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SHORT COMMUNICATION

Comparative genomic analyses reveal a lack of a substantial signature of host adaptation in *Rhodococcus equi* (“*Prescottella equi*”)

Vartul Sangal[1,2], Amanda L. Jones[2], Michael Goodfellow[3], Iain C. Sutcliffe[2] and Paul A. Hoskisson[1]

[1]Strathclyde Institute of Pharmacy and Biomedical Sciences, University of Strathclyde, 161 Cathedral Street, Glasgow G4 0RE, UK

[2]Faculty of Health and Life Sciences, Northumbria University, Newcastle upon Tyne NE1 8ST, UK

[3]School of Biology, University of Newcastle, Newcastle upon Tyne NE1 7RU, UK

Correspondence: Paul A. Hoskisson, Strathclyde Institute of Pharmacy and Biomedical Sciences, University of Strathclyde, 161 Cathedral Street, Glasgow G4 0RE, UK

Tel.: +44 (0)141 548 2819; Fax: +44 (0)141 548 4124; e-mail: paul.hoskisson@strath.ac.uk

Keywords: *Rhodococcus equi*, “*Prescottella equi*”, opportunistic pathogen, genome, metabolic differences

Abstract

Rhodococcus equi ("*Prescottella equi*") is a pathogenic actinomycete primarily infecting horses but has emerged as an opportunistic human pathogen. We have sequenced the genome of the type strain of this species, *R. equi* strain C7^{T}, and compared the genome with that of another foal isolate 103S and of a human isolate ATCC 33707. The *R. equi* strains are closely related to each other and yet distantly related to other rhodococci and *Nocardia brasiliensis*. The comparison of gene contents among *R. equi* strains revealed minor differences that could be associated with host adaptation from foals to humans, including the presence of a *paa* operon in the human isolate which is potentially involved in pathogenesis.

Rhodococcus equi, a Gram-positive coccobacillus that was formerly classified as *Corynebacterium equi*, is primarily a foal pathogen that causes fatal lymphadenitis and ulcerative enteritis in young foals (Prescott, 1991; Giguere, *et al.*, 2011; Vazquez-Boland, *et al.*, 2013). It has recently emerged as an important opportunistic human pathogen causing significant mortality among immunocompromised patients (Kedlaya, *et al.*, 2001; Yamshchikov, *et al.*, 2010) and is also associated with a wide range of other vertebrate hosts and with environmental reservoirs (Prescott, 1991).

In this study, we have sequenced the genome of the *R. equi* Type strain C7^T that was isolated from the lung abscess of a foal in 1922 (Goodfellow & Alderson, 1977). Comparative analyses were performed against the available genomes of *R. equi*, namely against those of strains 103S (Letek, *et al.*, 2010) and ATCC 33707 (Qin, *et al.*, 2010; GenBank Accession numbers NC_014659 and NZ_CM001149, respectively). The *R. equi* C7^T genome was sequenced on a Roche 454 GS-Junior instrument as described previously (Sangal, *et al.*, 2012a; Sangal, *et al.*, 2012b). A total of 172,478 reads with an average read length of 464 bp were assembled into 48 contigs (>200 bp) by GS *de novo* assembler v 2.7. The size of assembly was 5.197 MB with an average of 19 fold coverage. The genome was annotated using the NCBI PGAAP pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and RAST (Aziz, *et al.*, 2008). The draft genome of *R. equi* strain C7^T is estimated to have 5,033 features including 4,978 coding sequences and 55 tRNA genes. This genome has been submitted to GenBank and has the accession number APJC00000000.

The *R. equi* 103S and ATCC 33707 genomes were also annotated using RAST to ensure equivalence of annotation for comparative analyses. The CGView comparative tool analysis (Grant, *et al.*, 2012) revealed a very high conservation of both the nucleotide (Fig. 1A) and the protein sequences (Fig. 1B) among these genomes. Indeed, the genome-wide protein Blast searches, using the SEED Viewer (Aziz, *et al.*, 2012), revealed that only 69, 152 and 187

genes, mostly encoding hypothetical proteins, are specific to strains 103S, C7^T and ATCC 33707, respectively that returned no hits in the other *R. equi* genomes (Supplementary Table 1). Some of these strain specific genes belonged to mobile genetic elements (integrase, transposase and repeats) and only 10-13 genes are predicted to be involved in cellular activities (Supplementary Table 1). Interestingly, strain ATCC 33707 possessed a set of phenylacetate CoA ligase/oxygenase genes (PaaD, F-I, Z) that are absent in the genomes of strains 103S and C7^T. These genes have been implicated in virulence in various pathogens (Law, et al., 2008; Teufel, et al., 2010). Strain ATCC 33707 was isolated from a human abscess and strains 103S and C7^T from equine hosts. Putative PaaE is common to all three isolates and PaaJ and PaaK subunits of strain ATCC 33707 shared ~30% identities with two proteins (PaaD-like protein DUF59 involved in Fe-S cluster assembly and probable phenylacetic acid degradation NADH oxidoreductase PaaE, respectively; data not shown) in the genomes of strains 103S and C7^T. The genes encoding PaaD and PaaZ have been identified on an horizontally acquired region by the Alien Hunter (Vernikos & Parkhill, 2006) and a lack of these genes in equine isolates suggest that *paa* operon was potentially acquired by strain ATCC 33707 which may be associated with pathogenesis in human hosts. Alternatively, the *paa* operon may not be essential for pathogenesis in foals and may have been lost in equine isolates through genome reduction. Clearly, a wider analysis of a larger collection of *R. equi* isolates from humans and foals should be performed to confirm this finding.

