717980	723912	5932	OXZ25475.1	B9N52_03670	720977	723229	1	DNA repair protein Rad50
717980	723912	5932	OXZ25476.1	B9N52_03675	723232	723912	1	serine/threonine protein phosphatase
769989	780323	10334	OXZ25521.1	B9N52_03900	769989	770300	1	peptidoglycan-binding protein LysM
769989	780323	10334	OXZ25522.1	B9N52_03905	770376	771356	-1	recombinase XerC
769989	780323	10334		B9N52_03910	771463	772639	-1	aspartate aminotransferase
769989	780323	10334	OXZ25523.1	B9N52_03915	772626	773447	-1	metal-dependent phosphoesterase
769989	780323	10334	OXZ25524.1	B9N52_03920	773516	775057	-1	ribonuclease Y
769989	780323	10334	OXZ25525.1	B9N52_03925	775176	775838	-1	chromosome partitioning protein ParA
769989	780323	10334	OXZ25526.1	B9N52_03930	775825	776064	-1	hypothetical protein
769989	780323	10334	OXZ25527.1	B9N52_03935	776064	777647	-1	exonuclease SbcC
769989	780323	10334	OXZ25684.1	B9N52_03940	777647	778597	-1	phosphoesterase
769989	780323	10334	OXZ25528.1	B9N52_03945	778628	779719	-1	recombinase RecA
769989	780323	10334	OXZ25529.1	B9N52_03950	779787	780323	-1	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase tetracycline resistance determinant leader
1182570	1194616	12046	OXZ25283.1	B9N52_05820	1182570	1182686	-1	peptide
1182570	1194616	12046	OXZ25284.1	B9N52_05825	1182931	1183866	-1	conjugal transfer protein
1182570	1194616	12046	OXZ25285.1	B9N52_05830	1183863	1184864	-1	peptidase P60
1182570	1194616	12046	OXZ25286.1	B9N52_05835	1184861	1187038	-1	hypothetical protein
1182570	1194616	12046	OXZ25287.1	B9N52_05840	1187041	1189488	-1	ATP/GTP-binding protein
1182570	1194616	12046	OXZ25288.1	B9N52_05845	1189472	1189978	-1	conjugal transfer protein
1182570	1194616	12046	OXZ25289.1	B9N52_05850	1189953	1190450	-1	antirestriction protein ArdA
1182570	1194616	12046	OXZ25290.1	B9N52_05855	1190567	1190788	-1	hypothetical protein
1182570	1194616	12046	OXZ25291.1	B9N52_05860	1190831	1192036	-1	replication initiation protein
1182570	1194616	12046	OXZ25292.1	B9N52_05865	1192059	1192211	-1	conjugal transfer protein
1182570	1194616	12046	OXZ25293.1	B9N52_05870	1192214	1193599	-1	ATP-binding protein
1182570	1194616	12046	OXZ25294.1	B9N52_05875	1193628	1194014	-1	conjugal transfer protein
1182570	1194616	12046	OXZ25295.1	B9N52_05880	1194030	1194344	-1	conjugal transfer protein
1182570	1194616	12046	OXZ25296.1	B9N52_05885	1194529	1194616	-1	hypothetical protein
1215800	1221814	6014	OXZ25202.1	B9N52_05970	1215800	1216666	-1	hypothetical protein
1215800	1221814	6014	OXZ25179.1	B9N52_05975	1217667	1218396	-1	hypothetical protein
1215800	1221814	6014	OXZ25180.1	B9N52_05980	1218662	1220110	-1	hypothetical protein
1215800	1221814	6014	OXZ25181.1	B9N52_05985	1220372	1221814	-1	hypothetical protein
1385415	1465266	79851	OXZ25081.1	B9N52_06785	1385415	1385762	-1	hypothetical protein

1385415	1465266	79851	B9N52_06790	1385852	1386129	-1 hypothetical protein
1385415	1465266	79851 OXZ25076.1	B9N52_06795	1386361	1386897	-1 Rossman fold protein, TIGR00730 family
1385415	1465266	79851 OXZ25077.1	B9N52_06800	1387008	1388005	-1 macrolide ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ25019.1	B9N52_06805	1389211	1389657	-1 transposase
1385415	1465266	79851 OXZ25020.1	B9N52_06810	1389736	1391862	-1 catalase HP11
1385415	1465266	79851 OXZ25021.1	B9N52_06815	1392350	1392841	-1 protein-S-isoprenylcysteine methyltransferase
1385415	1465266	79851 OXZ25022.1	B9N52_06820	1392855	1393793	-1 esterase
1385415	1465266	79851 OXZ25023.1	B9N52_06825	1393862	1394488	-1 hypothetical protein
1385415	1465266	79851 OXZ25024.1	B9N52_06830	1394516	1395124	-1 SAM-dependent methyltransferase
1385415	1465266	79851 OXZ25025.1	B9N52_06835	1395340	1396089	-1 phosphorylase
1385415	1465266	79851 OXZ25026.1	B9N52_06840	1396219	1396576	-1 macrolide ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ25018.1	B9N52_06845	1397577	1398145	-1 macrolide ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ25017.1	B9N52_06850	1399146	1399876	-1 macrolide ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24933.1	B9N52_06855	1401405	1402019	-1 hypothetical protein
1385415	1465266	79851 OXZ24934.1	B9N52_06860	1402226	1403590	-1 ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24935.1	B9N52_06865	1403578	1404273	-1 cobalt ABC transporter permease
1385415	1465266	79851 OXZ24936.1	B9N52_06870	1404273	1404854	-1 hypothetical protein
1385415	1465266	79851 OXZ24937.1	B9N52_06875	1404914	1406257	-1 MATE family efflux transporter
1385415	1465266	79851 OXZ24938.1	B9N52_06880	1406269	1407990	-1 ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24939.1	B9N52_06885	1407974	1409728	-1 ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24940.1	B9N52_06890	1409889	1410881	1 AraC family transcriptional regulator
1385415	1465266	79851 OXZ24941.1	B9N52_06895	1411661	1412719	-1 arsenical-resistance protein
1385415	1465266	79851 OXZ24942.1	B9N52_06900	1412750	1414501	-1 arsenical pump-driving ATPase arsenical resistance operon transcriptional
1385415	1465266	79851 OXZ24943.1	B9N52_06905	1414520	1414885	-1 repressor ArsD
1385415	1465266	79851 OXZ24944.1	B9N52_06910	1414905	1415219	-1 transcriptional regulator
1385415	1465266	79851 OXZ24945.1	B9N52_06915	1415958	1416413	1 penicillinase repressor
1385415	1465266	79851	B9N52_06920	1416427	1418580	1 heavy metal translocating P-type ATPase
1385415	1465266	79851 OXZ24946.1	B9N52_06925	1419254	1419859	-1 cadmium resistance protein CadD
1385415	1465266	79851	B9N52_06930	1420153	1420370	-1 hypothetical protein
1385415	1465266	79851 OXZ24947.1	B9N52_06935	1420665	1421963	-1 AAA family ATPase
1385415	1465266	79851	B9N52_06940	1422588	1422925	-1 hypothetical protein
1385415	1465266	79851 OXZ24948.1	B9N52_06945	1423188	1423445	-1 hypothetical protein
1385415	1465266	79851 OXZ24949.1	B9N52_06950	1423468	1425903	-1 ABC transporter permease
1385415	1465266	79851 OXZ24950.1	B9N52_06955	1425896	1426576	-1 peptide ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24951.1	B9N52_06960	1426623	1427483	-1 two-component sensor histidine kinase
1385415	1465266	79851 OXZ24952.1	B9N52_06965	1427485	1428135	-1 DNA-binding response regulator
1385415	1465266	79851	B9N52_06970	1428709	1429124	-1 RNA polymerase subunit sigma
1385415	1465266	79851 OXZ24953.1	B9N52_06975	1429436	1430788	-1 MATE family efflux transporter
1385415	1465266	79851 OXZ24954.1	B9N52_06980	1430815	1432560	-1 ABC transporter permease
1385415	1465266	79851 OXZ24955.1	B9N52_06985	1432553	1434343	-1 ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24956.1	B9N52_06990	1434333	1435802	-1 ABC transporter
1385415	1465266	79851 OXZ24957.1	B9N52_06995	1435787	1436500	-1 ABC transporter permease
1385415	1465266	79851 OXZ24958.1	B9N52_07000	1436490	1437086	-1 hypothetical protein
1385415	1465266	79851 OXZ25016.1	B9N52_07005	1437210	1437848	-1 TetR family transcriptional regulator
1385415	1465266	79851 OXZ24959.1	B9N52_07010	1437920	1439482	-1 recombinase family protein
1385415	1465266	79851 OXZ24960.1	B9N52_07015	1439475	1439891	-1 integrase
1385415	1465266	79851 OXZ24961.1	B9N52_07020	1439884	1441446	-1 recombinase family protein
1385415	1465266	79851 OXZ24962.1	B9N52_07025	1441506	1441715	-1 hypothetical protein
1385415	1465266	79851 OXZ24963.1	B9N52_07030	1442081	1443817	-1 multidrug ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24964.1	B9N52_07035	1443810	1445531	-1 ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24965.1	B9N52_07040	1445569	1446921	-1 MATE family efflux transporter
1385415	1465266	79851 OXZ24966.1	B9N52_07045	1446934	1448382	-1 ABC transporter
1385415	1465266	79851 OXZ24967.1	B9N52_07050	1448379	1449068	-1 ABC transporter permease
1385415	1465266	79851 OXZ24968.1	B9N52_07055	1449068	1449646	-1 hypothetical protein
1385415	1465266	79851 OXZ24969.1	B9N52_07060	1449698	1450270	-1 TetR family transcriptional regulator
1385415	1465266	79851 OXZ24970.1	B9N52_07065	1450563	1450919	1 plasmid mobilization relaxosome protein MobC
1385415	1465266	79851	B9N52_07070	1450921	1452251	1 endonuclease
1385415	1465266	79851 OXZ24971.1	B9N52_07075	1452255	1453496	-1 DNA (cytosine-5-)-methyltransferase
1385415	1465266	79851 OXZ24972.1	B9N52_07080	1453493	1454986	-1 hypothetical protein
1385415	1465266	79851 OXZ24973.1	B9N52_07085	1454976	1457147	-1 hypothetical protein
1385415	1465266	79851 OXZ24974.1	B9N52_07090	1457198	1457419	-1 transcriptional regulator
1385415	1465266	79851	B9N52_07095	1457704	1458141	-1 hypothetical protein
1385415	1465266	79851 OXZ24975.1	B9N52_07100	1458874	1459461	-1 transcriptional regulator 23S rRNA (uracil(1939)-C(5))-methyltransferase
1385415	1465266	79851 OXZ24976.1	B9N52_07105	1459959	1461173	-1 RlmD
1385415	1465266	79851 OXZ24977.1	B9N52_07110	1461266	1463062	-1 ABC transporter
1385415	1465266	79851 OXZ24978.1	B9N52_07115	1463055	1464815	-1 multidrug ABC transporter ATP-binding protein
1385415	1465266	79851 OXZ24979.1	B9N52_07120	1464790	1465266	-1 MarR family transcriptional regulator
1399146	1406257	7111 OXZ25017.1	B9N52_06850	1399146	1399876	-1 macrolide ABC transporter ATP-binding protein
1399146	1406257	7111 OXZ24933.1	B9N52_06855	1401405	1402019	-1 hypothetical protein
1399146	1406257	7111 OXZ24934.1	B9N52_06860	1402226	1403590	-1 ABC transporter ATP-binding protein
1399146	1406257	7111 OXZ24935.1	B9N52_06865	1403578	1404273	-1 cobalt ABC transporter permease
1399146	1406257	7111 OXZ24936.1	B9N52_06870	1404273	1404854	-1 hypothetical protein
1399146	1406257	7111 OXZ24937.1	B9N52_06875	1404914	1406257	-1 MATE family efflux transporter
1420153	1425903	5750	B9N52_06930	1420153	1420370	-1 hypothetical protein
1420153	1425903	5750 OXZ24947.1	B9N52_06935	1420665	1421963	-1 AAA family ATPase
1420153	1425903	5750	B9N52_06940	1422588	1422925	-1 hypothetical protein
1420153	1425903	5750 OXZ24948.1	B9N52_06945	1423188	1423445	-1 hypothetical protein
1420153	1425903	5750 OXZ24949.1	B9N52_06950	1423468	1425903	-1 ABC transporter permease