Strain 103S shares 42 genes with strain C7^T that are absent from the genome of strain ATCC 33707 and 48 genes with strain ATCC 33707 that are absent from the genome of strain C7^T. Most of these genes encode hypothetical proteins and only 6-12 of these are potentially involved in cellular activities, including nucleotide/nucleoside (especially RNA) metabolism, carbohydrates and sulphur metabolism, and respiration (Supplementary Table 1). A gene encoding NADH-ubiquinone oxidoreductase chain H (fig|685727.5.peg.1900) and one

encoding a glycosyltransferase (fig|685727.5.peg.4060) are common between the genomes of strains 103S and ATCC 33707 but absent in that of strain C7^T. Similarly, two genes involved in sulphur metabolism (fig|685727.5.peg.436, fig|685727.5.peg.1276) are common between the genomes of strains C7^T and 103S but missing from the genome of strain ATCC 33707. Strains C7^T and ATCC 33707 share 84 genes that are absent from the genome of strain 103S, of which 23 are likely involved in a variety of metabolic activities (Supplementary Table 1). In addition, some genes showed poor identity (<50% protein sequence identity) between the different genomes that may also partly contribute to the functional divergence of these strains (data not shown). These variations potentially reflect the minor differences in lifestyle of individual strains. Overall, the two equine isolates and the human isolate share most of their gene content with 109-258 variable genes between strain pairs (Supplementary Table 1). These results are consistent with a recent report suggesting that *R. equi* isolates are very closely related to each other (Vazquez-Boland, *et al.*, 2013).

Single nucleotide polymorphisms (SNPs) were extracted from the genomic alignment of all three strains using Mauve (Darling, et al., 2004) and were annotated using 103S as the reference genome by TRAMS (Reumerman, *et al*., 2013), after excluding the SNPs with missing alleles. There were 49,903 SNPs between the genomes of 103S and C7^T, of which 4,976 were intergenic. These SNPs introduced 28,458 synonymous and 12,804 nonsynonymous changes in the genome of strain C7^T including 21 stop codons (Supplementary Table 2). Nine nonsense SNPs were present in genes encoding hypothetical proteins and two nonsense SNPs were present in a gene encoding a MCE family protein, Mce1F (Supplementary Table 2). A third nonsense SNP terminated another MCE family membrane protein. MCE family proteins were originally implicated as having an important role in the entry and survival of *Mycobacterium tuberculosis* inside host cells (Arruda, *et al*., 1993) although complex phenotypes are associated with *mce* loci (Clark *et al*. 2013) and it is likely that the direct

function of the MCE proteins is in transport of hydrophobic solutes such as sterols (Mohn *et al.* 2008). Other nonsense SNPs resulted in the inactivation of genes involved in putative ABC transporter ATP binding protein, putative esterase, YndJ, pyruvate oxidase, ribosyl nicotinamide transporter (PnuC-like), polyhydroxyalkanoic acid synthase, epoxide hydrolase, acetate kinase and long-chain fatty acid CoA ligase (Supplementary Table 2). It is not clear whether these changes reflect a difference in ability of this strain to utilize different carbon sources or if they have accumulated over long term culture to adapt to an *in vitro* lifestyle.

There are 43,350 SNPs between the genomes of strains 103S and ATCC 33707 that introduced 26,312 synonymous and 10,379 nonsynonymous changes including 19 stop codons (Supplementary Table 2). Seven nonsynonymous changes in genes for an ABC transporter ATP binding protein, a putative esterase, an acetate kinase and four hypothetical proteins are shared with the genome of strain $C7^T$ (Supplementary Table 2). Stop codons also inactivated eight other hypothetical proteins and genes encoding 3-oxoacyl-[acyl-carrier protein] reductase, secreted peptidase and an oxetanocin A resistance protein (Supplementary Table 2). 3-oxoacyl-[acyl-carrier protein] reductase is involved in fatty acid biosynthesis by reducing β-ketoacyl-ACP substrates to beta-hydroxyacyl-ACP products (Lai and Cronan, 2004) but it is unlikely to affect the strain fitness because there are multiple copies of the gene that encode this enzyme in the genome.

The draft genome of strain $C7^T$ is ~153 Kb larger than the chromosome of strain 103S but ~59 Kb smaller than the genome of the ATCC 33707 strain. Strains $C7^T$ and 103S were isolated from foals (Goodfellow & Alderson, 1977; de la Pena-Moctezuma & Prescott, 1995) and strain ATCC 33707 from a human skin abscess (Prescott, 1981). The $C7^T$ strain was isolated in 1922 but isolation dates are unknown for the remaining two strains. The smaller chromosome in strain 103S may represent degradation of the accessory genome that may not be essential for host infection. To identify horizontal gene acquisition by these strains, the

genomes were analysed by Alien Hunter (Vernikos & Parkhill, 2006) which identified 72 acquired regions in 103S (~662 Kb), 144 in C7^T (~1.2 Mb) and 115 in ATCC 33707 (~972 Kb; Supplementary Fig. 1). Most of the imports identified in the genome of strain 103S were also identified in those of strains C7^T and ATCC 33707, including two large regions that were previously described (Letek, *et al.*, 2010). The draft status of the C7^T (48 contigs) and ATCC 33707 (35 contigs) genomes might be largely responsible for identification of higher numbers of imports as some gaps may have divided them into more fragments. However, the total length of imports was also variable though most of the genes were conserved among these strains. The predicted horizontally acquired regions contributed to 376 of the total 582 variable genes identified by genome-wide protein Blast searches (Supplementary Table 1). The host jumps of *Staphylococcus aureus* have been characterized by gain or loss of accessory gene pool via mobile genetic elements (Lowder, *et al*., 2009; Resch, *et al*., 2013) and horizontal gene transfer also appears to have little impact on functional variation among *R. equi* strains (Supplementary Table 1). Some of the imported genes may be involved in virulence in particular hosts, but their functions remain to be characterized as most of them encode hypothetical proteins.

The virulence plasmid, which is essential for virulence in *R. equi* (Takai, *et al.*, 2000; Letek, *et al.*, 2008; Vazquez-Boland, *et al.*, 2013), is missing from strains C7^T and ATCC 33707, both of which are avirulent (Takai, et al., 1985; Prescott, 1991). The virulence plasmid has presumably been lost from these strains at some point during long term culture *in vitro*.

The phylogenetic relatedness of *R. equi* strains was investigated using PhyloPhlAn, a program designed to accurately calculate phylogenies from >400 proteins that can potentially resolve taxonomic groupings (Segata *et al.*, 2013). We also included the genome sequences of *Rhodococcus erythropolis* PR4 (Sekine, *et al.*, 2006; Letek, *et al.*, 2010), *Rhodococcus* strain RHA1 (McLeod, *et al.*, 2006), recently formally classified as *Rhodococcus jostii* (Jones *et al*., 2013a) and *Nocardia brasiliensis* ATCC 700358 (Vera-Cabrera, *et al.*, 2012) and used

Corynebacterium diphtheriae NCTC 03529 (Sangal, *et al.*, 2012b) as the outgroup (Accession numbers NC_012490, CP000431, NC_018681 and AJGI00000000, respectively). All of the *R. equi* strains grouped closely together but distantly to the other rhodococci and *N. brasiliensis* (Fig. 2), which supports our recent proposal of reclassifying *R. equi* into a separate genus as "*Prescottella equi*" (Jones, *et al.*, 2013b; Jones, *et al.*, 2013c). However, the name *Prescottella* has still to be validated, although the taxonomic status of *R. equi* has been questioned (Kämpfer et al. 2013). Further analyses incorporating a wider range of genomes of rhodococci and closely related bacteria are needed to remove any ambiguity over the proposal for the prospective new genus.

In summary, we report the draft genome of the type strain of an important pathogen, *R. equi* strain C7^{T}. *R. equi* strains are phylogenetically closely related and the nucleotide sequence and functional characteristics are highly conserved within this taxon. *R. equi* has recently emerged as an important opportunistic human pathogen but the comparison of equine and human isolates revealed only small differences in the gene content that may be associated with the host adaptation. The whole Genome Shotgun project of *R. equi* strain C7^{T} has been deposited at DDBJ/EMBL/GenBank under the accession no. APJC00000000. The version described in this paper is the first version, APJC01000000.