1420153	1425903	5750 OXZ24950.1	B9N52_06955	1425896	1426576	-1 peptide ABC transporter ATP-binding protein
1441506	1450919	9413 OXZ24962.1	B9N52_07025	1441506	1441715	-1 hypothetical protein
1441506	1450919	9413 OXZ24963.1	B9N52_07030	1442081	1443817	-1 multidrug ABC transporter ATP-binding protein
1441506	1450919	9413 OXZ24964.1	B9N52_07035	1443810	1445531	-1 ABC transporter ATP-binding protein
1441506	1450919	9413 OXZ24965.1	B9N52_07040	1445569	1446921	-1 MATE family efflux transporter
1441506	1450919	9413 OXZ24966.1	B9N52_07045	1446934	1448382	-1 ABC transporter
1441506	1450919	9413 OXZ24967.1	B9N52_07050	1448379	1449068	-1 ABC transporter permease
1441506	1450919	9413 OXZ24968.1	B9N52_07055	1449068	1449646	-1 hypothetical protein
1441506	1450919	9413 OXZ24969.1	B9N52_07060	1449698	1450270	-1 TetR family transcriptional regulator
1441506	1450919	9413 OXZ24970.1	B9N52_07065	1450563	1450919	1 plasmid mobilization relaxosome protein MobC
1771981	1789695	17714 OXZ24924.1	B9N52_08540	1771981	1773342	1 hypothetical protein
1771981	1789695	17714 OXZ24684.1	B9N52_08575	1774499	1775197	-1 hypothetical protein
1771981	1789695	17714 OXZ24685.1	B9N52_08580	1775356	1775895	-1 transposase
1771981	1789695	17714 OXZ24682.1	B9N52_08585	1784312	1784851	1 transposase
1771981	1789695	17714 OXZ24683.1	B9N52_08590	1784914	1785708	1 hypothetical protein
1771981	1789695	17714 OXZ24688.1	B9N52_08545	1788311	1789105	-1 transposase
1771981	1789695	17714 OXZ24689.1	B9N52_08550	1789129	1789695	-1 transposase
1774499	1789105	14606 OXZ24684.1	B9N52_08575	1774499	1775197	-1 hypothetical protein
1774499	1789105	14606 OXZ24685.1	B9N52_08580	1775356	1775895	-1 transposase
1774499	1789105	14606 OXZ24682.1	B9N52_08585	1784312	1784851	1 transposase
1774499	1789105	14606 OXZ24683.1	B9N52_08590	1784914	1785708	1 hypothetical protein
1774499	1789105	14606 OXZ24688.1	B9N52_08545	1788311	1789105	-1 transposase

Table S3K: Predicted genomic islands in the genome of "F. nericia" ATCC53516

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
235768	246338	10570	EFH93375.1	HMPREF0391_11033	235768	236637	1	hypothetical protein
235768	246338	10570	EFH93374.1	HMPREF0391_11032	236624	238612	1	DHHA1 domain protein
235768	246338	10570	EFH93373.1	HMPREF0391_11031	238593	239039	1	ribosomal protein L9
235768	246338	10570	EFH93372.1	HMPREF0391_11030	239073	240410	1	replicative DNA helicase
235768	246338	10570	EFH93371.1	HMPREF0391_11029	240407	240970	1	acetyltransferase, GNAT family
235768	246338	10570	EFH93370.1	HMPREF0391_11028	240954	241733	1	DnaD domain protein
235768	246338	10570	EFH93369.1	HMPREF0391_11027	241736	242713	1	DNA replication protein DnaC
235768	246338	10570	EFH93368.1	HMPREF0391_11026	242710	243354	1	YjeF-like protein
235768	246338	10570	EFH93367.1	HMPREF0391_11025	244071	244613	1	hypothetical protein
235768	246338	10570	EFH93366.1	HMPREF0391_11024	244597	245283	1	hypothetical protein
235768	246338	10570	EFH93365.1	HMPREF0391_11023	245337	246053	1	putative phage head-tail adaptor
235768	246338	10570	EFH93364.1	HMPREF0391_11022	246111	246338	1	hypothetical protein
294189	302405	8216	EFH93316.1	HMPREF0391_10974	294189	294389	1	DNA-binding helix-turn-helix protein
294189	302405	8216	EFH93315.1	HMPREF0391_10973	294390	294839	1	hypothetical protein
294189	302405	8216	EFH93314.1	HMPREF0391_10972	294976	295641	1	hypothetical protein
294189	302405	8216	EFH93313.1	HMPREF0391_10971	295802	296746	1	DnaJ domain protein
294189	302405	8216	EFH93312.1	HMPREF0391_10970	296765	299350	1	ATP-dependent chaperone protein ClpB
294189	302405	8216	EFH93311.1	HMPREF0391_10969	299626	300015	-1	hypothetical protein
294189	302405	8216	EFH93310.1	HMPREF0391_10968	300091	300954	1	UTP--glucose-1-phosphate uridylyltransferase
294189	302405	8216	EFH93309.1	HMPREF0391_10967	301037	301732	1	response regulator receiver domain protein
294189	302405	8216	EFH93308.1	HMPREF0391_10966	301740	302405	1	hypothetical protein
349541	354034	4493	EFH93269.1	HMPREF0391_10927	349438	349557	1	hypothetical protein
349541	354034	4493	EFH93268.1	HMPREF0391_10926	349541	349756	1	hypothetical protein
349541	354034	4493	EFH93267.1	HMPREF0391_10925	352820	354034	-1	transposase, Mutator family
494767	499382	4615	EFH93134.1	HMPREF0391_10792	494767	494967	1	hypothetical protein
494767	499382	4615	EFH93133.1	HMPREF0391_10791	495132	496514	-1	domain protein
494767	499382	4615	EFH93132.1	HMPREF0391_10790	496505	497164	-1	response regulator receiver domain protein
494767	499382	4615	EFH93131.1	HMPREF0391_10789	497197	497964	-1	antibiotic ABC transporter protein MutG
494767	499382	4615	EFH93130.1	HMPREF0391_10788	497937	498677	-1	mutacin ABC transporter protein, MutE
494767	499382	4615	EFH93129.1	HMPREF0391_10787	498681	499382	-1	MutF
971218	980556	9338	EFH92519.1	HMPREF0391_11491	971218	972198	-1	site-specific tyrosine recombinase XerC
971218	980556	9338	EFH92520.1	HMPREF0391_11492	972301	973476	-1	aminotransferase, class I/II
971218	980556	9338	EFH92521.1	HMPREF0391_11493	973463	974284	-1	PHP domain protein
971218	980556	9338	EFH92522.1	HMPREF0391_11494	974353	975894	-1	YmdA/YtgF family protein
971218	980556	9338	EFH92523.1	HMPREF0391_11495	976013	976675	-1	hypothetical protein
971218	980556	9338	EFH92524.1	HMPREF0391_11496	976662	976901	-1	hypothetical protein
971218	980556	9338	EFH92525.1	HMPREF0391_11497	976901	978484	-1	hypothetical protein
971218	980556	9338	EFH92526.1	HMPREF0391_11498	978484	979437	-1	phosphodiesterase family protein
971218	980556	9338	EFH92527.1	HMPREF0391_11499	979465	980556	-1	RecA protein
1135806	1139907	4101	EFH92677.1	HMPREF0391_11649	1135806	1136735	-1	ABC transporter, permease protein
1135806	1139907	4101	EFH92678.1	HMPREF0391_11650	1136737	1137441	-1	TOBE domain protein
1135806	1139907	4101	EFH92679.1	HMPREF0391_11651	1137658	1138644	1	integrase core domain protein
1135806	1139907	4101	EFH92680.1	HMPREF0391_11652	1138613	1138924	-1	protein
1135806	1139907	4101	EFH92681.1	HMPREF0391_11653	1139134	1139907	1	transcriptional regulator, DeoR family
1172805	1217320	44515	EFH92708.1	HMPREF0391_11680	1172805	1173215	-1	hypothetical protein
1172805	1217320	44515	EFH92709.1	HMPREF0391_11681	1173535	1174884	-1	MATE efflux family protein
1172805	1217320	44515	EFH92710.1	HMPREF0391_11682	1174921	1176654	-1	ABC transporter, ATP-binding protein
1172805	1217320	44515	EFH92711.1	HMPREF0391_11683	1176651	1178393	-1	ABC transporter, ATP-binding protein
1172805	1217320	44515	EFH92712.1	HMPREF0391_11684	1178429	1179820	-1	ABC transporter, ATP-binding protein
1172805	1217320	44515	EFH92713.1	HMPREF0391_11685	1179813	1180514	-1	cobalt transport protein
1172805	1217320	44515	EFH92714.1	HMPREF0391_11686	1180539	1181120	-1	conserved hypothetical protein TIGR02185
1172805	1217320	44515	EFH92715.1	HMPREF0391_11687	1181138	1181749	-1	transcriptional regulator, TetR family
1172805	1217320	44515	EFH92716.1	HMPREF0391_11688	1181938	1182417	1	hypothetical protein
1172805	1217320	44515	EFH92717.1	HMPREF0391_11689	1182419	1183750	1	relaxase/mobilization nuclease domain protein
1172805	1217320	44515	EFH92718.1	HMPREF0391_11690	1183771	1184268	-1	hypothetical protein
1172805	1217320	44515	EFH92719.1	HMPREF0391_11691	1184269	1185690	-1	hypothetical protein
1172805	1217320	44515	EFH92720.1	HMPREF0391_11692	1185725	1185940	-1	hypothetical protein
1172805	1217320	44515	EFH92721.1	HMPREF0391_11693	1186041	1186274	-1	hypothetical protein
1172805	1217320	44515	EFH92722.1	HMPREF0391_11694	1186387	1187049	-1	hypothetical protein
1172805	1217320	44515	EFH92723.1	HMPREF0391_11695	1187065	1194735	-1	helicase C-terminal domain protein
1172805	1217320	44515	EFH92724.1	HMPREF0391_11696	1194818	1197031	-1	hypothetical protein
1172805	1217320	44515	EFH92725.1	HMPREF0391_11697	1197067	1198029	-1	DNA (cytosine-5-)-methyltransferase
1172805	1217320	44515	EFH92726.1	HMPREF0391_11698	1198022	1199755	-1	DNA topoisomerase
1172805	1217320	44515	EFH92727.1	HMPREF0391_11699	1199807	1200673	-1	hypothetical protein
1172805	1217320	44515	EFH92728.1	HMPREF0391_11700	1200688	1201758	-1	copper amine oxidase domain protein
1172805	1217320	44515	EFH92729.1	HMPREF0391_11701	1201839	1203038	-1	hypothetical protein
1172805	1217320	44515	EFH92730.1	HMPREF0391_11702	1203025	1203264	-1	hypothetical protein
1172805	1217320	44515	EFH92731.1	HMPREF0391_11703	1203354	1204529	-1	NlpC/P60 family protein
1172805	1217320	44515	EFH92732.1	HMPREF0391_11704	1204692	1204973	-1	hypothetical protein
1172805	1217320	44515	EFH92733.1	HMPREF0391_11705	1205024	1205908	-1	transposase, Mutator family
1172805	1217320	44515	EFH92734.1	HMPREF0391_11706	1205958	1207439	-1	hypothetical protein
1172805	1217320	44515	EFH92735.1	HMPREF0391_11707	1207447	1209870	-1	hypothetical protein
1172805	1217320	44515	EFH92736.1	HMPREF0391_11708	1209761	1210171	-1	hypothetical protein
1172805	1217320	44515	EFH92737.1	HMPREF0391_11709	1210173	1210463	-1	hypothetical protein
1172805	1217320	44515	EFH92738.1	HMPREF0391_11710	1210473	1211336	-1	hypothetical protein
1172805	1217320	44515	EFH92739.1	HMPREF0391_11711	1211347	1211562	-1	hypothetical protein
1172805	1217320	44515	EFH92740.1	HMPREF0391_11712	1211564	1211875	-1	hypothetical protein
1172805	1217320	44515	EFH92741.1	HMPREF0391_11713	1212066	1212341	-1	hypothetical protein