Acknowledgements

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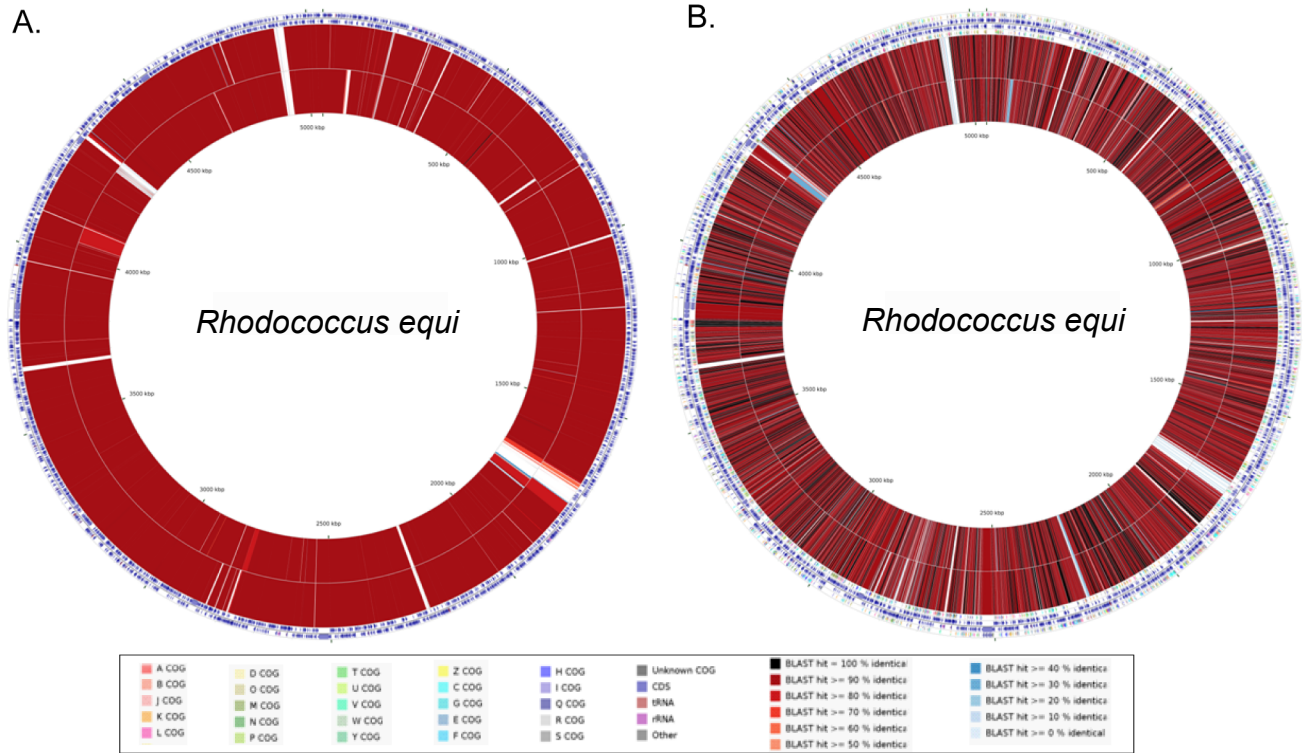
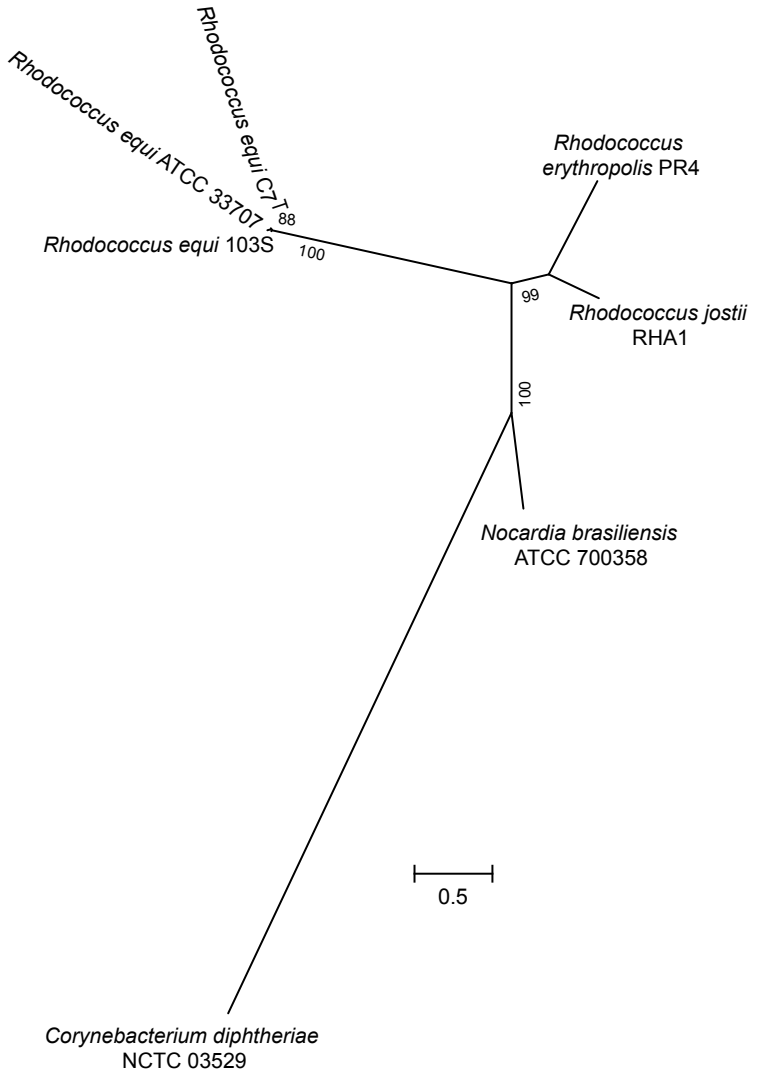
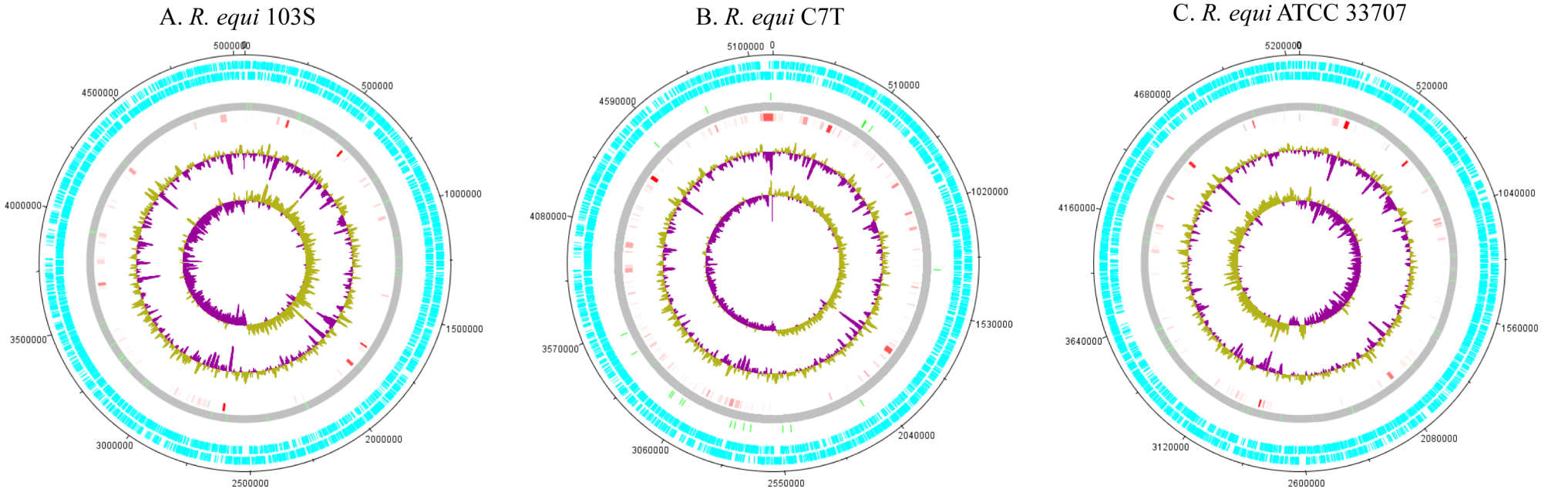
Figure Legends

Figure 1. Genomic blast maps of *R. equi* strain 103S against ATCC 33707 and C7^{T}. (A) DNA blast map, (B) CDS blast map. The colour scale (inset) shows the level of sequence identity with the respective sequences from strain C7^{T} (middle circle) and strain ATCC 33707 (inner circle).

Figure 2. Phylogenetic tree from >400 universal proteins showing the genomic relationship of *R. equi* to representatives of closely related taxa. Scale bar shows mean nucleotide substitutions per site.


A.
B.
Rhodococcus equi
Rhodococcus equi
500 kbp
1000 kbp
1500 kbp
2000 kbp
2500 kbp
3000 kbp
3500 kbp
4000 kbp
4500 kbp
5000 kbp
A COG
B COG
J COG
K COG
L COG
D COG
O COG
M COG
N COG
P COG
T COG
U COG
V COG
W COG
Y COG
Z COG
C COG
G COG
E COG
F COG
H COG
I COG
Q COG
R COG
S COG
Unknown COG
CDS
tRNA
rRNA
Other
BLAST hit = 100 % identica
BLAST hit >= 90 % identica
BLAST hit >= 80 % identica
BLAST hit >= 70 % identica
BLAST hit >= 60 % identica
BLAST hit >= 50 % identica
BLAST hit >= 40 % identica
BLAST hit >= 30 % identica
BLAST hit >= 20 % identica
BLAST hit >= 10 % identica
BLAST hit >= 0 % identical


Rhodococcus equi C7T
Rhodococcus equi ATCC 33707
88
Rhodococcus equi 103S
100
Rhodococcus erythropolis PR4
99
Rhodococcus jostii RHA1
100
Nocardia brasiliensis ATCC 700358
0.5
Corynebacterium diphtheriae NCTC 03529



Supplementary Figure 1. Circular diagrams of *R. equi* chromosomes. Outer two rings are the coding sequences on forward and reverse strands. The genomic islands predicted by AlienHunter are shown in red colour followed by GC plot and GC skew, respectively.

Supplementary Table 1. Differences in the gene content between 103S, ATCC33707 and 103S based on the bidirectional protein blast searches