1172805	1217320	44515	EFH92742.1	HMPREF0391_11714	1212360	1214156	-1 TraG/TraD family protein
1172805	1217320	44515	EFH92743.1	HMPREF0391_11715	1214149	1214883	-1 BRO family, N-terminal domain protein
1172805	1217320	44515	EFH92744.1	HMPREF0391_11716	1214880	1215365	-1 hypothetical protein
1172805	1217320	44515	EFH92745.1	HMPREF0391_11717	1215358	1216185	-1 chromosomal replication initiator protein DnaA
1172805	1217320	44515	EFH92746.1	HMPREF0391_11718	1216182	1216955	-1 replication initiator protein A domain protein
1172805	1217320	44515	EFH92747.1	HMPREF0391_11719	1217039	1217320	-1 hypothetical protein
1203025	1207439	4414	EFH92729.1	HMPREF0391_11701	1201839	1203038	-1 hypothetical protein
1203025	1207439	4414	EFH92730.1	HMPREF0391_11702	1203025	1203264	-1 hypothetical protein
1203025	1207439	4414	EFH92731.1	HMPREF0391_11703	1203354	1204529	-1 NlpC/P60 family protein
1203025	1207439	4414	EFH92732.1	HMPREF0391_11704	1204692	1204973	-1 hypothetical protein
1203025	1207439	4414	EFH92733.1	HMPREF0391_11705	1205024	1205908	-1 transposase, Mutator family
1203025	1207439	4414	EFH92734.1	HMPREF0391_11706	1205958	1207439	-1 hypothetical protein
1211564	1217320	5756	EFH92740.1	HMPREF0391_11712	1211564	1211875	-1 hypothetical protein
1211564	1217320	5756	EFH92741.1	HMPREF0391_11713	1212066	1212341	-1 hypothetical protein
1211564	1217320	5756	EFH92742.1	HMPREF0391_11714	1212360	1214156	-1 TraG/TraD family protein
1211564	1217320	5756	EFH92743.1	HMPREF0391_11715	1214149	1214883	-1 BRO family, N-terminal domain protein
1211564	1217320	5756	EFH92744.1	HMPREF0391_11716	1214880	1215365	-1 hypothetical protein
1211564	1217320	5756	EFH92745.1	HMPREF0391_11717	1215358	1216185	-1 chromosomal replication initiator protein DnaA
1211564	1217320	5756	EFH92746.1	HMPREF0391_11718	1216182	1216955	-1 replication initiator protein A domain protein
1211564	1217320	5756	EFH92747.1	HMPREF0391_11719	1217039	1217320	-1 hypothetical protein
1349537	1383336	33799	EFH93638.1	HMPREF0391_10006	1348897	1349553	-1 chain length determinant protein
1349537	1383336	33799	EFH93639.1	HMPREF0391_10007	1349537	1350316	-1 hypothetical protein
1349537	1383336	33799	EFH93640.1	HMPREF0391_10008	1350317	1350739	-1 SH3 domain protein
1349537	1383336	33799	EFH93641.1	HMPREF0391_10009	1350920	1351444	1 topology modulation protein
1349537	1383336	33799	EFH93642.1	HMPREF0391_10010	1351534	1352748	1 transposase, Mutator family
1349537	1383336	33799	EFH93643.1	HMPREF0391_10011	1353139	1361259	-1 LPXTG-motif cell wall anchor domain protein
1349537	1383336	33799	EFH93644.1	HMPREF0391_10012	1362088	1363713	-1 LPXTG-motif cell wall anchor domain protein
1349537	1383336	33799	EFH93645.1	HMPREF0391_10013	1363706	1363873	1 hypothetical protein
1349537	1383336	33799	EFH93646.1	HMPREF0391_10014	1367492	1367641	-1 hypothetical protein
1349537	1383336	33799	EFH93647.1	HMPREF0391_10015	1367678	1371538	-1 hypothetical protein
1349537	1383336	33799	EFH93648.1	HMPREF0391_10016	1371646	1371777	-1 hypothetical protein
1349537	1383336	33799	EFH93649.1	HMPREF0391_10017	1373225	1375135	-1 LPXTG-motif cell wall anchor domain protein
1349537	1383336	33799	EFH93650.1	HMPREF0391_10018	1375655	1375777	-1 hypothetical protein
1349537	1383336	33799	EFH93651.1	HMPREF0391_10019	1375808	1376242	-1 acetyltransferase, GNAT family
1349537	1383336	33799	EFH93652.1	HMPREF0391_10020	1376265	1376963	-1 putative TIGR02206 family protein
1349537	1383336	33799	EFH93653.1	HMPREF0391_10021	1376963	1377682	-1 hypothetical protein
1349537	1383336	33799	EFH93654.1	HMPREF0391_10022	1378623	1381976	-1 efflux ABC transporter, permease protein
1349537	1383336	33799	EFH93655.1	HMPREF0391_10023	1381978	1382679	-1 ABC transporter, ATP-binding protein
1349537	1383336	33799	EFH93656.1	HMPREF0391_10024	1382791	1383336	1 transcriptional regulator, TetR family
1431249	1529242	97993	EFH93711.1	HMPREF0391_10079	1431249	1431857	-1 methyltransferase domain protein
1431249	1529242	97993	EFH93712.1	HMPREF0391_10080	1431960	1432244	-1 hypothetical protein
1431249	1529242	97993	EFH93713.1	HMPREF0391_10081	1432455	1432946	-1 hypothetical protein
1431249	1529242	97993	EFH93714.1	HMPREF0391_10082	1433194	1433943	-1 hypothetical protein
1431249	1529242	97993	EFH93715.1	HMPREF0391_10083	1434203	1435807	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93716.1	HMPREF0391_10084	1436535	1437149	-1 hypothetical protein
1431249	1529242	97993	EFH93717.1	HMPREF0391_10085	1437358	1438722	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93718.1	HMPREF0391_10086	1438716	1439405	-1 cobalt transport protein
1431249	1529242	97993	EFH93719.1	HMPREF0391_10087	1439405	1439989	-1 conserved hypothetical protein TIGR02185
1431249	1529242	97993	EFH93720.1	HMPREF0391_10088	1440049	1441407	-1 MATE efflux family protein
1431249	1529242	97993	EFH93721.1	HMPREF0391_10089	1441404	1443125	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93722.1	HMPREF0391_10090	1443109	1444869	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93723.1	HMPREF0391_10091	1445024	1446016	1 transcriptional regulator, AraC family
1431249	1529242	97993	EFH93724.1	HMPREF0391_10092	1446278	1446817	1 transposase
1431249	1529242	97993	EFH93725.1	HMPREF0391_10093	1447012	1447716	1 integrase core domain protein
1431249	1529242	97993	EFH93726.1	HMPREF0391_10094	1447946	1449160	-1 transposase, Mutator family
1431249	1529242	97993	EFH93727.1	HMPREF0391_10095	1449521	1450117	-1 hypothetical protein
1431249	1529242	97993	EFH93728.1	HMPREF0391_10096	1450260	1452002	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93729.1	HMPREF0391_10097	1451989	1453710	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93730.1	HMPREF0391_10098	1453710	1455173	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93731.1	HMPREF0391_10099	1455175	1455846	-1 cobalt transport protein
1431249	1529242	97993	EFH93732.1	HMPREF0391_10100	1455843	1456433	-1 conserved hypothetical protein TIGR02185
1431249	1529242	97993	EFH93733.1	HMPREF0391_10101	1456500	1457477	-1 transcriptional regulator, AraC family
1431249	1529242	97993	EFH93734.1	HMPREF0391_10102	1457487	1458089	-1 transcriptional regulator, TetR family
1431249	1529242	97993	EFH93735.1	HMPREF0391_10103	1458205	1458381	-1 hypothetical protein
1431249	1529242	97993	EFH93736.1	HMPREF0391_10104	1458528	1458791	1 hypothetical protein
1431249	1529242	97993	EFH93737.1	HMPREF0391_10105	1459309	1459572	-1 hypothetical protein
1431249	1529242	97993	EFH93738.1	HMPREF0391_10106	1459749	1460726	-1 caspase domain protein
1431249	1529242	97993	EFH93739.1	HMPREF0391_10107	1460746	1461123	-1 hypothetical protein
1431249	1529242	97993	EFH93740.1	HMPREF0391_10108	1461126	1461293	-1 hypothetical protein
1431249	1529242	97993	EFH93741.1	HMPREF0391_10109	1461517	1461984	-1 hypothetical protein
1431249	1529242	97993	EFH93742.1	HMPREF0391_10110	1462046	1462837	-1 CAAX amino terminal protease family protein
1431249	1529242	97993	EFH93743.1	HMPREF0391_10111	1463678	1464328	-1 hypothetical protein
1431249	1529242	97993	EFH93744.1	HMPREF0391_10112	1464635	1465384	-1 hypothetical protein
1431249	1529242	97993	EFH93745.1	HMPREF0391_10113	1465957	1467390	-1 hypothetical protein
1431249	1529242	97993	EFH93746.1	HMPREF0391_10114	1467431	1467751	-1 hypothetical protein
1431249	1529242	97993	EFH93747.1	HMPREF0391_10115	1467931	1468203	-1 hypothetical protein
1431249	1529242	97993	EFH93748.1	HMPREF0391_10116	1468489	1469475	1 integrase core domain protein
1431249	1529242	97993	EFH93749.1	HMPREF0391_10117	1469778	1471130	-1 MATE efflux family protein
1431249	1529242	97993	EFH93750.1	HMPREF0391_10118	1471157	1472902	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93751.1	HMPREF0391_10119	1472895	1474688	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93752.1	HMPREF0391_10120	1474675	1476144	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93753.1	HMPREF0391_10121	1476129	1476842	-1 cobalt transport protein

1431249	1529242	97993	EFH93754.1	HMPREF0391_10122	1476832	1477428	-1 conserved hypothetical protein TIGR02185
1431249	1529242	97993	EFH93755.1	HMPREF0391_10123	1477552	1478271	-1 transcriptional regulator, TetR family
1431249	1529242	97993	EFH93756.1	HMPREF0391_10124	1478262	1479827	-1 resolvase, N-terminal domain protein
1431249	1529242	97993	EFH93757.1	HMPREF0391_10125	1479817	1480233	-1 recombinase
1431249	1529242	97993	EFH93758.1	HMPREF0391_10126	1480226	1481788	-1 resolvase, N-terminal domain protein
1431249	1529242	97993	EFH93759.1	HMPREF0391_10127	1481848	1482057	-1 hypothetical protein
1431249	1529242	97993	EFH93760.1	HMPREF0391_10128	1482421	1484157	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93761.1	HMPREF0391_10129	1484150	1485889	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93762.1	HMPREF0391_10130	1485873	1486496	-1 transcriptional regulator, TetR family
1431249	1529242	97993	EFH93763.1	HMPREF0391_10131	1486640	1487449	-1 Cpl-7 lysozyme C-terminal domain protein
1431249	1529242	97993	EFH93764.1	HMPREF0391_10132	1487450	1487851	-1 toxin secretion/phage lysis holin
1431249	1529242	97993	EFH93765.1	HMPREF0391_10133	1487853	1489232	-1 hypothetical protein
1431249	1529242	97993	EFH93766.1	HMPREF0391_10134	1489219	1491090	-1 hypothetical protein
1431249	1529242	97993	EFH93767.1	HMPREF0391_10135	1491090	1491452	-1 hypothetical protein
1431249	1529242	97993	EFH93768.1	HMPREF0391_10136	1491452	1492948	-1 TMP repeat protein
1431249	1529242	97993	EFH93769.1	HMPREF0391_10137	1492818	1494518	-1 phage tail tape measure protein, TP901 family
1431249	1529242	97993	EFH93770.1	HMPREF0391_10138	1494581	1494907	-1 hypothetical protein
1431249	1529242	97993	EFH93771.1	HMPREF0391_10139	1494946	1495110	-1 hypothetical protein
1431249	1529242	97993	EFH93772.1	HMPREF0391_10140	1495128	1495484	-1 hypothetical protein
1431249	1529242	97993	EFH93773.1	HMPREF0391_10141	1495487	1496083	-1 phage major tail protein, phi13 family
1431249	1529242	97993	EFH93774.1	HMPREF0391_10142	1496073	1496420	-1 hypothetical protein
1431249	1529242	97993	EFH93775.1	HMPREF0391_10143	1496413	1496793	-1 hypothetical protein
1431249	1529242	97993	EFH93776.1	HMPREF0391_10144	1496790	1497122	-1 putative phage head-tail adaptor
1431249	1529242	97993	EFH93777.1	HMPREF0391_10145	1497122	1497394	-1 phage DNA packaging protein
1431249	1529242	97993	EFH93778.1	HMPREF0391_10146	1497405	1498595	-1 phage major capsid protein, HK97 family
1431249	1529242	97993	EFH93779.1	HMPREF0391_10147	1498598	1499284	-1 endopeptidase Clp
1431249	1529242	97993	EFH93780.1	HMPREF0391_10148	1499271	1500548	-1 phage portal protein, HK97 family
1431249	1529242	97993	EFH93781.1	HMPREF0391_10149	1500593	1501012	-1 hypothetical protein
1431249	1529242	97993	EFH93782.1	HMPREF0391_10150	1501057	1502646	-1 putative phage terminase, large subunit
1431249	1529242	97993	EFH93783.1	HMPREF0391_10151	1502742	1503062	-1 hypothetical protein
1431249	1529242	97993	EFH93784.1	HMPREF0391_10152	1503123	1503518	-1 hypothetical protein
1431249	1529242	97993	EFH93785.1	HMPREF0391_10153	1503563	1503778	-1 hypothetical protein
1431249	1529242	97993	EFH93786.1	HMPREF0391_10154	1503822	1505072	-1 DNA (cytosine-5-)-methyltransferase
1431249	1529242	97993	EFH93787.1	HMPREF0391_10155	1505072	1505854	-1 hypothetical protein
1431249	1529242	97993	EFH93788.1	HMPREF0391_10156	1505858	1506370	-1 HNH endonuclease domain protein
1431249	1529242	97993	EFH93789.1	HMPREF0391_10157	1506380	1507027	-1 hypothetical protein
1431249	1529242	97993	EFH93790.1	HMPREF0391_10158	1507081	1507479	-1 HNH endonuclease domain protein
1431249	1529242	97993	EFH93791.1	HMPREF0391_10159	1507626	1507883	1 transcriptional regulator, AbrB family
1431249	1529242	97993	EFH93792.1	HMPREF0391_10160	1507883	1508149	1 addiction module toxin, RelE/StbE family
1431249	1529242	97993	EFH93793.1	HMPREF0391_10161	1508226	1508627	-1 hypothetical protein
1431249	1529242	97993	EFH93794.1	HMPREF0391_10162	1508675	1510018	-1 type III restriction enzyme, res subunit
1431249	1529242	97993	EFH93795.1	HMPREF0391_10163	1510019	1510216	-1 VRR-NUC domain protein
1431249	1529242	97993	EFH93796.1	HMPREF0391_10164	1510258	1510497	-1 hypothetical protein
1431249	1529242	97993	EFH93797.1	HMPREF0391_10165	1510779	1512980	-1 protein
1431249	1529242	97993	EFH93798.1	HMPREF0391_10166	1512981	1513367	-1 hypothetical protein
1431249	1529242	97993	EFH93799.1	HMPREF0391_10167	1513360	1513602	-1 hypothetical protein
1431249	1529242	97993	EFH93800.1	HMPREF0391_10168	1513574	1515505	-1 putative DNA-directed DNA polymerase
1431249	1529242	97993	EFH93801.1	HMPREF0391_10169	1515480	1515680	-1 hypothetical protein
1431249	1529242	97993	EFH93802.1	HMPREF0391_10170	1515690	1516232	-1 hypothetical protein
1431249	1529242	97993	EFH93803.1	HMPREF0391_10171	1516222	1517346	-1 hypothetical protein
1431249	1529242	97993	EFH93804.1	HMPREF0391_10172	1517346	1517621	-1 hypothetical protein
1431249	1529242	97993	EFH93805.1	HMPREF0391_10173	1517584	1517748	-1 hypothetical protein
1431249	1529242	97993	EFH93806.1	HMPREF0391_10174	1517739	1517909	-1 hypothetical protein
1431249	1529242	97993	EFH93807.1	HMPREF0391_10175	1517943	1518461	-1 RNA polymerase sigma factor, sigma-70 family
1431249	1529242	97993	EFH93808.1	HMPREF0391_10176	1518796	1518960	-1 hypothetical protein
1431249	1529242	97993	EFH93809.1	HMPREF0391_10177	1519033	1519818	-1 hypothetical protein
1431249	1529242	97993	EFH93810.1	HMPREF0391_10178	1519821	1520192	-1 DNA-binding helix-turn-helix protein
1431249	1529242	97993	EFH93811.1	HMPREF0391_10179	1520443	1521657	-1 23S rRNA (uracil-5-)-methyltransferase RumA
1431249	1529242	97993	EFH93812.1	HMPREF0391_10180	1521740	1523536	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93813.1	HMPREF0391_10181	1523529	1525289	-1 ABC transporter, ATP-binding protein
1431249	1529242	97993	EFH93814.1	HMPREF0391_10182	1525264	1525740	-1 transcriptional regulator, MarR family
1431249	1529242	97993	EFH93815.1	HMPREF0391_10183	1525745	1525873	-1 hypothetical protein
1431249	1529242	97993	EFH93816.1	HMPREF0391_10184	1525897	1527198	-1 thiamine biosynthesis protein ThiC
1431249	1529242	97993	EFH93817.1	HMPREF0391_10185	1527379	1528293	-1 molybdenum cofactor biosynthesis protein C
1431249	1529242	97993	EFH93818.1	HMPREF0391_10186	1528295	1529242	-1 molybdenum cofactor biosynthesis protein A
1453710	1469475	15765	EFH93730.1	HMPREF0391_10098	1453710	1455173	-1 ABC transporter, ATP-binding protein
1453710	1469475	15765	EFH93731.1	HMPREF0391_10099	1455175	1455846	-1 cobalt transport protein
1453710	1469475	15765	EFH93732.1	HMPREF0391_10100	1455843	1456433	-1 conserved hypothetical protein TIGR02185
1453710	1469475	15765	EFH93733.1	HMPREF0391_10101	1456500	1457477	-1 transcriptional regulator, AraC family
1453710	1469475	15765	EFH93734.1	HMPREF0391_10102	1457487	1458089	-1 transcriptional regulator, TetR family
1453710	1469475	15765	EFH93735.1	HMPREF0391_10103	1458205	1458381	-1 hypothetical protein
1453710	1469475	15765	EFH93736.1	HMPREF0391_10104	1458528	1458791	1 hypothetical protein
1453710	1469475	15765	EFH93737.1	HMPREF0391_10105	1459309	1459572	-1 hypothetical protein
1453710	1469475	15765	EFH93738.1	HMPREF0391_10106	1459749	1460726	-1 caspase domain protein
1453710	1469475	15765	EFH93739.1	HMPREF0391_10107	1460746	1461123	-1 hypothetical protein
1453710	1469475	15765	EFH93740.1	HMPREF0391_10108	1461126	1461293	-1 hypothetical protein
1453710	1469475	15765	EFH93741.1	HMPREF0391_10109	1461517	1461984	-1 hypothetical protein
1453710	1469475	15765	EFH93742.1	HMPREF0391_10110	1462046	1462837	-1 CAAX amino terminal protease family protein
1453710	1469475	15765	EFH93743.1	HMPREF0391_10111	1463678	1464328	-1 hypothetical protein
1453710	1469475	15765	EFH93744.1	HMPREF0391_10112	1464635	1465384	-1 hypothetical protein
1453710	1469475	15765	EFH93745.1	HMPREF0391_10113	1465957	1467390	-1 hypothetical protein
1453710	1469475	15765	EFH93746.1	HMPREF0391_10114	1467431	1467751	-1 hypothetical protein