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	41	fig|685727.5.peg.65 (Q)	fig|525370.5.peg.4858 (97.5)		ATCC33707
hypothetical protein	216	fig|685727.5.peg.69 (Q)	fig|525370.5.peg.4854 (100)		ATCC33707
Hydantoin racemase (EC 5.1.99.-)	252	fig|685727.5.peg.75 (Q)	fig|525370.5.peg.4848 (99.6)		
hypothetical protein	64	fig|685727.5.peg.98 (Q)		fig|1219013.3.peg.93 (98.41)	
hypothetical protein	44	fig|685727.5.peg.101 (Q)	fig|525370.5.peg.4821 (100)		
FIG022958: hypothetical protein	210	fig|685727.5.peg.122 (Q)	fig|525370.5.peg.4977 (100)		
Permease of the drug/metabolite transporter (DMT) superfamily	51	fig|685727.5.peg.242 (Q)		fig|1219013.3.peg.240 (97.73)	
hypothetical protein	69	fig|685727.5.peg.264 (Q)		fig|1219013.3.peg.268 (100)	C7
hypothetical protein	110	fig|685727.5.peg.265 (Q)		fig|1219013.3.peg.269 (98.11)	C7
hypothetical protein	151	fig|685727.5.peg.266 (Q)		fig|1219013.3.peg.270 (98.67)	C7
hypothetical protein	39	fig|685727.5.peg.300 (Q)	fig|525370.5.peg.3529 (100)		
hypothetical protein	56	fig|685727.5.peg.306 (Q)			
hypothetical protein	178	fig|685727.5.peg.313 (Q)			
Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent	778	fig|685727.5.peg.328 (Q)			
hypothetical protein	221	fig|685727.5.peg.329 (Q)			
hypothetical protein	56	fig|685727.5.peg.404 (Q)			
Arylsulfatase (EC 3.1.6.1)	48	fig|685727.5.peg.436 (Q)		fig|1219013.3.peg.462 (100)	
hypothetical protein	42	fig|685727.5.peg.461 (Q)		fig|1219013.3.peg.487 (100)	C7
hypothetical protein	85	fig|685727.5.peg.477 (Q)	fig|525370.5.peg.713 (100)		
hypothetical protein	98	fig|685727.5.peg.484 (Q)		fig|1219013.3.peg.514 (98.97)	
hypothetical protein	42	fig|685727.5.peg.509 (Q)	fig|525370.5.peg.2715 (100)		
hypothetical protein	66	fig|685727.5.peg.558 (Q)			
hypothetical protein	50	fig|685727.5.peg.563 (Q)			
hypothetical protein	71	fig|685727.5.peg.650 (Q)			
hypothetical protein	149	fig|685727.5.peg.759 (Q)		fig|1219013.3.peg.838 (98.65)	
putative ABC transporter ATP binding protein	612	fig|685727.5.peg.791 (Q)		fig|1219013.3.peg.4071 (28.26)	
hypothetical protein	62	fig|685727.5.peg.892 (Q)		fig|1219013.3.peg.987 (90.16)	
hypothetical protein	71	fig|685727.5.peg.921 (Q)	fig|525370.5.peg.2059 (100)		
hypothetical protein	39	fig|685727.5.peg.947 (Q)			
hypothetical protein	40	fig|685727.5.peg.960 (Q)			103S
hypothetical protein	61	fig|685727.5.peg.961 (Q)			103S
Putative membrane protein	182	fig|685727.5.peg.981 (Q)		fig|1219013.3.peg.1085 (98.34)	
hypothetical protein	51	fig|685727.5.peg.1008 (Q)		fig|1219013.3.peg.1113 (100)	
hypothetical protein	43	fig|685727.5.peg.1059 (Q)			
hypothetical protein	202	fig|685727.5.peg.1103 (Q)	fig|525370.5.peg.3802 (97.5)		
hypothetical protein	45	fig|685727.5.peg.1129 (Q)		fig|1219013.3.peg.1237 (100)	
hypothetical protein	53	fig|685727.5.peg.1285 (Q)			
hypothetical protein	77	fig|685727.5.peg.1334 (Q)	fig|525370.5.peg.3954 (98.67)		
hypothetical protein	43	fig|685727.5.peg.1461 (Q)			
hypothetical protein	60	fig|685727.5.peg.1552 (Q)		fig|1219013.3.peg.1665 (98.31)	C7
hypothetical protein	53	fig|685727.5.peg.1639 (Q)		fig|1219013.3.peg.1757 (100)	C7
hypothetical protein	200	fig|685727.5.peg.1640 (Q)		fig|1219013.3.peg.1757 (98.99)	
hypothetical protein	139	fig|685727.5.peg.1641 (Q)	fig|525370.5.peg.1120 (42.97)		
hypothetical protein	152	fig|685727.5.peg.1645 (Q)	fig|525370.5.peg.1116 (84.21)		ATCC33707-103S
hypothetical protein	321	fig|685727.5.peg.1646 (Q)	fig|525370.5.peg.1084 (31.85)		ATCC33707-103S
hypothetical protein	487	fig|685727.5.peg.1647 (Q)			103S
hypothetical protein	255	fig|685727.5.peg.1649 (Q)	fig|525370.5.peg.1109 (98.82)		ATCC33707-103S
DNA helicase related protein	1828	fig|685727.5.peg.1655 (Q)	fig|525370.5.peg.1095 (23.18)		ATCC33707-103S
hypothetical protein	92	fig|685727.5.peg.1656 (Q)			103S
hypothetical protein	924	fig|685727.5.peg.1658 (Q)			103S
Helicase, C-terminal:Type III restriction enzyme, res subunit:DEAD/DEAH box helicase, N-terminal	2130	fig|685727.5.peg.1659 (Q)			103S
Type II restriction enzyme, methylase subunits	1530	fig|685727.5.peg.1660 (Q)			103S
putative ATP-dependent helicase	960	fig|685727.5.peg.1661 (Q)	fig|525370.5.peg.2722 (22.42)		
hypothetical protein	1135	fig|685727.5.peg.1662 (Q)			
hypothetical protein	114	fig|685727.5.peg.1664 (Q)			103S
hypothetical protein	444	fig|685727.5.peg.1665 (Q)			103S
hypothetical protein	63	fig|685727.5.peg.1666 (Q)			103S
hypothetical protein	118	fig|685727.5.peg.1667 (Q)			103S
hypothetical protein	94	fig|685727.5.peg.1669 (Q)	fig|525370.5.peg.1077 (86.02)		ATCC33707-103S
hypothetical protein	173	fig|685727.5.peg.1670 (Q)	fig|525370.5.peg.1076 (88.95)		
hypothetical protein	55	fig|685727.5.peg.1681 (Q)	fig|525370.5.peg.1064 (100)		
cyclase/dehydrase	173	fig|685727.5.peg.1707 (Q)	fig|525370.5.peg.1038 (100)		
hypothetical protein	72	fig|685727.5.peg.1708 (Q)	fig|525370.5.peg.1037 (98.59)		
putative isomerase	122	fig|685727.5.peg.1709 (Q)	fig|525370.5.peg.1036 (100)		
NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)	435	fig|685727.5.peg.1900 (Q)	fig|525370.5.peg.4090 (99.08)		
hypothetical protein	38	fig|685727.5.peg.1908 (Q)			

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	65	fig|685727.5.peg.1998 (Q)			
COG1359: Uncharacterized conserved protein	79	fig|685727.5.peg.2112 (Q)			103S
hypothetical protein	61	fig|685727.5.peg.2114 (Q)			103S
hypothetical protein	123	fig|685727.5.peg.2116 (Q)			103S
Non-heme chloroperoxidase (EC 1.11.1.10)	52	fig|685727.5.peg.2118 (Q)			
alpha/beta hydrolase fold(EC:1.11.1.10)	64	fig|685727.5.peg.2119 (Q)			
hypothetical protein	38	fig|685727.5.peg.2121 (Q)			
hypothetical protein	82	fig|685727.5.peg.2133 (Q)			
hypothetical protein	58	fig|685727.5.peg.2218 (Q)			
hypothetical protein	38	fig|685727.5.peg.2265 (Q)		fig|1219013.3.peg.2377 (100)	
hypothetical protein	116	fig|685727.5.peg.2347 (Q)	fig|525370.5.peg.4220 (88.89)		
hypothetical protein	57	fig|685727.5.peg.2390 (Q)	fig|525370.5.peg.4177 (100)		
hypothetical protein	444	fig|685727.5.peg.2393 (Q)			
hypothetical protein	43	fig|685727.5.peg.2401 (Q)			
hypothetical protein	82	fig|685727.5.peg.2435 (Q)	fig|525370.5.peg.1805 (98.77)		
hypothetical protein	84	fig|685727.5.peg.2475 (Q)	fig|525370.5.peg.1704 (98.78)		ATCC33707-103S
hypothetical protein	67	fig|685727.5.peg.2533 (Q)		fig|1219013.3.peg.2646 (98.48)	
hypothetical protein	42	fig|685727.5.peg.2566 (Q)			103S
hypothetical protein	56	fig|685727.5.peg.2569 (Q)	fig|525370.5.peg.1612 (100)		ATCC33707-103S
hypothetical protein	86	fig|685727.5.peg.2580 (Q)		fig|1219013.3.peg.2691 (100)	C7-103S
FIG01136303: hypothetical protein	115	fig|685727.5.peg.2585 (Q)		fig|1219013.3.peg.2699 (95.12)	103S
hypothetical protein	86	fig|685727.5.peg.2586 (Q)	fig|525370.5.peg.1595 (95.56)		ATCC33707-103S
hypothetical protein	84	fig|685727.5.peg.2615 (Q)	fig|525370.5.peg.1965 (89.16)		ATCC33707-103S
hypothetical protein	260	fig|685727.5.peg.2617 (Q)		fig|1219013.3.peg.2734 (96.91)	C7-103S
hypothetical protein	100	fig|685727.5.peg.2618 (Q)		fig|1219013.3.peg.2735 (94.95)	C7-103S
putative acetyltransferase	143	fig|685727.5.peg.2658 (Q)			103S
hypothetical protein	195	fig|685727.5.peg.2660 (Q)			103S
hypothetical protein	288	fig|685727.5.peg.2684 (Q)		fig|1219013.3.peg.2803 (100)	C7-103S
hypothetical protein	333	fig|685727.5.peg.2685 (Q)		fig|1219013.3.peg.2804 (99.7)	C7-103S
hypothetical protein	356	fig|685727.5.peg.2687 (Q)		fig|1219013.3.peg.2806 (98.87)	C7-103S
hypothetical protein	425	fig|685727.5.peg.2688 (Q)		fig|1219013.3.peg.4267 (29.87)	103S
hypothetical protein	171	fig|685727.5.peg.2701 (Q)		fig|1219013.3.peg.2818 (97.06)	C7
hypothetical protein	38	fig|685727.5.peg.3012 (Q)			
hypothetical protein	48	fig|685727.5.peg.3094 (Q)			
hypothetical protein	43	fig|685727.5.peg.3095 (Q)		fig|1219013.3.peg.3228 (92.86)	C7
hypothetical protein	64	fig|685727.5.peg.3272 (Q)		fig|1219013.3.peg.3411 (96.83)	
hypothetical protein	48	fig|685727.5.peg.3310 (Q)	fig|525370.5.peg.3144 (100)		ATCC33707-103S
hypothetical protein	38	fig|685727.5.peg.3318 (Q)			
hypothetical protein	63	fig|685727.5.peg.3447 (Q)			103S
hypothetical protein	65	fig|685727.5.peg.3448 (Q)			103S
hypothetical protein	124	fig|685727.5.peg.3449 (Q)			103S
hypothetical protein	256	fig|685727.5.peg.3450 (Q)			103S
hypothetical protein	281	fig|685727.5.peg.3451 (Q)			103S
hypothetical protein	613	fig|685727.5.peg.3452 (Q)		fig|1219013.3.peg.1777 (32.39)	C7-103S
hypothetical protein	38	fig|685727.5.peg.3480 (Q)		fig|1219013.3.peg.3618 (100)	
hypothetical protein	97	fig|685727.5.peg.3522 (Q)		fig|1219013.3.peg.3660 (97.92)	
YgjD/Kae1/Qri7 family, required for threonylcarbamoyladenosine (t(6)A) formation in tRNA	347	fig|685727.5.peg.3523 (Q)		fig|1219013.3.peg.3661 (99.71)	
hypothetical protein	167	fig|685727.5.peg.3799 (Q)	fig|525370.5.peg.1498 (96.99)		
hypothetical protein	161	fig|685727.5.peg.3853 (Q)			103S
hypothetical protein	45	fig|685727.5.peg.4055 (Q)			103S
hypothetical protein	48	fig|685727.5.peg.4057 (Q)			103S
GumJ protein	504	fig|685727.5.peg.4058 (Q)			103S
hypothetical protein	363	fig|685727.5.peg.4059 (Q)			103S
hypothetical protein	44	fig|685727.5.peg.4063 (Q)	fig|525370.5.peg.673 (95.35)		ATCC33707-103S
hypothetical protein	106	fig|685727.5.peg.4065 (Q)			103S
hypothetical protein	47	fig|685727.5.peg.4066 (Q)	fig|525370.5.peg.671 (89.13)		ATCC33707-103S
hypothetical protein	90	fig|685727.5.peg.4069 (Q)	fig|525370.5.peg.668 (100)		ATCC33707-103S
hypothetical protein	54	fig|685727.5.peg.4140 (Q)	fig|525370.5.peg.4557 (91.07)		
hypothetical protein	53	fig|685727.5.peg.4187 (Q)		fig|1219013.3.peg.4353 (98.08)	
hypothetical protein	38	fig|685727.5.peg.4392 (Q)	fig|525370.5.peg.513 (100)		
hypothetical protein	44	fig|685727.5.peg.4462 (Q)		fig|1219013.3.peg.4643 (97.67)	C7-103S
hypothetical protein	39	fig|685727.5.peg.4465 (Q)		fig|1219013.3.peg.4646 (100)	C7-103S
hypothetical protein	42	fig|685727.5.peg.4466 (Q)		fig|1219013.3.peg.4647 (97.56)	C7-103S
hypothetical protein	39	fig|685727.5.peg.4517 (Q)		fig|1219013.3.peg.4700 (100)	
hypothetical protein	88	fig|685727.5.peg.4520 (Q)		fig|1219013.3.peg.4703 (93.1)	
hypothetical protein	45	fig|685727.5.peg.4524 (Q)	fig|525370.5.peg.382 (97.73)		ATCC33707