1453710	1469475	15765 EFH93747.1	HMPREF0391_10115	1467931	1468203	-1 hypothetical protein
1453710	1469475	15765 EFH93748.1	HMPREF0391_10116	1468489	1469475	1 integrase core domain protein
1570342	1579874	9532 EFH93858.1	HMPREF0391_10226	1570342	1571268	1 hypothetical protein
1570342	1579874	9532 EFH93859.1	HMPREF0391_10227	1571298	1571957	1 hypothetical protein
1570342	1579874	9532 EFH93860.1	HMPREF0391_10228	1572230	1572361	1 hypothetical protein
1570342	1579874	9532 EFH93861.1	HMPREF0391_10229	1572354	1573454	1 transposase
1570342	1579874	9532 EFH93862.1	HMPREF0391_10230	1573710	1573952	1 prevent-host-death family protein
1570342	1579874	9532 EFH93863.1	HMPREF0391_10231	1574033	1575247	1 transposase, Mutator family
1570342	1579874	9532 EFH93864.1	HMPREF0391_10232	1576090	1576665	-1 Fic family protein
1570342	1579874	9532 EFH93865.1	HMPREF0391_10233	1577843	1578577	-1 hydrolase, carbon-nitrogen family
1570342	1579874	9532 EFH93866.1	HMPREF0391_10234	1578577	1579080	-1 hypothetical protein
1570342	1579874	9532 EFH93867.1	HMPREF0391_10235	1579233	1579874	1 channel protein, hemolysin III family
1806496	1818737	12241 EFH94054.1	HMPREF0391_10422	1806496	1806795	-1 hypothetical protein
1806496	1818737	12241 EFH94055.1	HMPREF0391_10423	1807324	1807638	1 hypothetical protein
1806496	1818737	12241 EFH94056.1	HMPREF0391_10424	1807654	1808040	1 hypothetical protein
1806496	1818737	12241 EFH94057.1	HMPREF0391_10425	1808069	1809454	1 FtsK/SpoIIIE family protein
1806496	1818737	12241 EFH94058.1	HMPREF0391_10426	1809457	1809609	1 hypothetical protein
1806496	1818737	12241 EFH94059.1	HMPREF0391_10427	1809632	1810837	1 DNA-binding helix-turn-helix protein
1806496	1818737	12241 EFH94060.1	HMPREF0391_10428	1810880	1811101	1 hypothetical protein
1806496	1818737	12241 EFH94061.1	HMPREF0391_10429	1811218	1811715	1 antirestriction protein ArdA
1806496	1818737	12241 EFH94062.1	HMPREF0391_10430	1811690	1812196	1 hypothetical protein
1806496	1818737	12241 EFH94063.1	HMPREF0391_10431	1812180	1814627	1 hypothetical protein
1806496	1818737	12241 EFH94064.1	HMPREF0391_10432	1814630	1816807	1 hypothetical protein
1806496	1818737	12241 EFH94065.1	HMPREF0391_10433	1816804	1817805	1 NlpC/P60 family protein
1806496	1818737	12241 EFH94066.1	HMPREF0391_10434	1817802	1818737	1 hypothetical protein
1888259	1904566	16307 EFH94139.1	HMPREF0391_10507	1888259	1888393	-1 hypothetical protein
1888259	1904566	16307 EFH94140.1	HMPREF0391_10508	1889426	1889770	-1 hypothetical protein
1888259	1904566	16307 EFH94141.1	HMPREF0391_10509	1889757	1891727	-1 oligopeptide transporter, OPT family
1888259	1904566	16307 EFH94142.1	HMPREF0391_10510	1891902	1892507	1 hypothetical protein
1888259	1904566	16307 EFH94143.1	HMPREF0391_10511	1892871	1893791	-1 transposase, Mutator family
1888259	1904566	16307 EFH94144.1	HMPREF0391_10512	1893839	1894084	-1 hypothetical protein
1888259	1904566	16307 EFH94145.1	HMPREF0391_10513	1894683	1895966	-1 hypothetical protein
1888259	1904566	16307 EFH94146.1	HMPREF0391_10514	1895969	1897267	-1 hypothetical protein
1888259	1904566	16307 EFH94147.1	HMPREF0391_10515	1897280	1898029	-1 hypothetical protein
1888259	1904566	16307 EFH94148.1	HMPREF0391_10516	1898022	1898333	-1 hypothetical protein
1888259	1904566	16307 EFH94149.1	HMPREF0391_10517	1898350	1900155	-1 hypothetical protein
1888259	1904566	16307 EFH94150.1	HMPREF0391_10518	1900143	1900892	-1 hypothetical protein
1888259	1904566	16307 EFH94151.1	HMPREF0391_10519	1900918	1902234	-1 hypothetical protein
1888259	1904566	16307 EFH94152.1	HMPREF0391_10520	1902530	1904566	1 hypothetical protein
1892871	1900892	8021 EFH94143.1	HMPREF0391_10511	1892871	1893791	-1 transposase, Mutator family
1892871	1900892	8021 EFH94144.1	HMPREF0391_10512	1893839	1894084	-1 hypothetical protein
1892871	1900892	8021 EFH94145.1	HMPREF0391_10513	1894683	1895966	-1 hypothetical protein
1892871	1900892	8021 EFH94146.1	HMPREF0391_10514	1895969	1897267	-1 hypothetical protein
1892871	1900892	8021 EFH94147.1	HMPREF0391_10515	1897280	1898029	-1 hypothetical protein
1892871	1900892	8021 EFH94148.1	HMPREF0391_10516	1898022	1898333	-1 hypothetical protein
1892871	1900892	8021 EFH94149.1	HMPREF0391_10517	1898350	1900155	-1 hypothetical protein
1892871	1900892	8021 EFH94150.1	HMPREF0391_10518	1900143	1900892	-1 hypothetical protein
1904633	1910011	5378 EFH94153.1	HMPREF0391_10521	1904633	1906318	1 hypothetical protein
1904633	1910011	5378 EFH94154.1	HMPREF0391_10522	1906315	1907400	1 hypothetical protein
1904633	1910011	5378 EFH94155.1	HMPREF0391_10523	1907437	1908018	1 hypothetical protein
1904633	1910011	5378 EFH94156.1	HMPREF0391_10524	1909789	1910011	-1 hypothetical protein

Table S3L: Predicted genomic islands in the genome of *F. magna* ATCC29328

Shown are genes of genomic islands predicted by IslandViewer4

Island start	Island end	Length	Gene name	Locus	Gene start	Gene end	Strand	Product
777457	788164	10707	WP_002838404.1	FMG_RS03870	777457	778155	1	DNA-binding response regulator
777457	788164	10707	WP_012290581.1	FMG_RS03875	778196	778780	1	peptidyl-prolyl cis-trans isomerase
777457	788164	10707	WP_012290582.1	FMG_RS03880	778782	779414	1	thymidine kinase
777457	788164	10707	WP_002841719.1	FMG_RS03885	779436	779906	-1	S-ribosylhomocysteine lyase
777457	788164	10707	WP_012290583.1	FMG_RS03890	779915	781018	-1	rod shape-determining protein RodA
777457	788164	10707	WP_002841740.1	FMG_RS03895	781093	781926	1	endonuclease
777457	788164	10707	WP_002838210.1	FMG_RS03900	781907	782533	1	endonuclease III
777457	788164	10707	WP_002841720.1	FMG_RS03905	782601	783521	1	aspartate carbamoyltransferase aspartate carbamoyltransferase regulatory
777457	788164	10707	WP_012290584.1	FMG_RS03910	783521	783949	1	subunit
777457	788164	10707	WP_012290585.1	FMG_RS03915	783949	785145	1	dihydroorotase
777457	788164	10707	WP_012290586.1	FMG_RS03920	785132	785983	1	orotidine 5'-phosphate decarboxylase dihydroorotate dehydrogenase electron transfer
777457	788164	10707	WP_012290587.1	FMG_RS03925	785976	786692	1	subunit
777457	788164	10707	WP_012290588.1	FMG_RS03930	786685	787581	1	dihydroorotate dehydrogenase
777457	788164	10707	WP_012290589.1	FMG_RS03935	787592	788164	1	orotate phosphoribosyltransferase
800334	806465	6131	WP_012290598.1	FMG_RS03995	800334	802022	1	hypothetical protein bifunctional ([pyruvate, phosphate dikinase] phosphate) phosphotransferase/[pyruvate,
800334	806465	6131	WP_002838113.1	FMG_RS04000	802033	802830	1	phosphate diki
800334	806465	6131	WP_012290599.1	FMG_RS04005	802914	804347	1	serine/threonine protein kinase
800334	806465	6131	WP_012290600.1	FMG_RS04010	804349	805023	1	protein phosphatase tRNA (N6-isopentenyl adenosine(37)-C2)-
800334	806465	6131	WP_002838381.1	FMG_RS04015	805080	806465	1	methylthiotransferase MiaB
991864	1059050	67186	WP_012290711.1	FMG_RS04885	991864	993141	-1	ABC transporter permease
991864	1059050	67186	WP_012290712.1	FMG_RS04890	993339	993626	-1	cupin
991864	1059050	67186	WP_012290713.1	FMG_RS04895	993694	994266	-1	uracil-DNA glycosylase
991864	1059050	67186	WP_012290714.1	FMG_RS04900	994598	994882	-1	hypothetical protein
991864	1059050	67186		FMG_RS04905	994940	995686	-1	ABC transporter
991864	1059050	67186		FMG_RS04910	995673	996392	-1	iron ABC transporter permease
991864	1059050	67186	WP_002840481.1	FMG_RS04915	996452	997210	-1	methyltransferase
991864	1059050	67186	WP_002837989.1	FMG_RS04920	997305	997898	1	hypothetical protein
991864	1059050	67186	WP_012290720.1	FMG_RS04925	998668	998937	1	transposase
991864	1059050	67186	WP_041250650.1	FMG_RS04930	999050	999847	1	transposase
991864	1059050	67186	WP_002840495.1	FMG_RS04935	1000078	1001280	-1	ABC transporter substrate-binding protein
991864	1059050	67186	WP_012290722.1	FMG_RS04940	1001280	1001819	-1	FMN-binding domain-containing protein
991864	1059050	67186	WP_012290723.1	FMG_RS04945	1001925	1002371	-1	hypothetical protein
991864	1059050	67186	WP_012290724.1	FMG_RS04950	1002528	1003763	-1	site-specific integrase
991864	1059050	67186	WP_009345237.1	FMG_RS04955	1003841	1004050	-1	transposase
991864	1059050	67186	WP_009345230.1	FMG_RS04960	1004486	1004896	-1	sigma factor
991864	1059050	67186	WP_041250601.1	FMG_RS04965	1005216	1006565	-1	multidrug transporter MatE
991864	1059050	67186	WP_012290726.1	FMG_RS04970	1006602	1008335	-1	multidrug ABC transporter ATP-binding protein
991864	1059050	67186	WP_012290727.1	FMG_RS04975	1008332	1010074	-1	ABC transporter ATP-binding protein
991864	1059050	67186	WP_012290728.1	FMG_RS04980	1010110	1011501	-1	ABC transporter ATP-binding protein
991864	1059050	67186	WP_012290729.1	FMG_RS04985	1011494	1012195	-1	ABC transporter permease
991864	1059050	67186	WP_002836642.1	FMG_RS04990	1012220	1012801	-1	membrane protein
991864	1059050	67186	WP_012290730.1	FMG_RS04995	1012819	1013412	-1	TetR family transcriptional regulator
991864	1059050	67186	WP_012290731.1	FMG_RS05000	1013743	1014099	1	conjugal transfer protein
991864	1059050	67186	WP_041250602.1	FMG_RS05005	1014101	1015432	1	endonuclease
991864	1059050	67186	WP_012290734.1	FMG_RS05010	1015796	1018231	-1	ABC transporter permease
991864	1059050	67186	WP_012290735.1	FMG_RS05015	1018224	1018904	-1	peptide ABC transporter ATP-binding protein
991864	1059050	67186	WP_012290736.1	FMG_RS05020	1018957	1019817	-1	two-component sensor histidine kinase
991864	1059050	67186	WP_012290737.1	FMG_RS05025	1019819	1020469	-1	DNA-binding response regulator
991864	1059050	67186	WP_012290738.1	FMG_RS05030	1020651	1021754	-1	ATP-dependent DNA helicase
991864	1059050	67186	WP_012290739.1	FMG_RS05035	1021744	1023372	-1	DNA recombinase
991864	1059050	67186	WP_012290740.1	FMG_RS05040	1023395	1023601	-1	transcriptional regulator
991864	1059050	67186	WP_012290741.1	FMG_RS05045	1023780	1024436	-1	hypothetical protein
991864	1059050	67186	WP_012290742.1	FMG_RS05050	1024480	1032123	-1	DNA helicase
991864	1059050	67186	WP_002836656.1	FMG_RS05055	1032206	1034419	-1	hypothetical protein
991864	1059050	67186	WP_002836657.1	FMG_RS05060	1034455	1035417	-1	type II restriction endonuclease subunit M
991864	1059050	67186	WP_012290743.1	FMG_RS05065	1035410	1037131	-1	DNA topoisomerase III
991864	1059050	67186	WP_002836659.1	FMG_RS05070	1037195	1038061	-1	bacteriocin
991864	1059050	67186	WP_004817210.1	FMG_RS05075	1038076	1040427	-1	copper amine oxidase
991864	1059050	67186	WP_001080402.1	FMG_RS05080	1040414	1040653	-1	hypothetical protein
991864	1059050	67186	WP_012290744.1	FMG_RS05085	1040668	1043247	-1	hypothetical protein
991864	1059050	67186	WP_041250652.1	FMG_RS05090	1043255	1045498	-1	conjugal transfer protein TraE
991864	1059050	67186	WP_008902108.1	FMG_RS05095	1045569	1045979	-1	transposase
991864	1059050	67186	WP_002838520.1	FMG_RS05100	1045981	1046271	-1	hypothetical protein
991864	1059050	67186	WP_000466919.1	FMG_RS05105	1046281	1047144	-1	hypothetical protein
991864	1059050	67186	WP_000394203.1	FMG_RS05110	1047155	1047370	-1	conjugal transfer protein
991864	1059050	67186	WP_002839977.1	FMG_RS05115	1047372	1047683	-1	hypothetical protein
991864	1059050	67186	WP_001105422.1	FMG_RS05120	1047879	1049348	-1	hypothetical protein
991864	1059050	67186	WP_001258251.1	FMG_RS05125	1049366	1049902	-1	hypothetical protein
991864	1059050	67186	WP_002839985.1	FMG_RS05130	1049964	1050683	-1	conjugal transfer protein TraG
991864	1059050	67186	WP_002838479.1	FMG_RS05135	1050785	1050970	-1	transposase
991864	1059050	67186	WP_002838522.1	FMG_RS05140	1051072	1052061	-1	hypothetical protein
991864	1059050	67186	WP_012290746.1	FMG_RS05145	1052135	1052458	-1	hypothetical protein
991864	1059050	67186	WP_012290747.1	FMG_RS05150	1052641	1053354	-1	hypothetical protein
991864	1059050	67186	WP_012290748.1	FMG_RS05155	1053436	1055076	-1	nickase
991864	1059050	67186	WP_012290749.1	FMG_RS05160	1055391	1055765	-1	hypothetical protein
991864	1059050	67186	WP_002416386.1	FMG_RS05165	1055852	1056268	-1	hypothetical protein
991864	1059050	67186	WP_002416388.1	FMG_RS05170	1056555	1056788	-1	hypothetical protein
991864	1059050	67186	WP_012290750.1	FMG_RS05175	1056801	1058822	-1	ferrous iron transporter B
991864	1059050	67186	WP_012290751.1	FMG_RS05180	1058826	1059050	-1	iron transporter FeoA

991864	1059050	67186 WP_012290752.1	FMG_RS05185	1059037	1060785	-1 multidrug ABC transporter
994598	1001280	6682 WP_012290714.1	FMG_RS04900	994598	994882	-1 hypothetical protein
994598	1001280	6682	FMG_RS04905	994940	995686	-1 ABC transporter
994598	1001280	6682	FMG_RS04910	995673	996392	-1 iron ABC transporter permease
994598	1001280	6682 WP_002840481.1	FMG_RS04915	996452	997210	-1 methyltransferase
994598	1001280	6682 WP_002837989.1	FMG_RS04920	997305	997898	1 hypothetical protein
994598	1001280	6682 WP_012290720.1	FMG_RS04925	998668	998937	1 transposase
994598	1001280	6682 WP_041250650.1	FMG_RS04930	999050	999847	1 transposase
994598	1001280	6682 WP_002840495.1	FMG_RS04935	1000078	1001280	-1 ABC transporter substrate-binding protein
1018957	1024436	5479 WP_012290736.1	FMG_RS05020	1018957	1019817	-1 two-component sensor histidine kinase
1018957	1024436	5479 WP_012290737.1	FMG_RS05025	1019819	1020469	-1 DNA-binding response regulator
1018957	1024436	5479 WP_012290738.1	FMG_RS05030	1020651	1021754	-1 ATP-dependent DNA helicase
1018957	1024436	5479 WP_012290739.1	FMG_RS05035	1021744	1023372	-1 DNA recombinase
1018957	1024436	5479 WP_012290740.1	FMG_RS05040	1023395	1023601	-1 transcriptional regulator
1018957	1024436	5479 WP_012290741.1	FMG_RS05045	1023780	1024436	-1 hypothetical protein
1538370	1546110	7740 WP_012291054.1	FMG_RS07340	1538370	1539119	-1 phosphorylase
1538370	1546110	7740 WP_012291055.1	FMG_RS07345	1539249	1540850	-1 macrolide ABC transporter ATP-binding protein
1538370	1546110	7740 WP_012291056.1	FMG_RS07350	1541255	1541869	-1 hypothetical protein
1538370	1546110	7740 WP_012291057.1	FMG_RS07355	1542076	1543440	-1 ABC transporter ATP-binding protein
1538370	1546110	7740 WP_012291058.1	FMG_RS07360	1543428	1544123	-1 cobalt ABC transporter permease
1538370	1546110	7740 WP_012291059.1	FMG_RS07365	1544123	1544707	-1 membrane protein
1538370	1546110	7740 WP_041250667.1	FMG_RS07370	1544767	1546110	-1 MATE family efflux transporter
1553812	1571194	17382 WP_002836976.1	FMG_RS07405	1553812	1554507	1 DNA-binding response regulator
1553812	1571194	17382 WP_012291067.1	FMG_RS07410	1554509	1555804	1 two-component sensor histidine kinase
1553812	1571194	17382 WP_041250623.1	FMG_RS07415	1556528	1556734	-1 hypothetical protein
1553812	1571194	17382 WP_041250624.1	FMG_RS07420	1557057	1557284	-1 hypothetical protein
1553812	1571194	17382 WP_012291068.1	FMG_RS07425	1557281	1559017	-1 multidrug ABC transporter ATP-binding protein
1553812	1571194	17382 WP_012291069.1	FMG_RS07430	1559010	1560731	-1 ABC transporter ATP-binding protein
1553812	1571194	17382 WP_012291070.1	FMG_RS07435	1560769	1562121	-1 MATE family efflux transporter
1553812	1571194	17382 WP_012291071.1	FMG_RS07440	1562134	1563582	-1 ABC transporter
1553812	1571194	17382 WP_012291072.1	FMG_RS07445	1563579	1564259	-1 ABC transporter permease
1553812	1571194	17382 WP_005956598.1	FMG_RS07450	1564259	1564837	-1 hypothetical protein
1553812	1571194	17382 WP_041250625.1	FMG_RS07455	1564889	1565461	-1 TetR family transcriptional regulator
1553812	1571194	17382 WP_012291075.1	FMG_RS07460	1565754	1566110	1 conjugal transfer protein
1553812	1571194	17382 WP_004838629.1	FMG_RS07470	1566622	1568316	-1 hypothetical protein
1553812	1571194	17382 WP_041250668.1	FMG_RS07475	1568316	1569320	-1 hypothetical protein
1553812	1571194	17382	FMG_RS07480	1569768	1570610	-1 abortive phage infection protein
1553812	1571194	17382 WP_012291079.1	FMG_RS07485	1570607	1571194	-1 transcriptional regulator

Table S4A: Blast results showing protein L homologs in 12 *Fingoldia* genomes.

As query, protein L from strain 312 (locus ID: M86697) was taken. As Blast cutoff: e-value < e-10

Species	strain	gene	Prokka annotation	score	e-value
<i>"F. nericia"</i>	ATCC53516	12510	Peptostreptococcal albumin-binding protein precursor	1099	0.0
<i>"F. nericia"</i>	T160124	15430	Peptostreptococcal albumin-binding protein precursor	357	e-112
<i>"F. nericia"</i>	CCUG54800	17560	Peptostreptococcal albumin-binding protein precursor	334	e-104
<i>"F. nericia"</i>	12T273	18110	Peptostreptococcal albumin-binding protein precursor	286	7e-85
<i>"F. nericia"</i>	12T306	16410	Peptostreptococcal albumin-binding protein precursor	218	3e-59
<i>"F. nericia"</i>	CCUG54800	10280	IgA FC receptor precursor	90	1e-18
<i>"F. nericia"</i>	12T272	07960	IgA FC receptor precursor	89	3e-18
<i>"F. nericia"</i>	T160124	15840	Surface protein G precursor	71	1e-12
<i>F. magna</i>	08T492	16540	Peptostreptococcal albumin-binding protein precursor	69	1e-12
<i>F. magna</i>	07T609	13520	Extracellular matrix-binding protein ebh precursor	68	1e-11
<i>"F. nericia"</i>	12T273	17160	Platelet binding protein GspB precursor	65	5e-11
<i>"F. nericia"</i>	CCUG54800	15040	Rib/alpha-like repeat protein	65	5e-11

Table S4B: Blast results showing peptostreptococcal albumin-binding protein (PAB) homologs in 12 *Fingoldia* genomes. As query, the PAB protein of strain ALB8 (locus ID: X77864) was taken. As Blast cutoff: e-value < e-10.

Species	strain	gene	Prokka annotation	score	e-value
<i>F. magna</i>	08T492	16540	Peptostreptococcal albumin-binding protein precursor	149	1e-40
<i>F. magna</i>	07T609	15520	Peptostreptococcal albumin-binding protein precursor	140	1e-38
<i>"F. nericia"</i>	12T306	16410	Peptostreptococcal albumin-binding protein precursor	123	4e-30
<i>"F. nericia"</i>	T160124	15430	Peptostreptococcal albumin-binding protein precursor	99	8e-23
<i>"F. nericia"</i>	CCUG54800	17560	Peptostreptococcal albumin-binding protein precursor	99	1e-22
<i>"F. nericia"</i>	12T273	18110	Peptostreptococcal albumin-binding protein precursor	65	1e-11
<i>"F. nericia"</i>	CCUG54800	17400	Internalin-A precursor	64	6e-11

Table S4C: Blast results showing GA-module containing proteins in 12 *Fingoldia* genomes. As query, the GA module of the PAB protein of strain ALB8 (locus ID: X77864) was taken. As Blast cutoff: e-value < e-10.

Species	strain	gene	Prokka annotation	score	e-value
<i>F. magna</i>	07T609	15520	Peptostreptococcal albumin-binding protein precursor	78	9e-20
<i>F. magna</i>	08T492	16540	Peptostreptococcal albumin-binding protein precursor	78	5e-19
" <i>F. nericia</i> "	T160124	15430	Peptostreptococcal albumin-binding protein precursor	77	2e-18
" <i>F. nericia</i> "	CCUG54800	17560	Peptostreptococcal albumin-binding protein precursor	74	4e-17
" <i>F. nericia</i> "	12T306	16410	Peptostreptococcal albumin-binding protein precursor	74	5e-17
" <i>F. nericia</i> "	CCUG54800	17400	Internalin-A precursor	60	3e-12
" <i>F. nericia</i> "	12T273	18110	Peptostreptococcal albumin-binding protein precursor	59	6e-12
" <i>F. nericia</i> "	12T306	16250	Internalin-A precursor	58	1e-11
" <i>F. nericia</i> "	09T494	18050	N-acetylmuramoyl-L-alanine amidase LytC	58	2e-11
" <i>F. nericia</i> "	12T273	04210	N-acetylmuramoyl-L-alanine amidase LytC	58	2e-11
<i>F. magna</i>	07T609	15360	Internalin-A precursor	58	2e-11
" <i>F. nericia</i> "	ATCC53516	09600	N-acetylmuramoyl-L-alanine amidase LytC	58	2e-11
" <i>F. nericia</i> "	T160124	15270	Internalin-A precursor	57	2e-11
<i>F. magna</i>	08T492	16380	N-acetylmuramoyl-L-alanine amidase LytC	57	3e-11
" <i>F. nericia</i> "	12T272	15560	N-acetylmuramoyl-L-alanine amidase LytC	56	6e-11
<i>F. magna</i>	ATCC29328	15850	N-acetylmuramoyl-L-alanine amidase LytC	56	8e-11

Table S4D: Blast results showing SufA homologs in 12 *Fingoldia* genomes. As query, SufA of strain ALB8 (locus ID: DQ679960) was taken. As Blast cutoff: e-value < e-10.

Species	strain	gene	Prokka annotation	score	e-value
<i>F. magna</i>	08T492	17920	Pll-type proteinase precursor	1971	0.0
" <i>F. nericia</i> "	12T273	01050	Plll-type proteinase precursor	1865	0.0
" <i>F. nericia</i> "	T160124	16880	Plll-type proteinase precursor	1827	0.0
" <i>F. nericia</i> "	ATCC53516	10860	Pll-type proteinase precursor	1823	0.0
" <i>F. nericia</i> "	T151023	00620	Pll-type proteinase precursor	1779	0.0
" <i>F. nericia</i> "	12T306	00480	Pll-type proteinase precursor	1771	0.0
" <i>F. nericia</i> "	09T494	01650	Pll-type proteinase precursor	1747	0.0
" <i>F. nericia</i> "	12T272	18030	Plll-type proteinase precursor	1725	0.0
<i>F. magna</i>	ATCC29328	00370	Pll-type proteinase precursor	1678	0.0
<i>F. magna</i>	09T408	03220	Pll-type proteinase precursor	157	5e-39
" <i>F. nericia</i> "	09T494	03870	Plll-type proteinase precursor	156	1e-38
<i>F. magna</i>	07T609	03110	Pll-type proteinase precursor	154	9e-38
" <i>F. nericia</i> "	12T273	06640	Pll-type proteinase precursor	153	1e-37
" <i>F. nericia</i> "	12T306	04830	Pll-type proteinase precursor	153	1e-37
" <i>F. nericia</i> "	12T272	01600	Pll-type proteinase precursor	153	1e-37
<i>F. magna</i>	08T492	02790	Pll-type proteinase precursor	153	1e-37
" <i>F. nericia</i> "	CCUG54800	04020	Pll-type proteinase precursor	153	2e-37
" <i>F. nericia</i> "	ATCC53516	07750	Pll-type proteinase precursor	146	2e-35
" <i>F. nericia</i> "	T160124	03150	Pll-type proteinase precursor	146	2e-35

Table S4E: Blast results showing FAF (*F. magna* adhesion factor) homologs in 12 *Fingoldia* genomes. As query, the FAF protein of strain ALB8 (locus ID: AAO46090) was taken. As Blast cutoff: e-value < e-10.

Species	strain	gene	Prokka annotation	score	e-value
<i>F. magna</i>	08T492	14650	Cna protein B-type domain protein	471	e-158
<i>F. magna</i>	ATCC29328	14170	Cna protein B-type domain protein	467	e-156
" <i>F. nericia</i> "	CCUG54800	15060	Cna protein B-type domain protein	451	e-150
" <i>F. nericia</i> "	T160124	12940	Cna protein B-type domain protein	436	e-144
<i>F. magna</i>	07T609	13570	Cna protein B-type domain protein	399	e-130
" <i>F. nericia</i> "	ATCC53516	00150	Cna protein B-type domain protein	314	9e-98
" <i>F. nericia</i> "	12T273	17180	Cna protein B-type domain protein	306	2e-94
" <i>F. nericia</i> "	T151023	14140	Cna protein B-type domain protein	239	6e-71
" <i>F. nericia</i> "	12T272	13990	Cna protein B-type domain protein	117	3e-29
" <i>F. nericia</i> "	12T272	14000	Hypothetical protein	111	4e-27
" <i>F. nericia</i> "	T151023	14150	Hypothetical protein	75	1e-15

Table S5: *Finogoldia* sp. strains tested in the RAPID ANA II system

strain	URE	BLTS	aARA	ONPG	aGLU	BGLU	aGAL	aFUC	NAG	PO4	LGY	GLY	PRO	PAL	ARG	SER	PYR	IND
<i>F. magna</i> 07T609	÷	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	÷*	+	+	+	+	÷
<i>F. magna</i> 08T492	÷	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	÷*	+	+	+	+	÷
<i>F. magna</i> 09T408	÷	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " 09T494	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " 12T272	÷	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " 12T273	÷	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " 12T306	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " CCUG54800	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " 15T1023	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	+	÷*	+	+	+	+	÷
" <i>F. nericia</i> " 16T0124	÷	÷	÷	÷	÷	÷	÷	÷	÷	+	+	+	÷*	+	+	+	+	÷

* very light pink

Reaction	Substrate
URE:	Urea
BLTS:	p-Nitrophenyl-β, D-disaccharide
aARA:	p-Nitrophenyl-α, L-arabinoside
ONPG:	σ-Nitrophenyl-β, D-galactoside
aGLU:	p-Nitrophenyl-α, D-glucoside
BGLU:	p-Nitrophenyl-β, D-glucoside
aGAL:	p-Nitrophenyl-α, D-galactoside
aFUC:	p-Nitrophenyl-α, L-fucoside
NAG:	p-Nitrophenyl-n-acetyl-β, D-glucosaminide
PO4:	p-Nitrophenylphosphate
LGY:	Leucyl-glycine-β-naphthylamide
GLY:	Glycine-β-naphthylamide
PRO:	Proline-β-naphthylamide
PAL:	Phenylalanine-β-naphthylamide
ARG:	Arginine-β-naphthylamide
SER:	Serine-β-naphthylamide
PYR:	Pyrrolidonyl-β-naphthylamide
IND:	Tryptophane