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	48	fig|685727.5.peg.4559 (Q)	fig|525370.5.peg.347 (95.74)		
hypothetical protein	56	fig|685727.5.peg.4616 (Q)			103S
hypothetical protein	48	fig|685727.5.peg.4617 (Q)			103S
hypothetical protein	41	fig|685727.5.peg.4618 (Q)			103S
similar to Ketosteroid isomerase-related protein	136	fig|685727.5.peg.4620 (Q)			103S
hypothetical protein	45	fig|685727.5.peg.4621 (Q)			103S
Transposase	80	fig|685727.5.peg.4622 (Q)			103S
transposase, IS4 family protein	99	fig|685727.5.peg.4623 (Q)			103S
Mobile element protein	71	fig|685727.5.peg.4624 (Q)			103S
hypothetical protein	85	fig|685727.5.peg.4627 (Q)			103S
hypothetical protein	466	fig|685727.5.peg.4628 (Q)			103S
hypothetical protein	245	fig|685727.5.peg.4629 (Q)			103S
Putative DNA-binding protein	277	fig|685727.5.peg.4631 (Q)	fig|525370.5.peg.1035 (31.78)		103S
hypothetical protein	41	fig|685727.5.peg.4632 (Q)			103S
hypothetical protein	849	fig|685727.5.peg.4634 (Q)			103S
hypothetical protein	255	fig|685727.5.peg.4635 (Q)			103S
Integrase	279	fig|685727.5.peg.4636 (Q)			103S
hypothetical protein	932	fig|685727.5.peg.4637 (Q)			103S
hypothetical protein	138	fig|685727.5.peg.4639 (Q)	fig|525370.5.peg.287 (96.35)		ATCC33707-103S
hypothetical protein	42	fig|685727.5.peg.4734 (Q)	fig|525370.5.peg.4931 (100)		ATCC33707-103S
rRNA small subunit 7-methylguanosine (m7G) methyltransferase GidB	224	fig|685727.5.peg.4735 (Q)	fig|525370.5.peg.4930 (96.41)		ATCC33707-103S
hypothetical protein	40		fig|525370.5.peg.120 (Q)		
hypothetical protein	41		fig|525370.5.peg.134 (Q)		
hypothetical protein	40		fig|525370.5.peg.344 (Q)		
hypothetical protein	38		fig|525370.5.peg.440 (Q)		
hypothetical protein	611		fig|525370.5.peg.464 (Q)		ATCC33707
ATP-dependent DNA helicase UvrD/PcrA	567		fig|525370.5.peg.465 (Q)		ATCC33707
hypothetical protein	39		fig|525370.5.peg.479 (Q)		ATCC33707
hypothetical protein	306		fig|525370.5.peg.621 (Q)		
hypothetical protein	583		fig|525370.5.peg.622 (Q)		
hypothetical protein	45		fig|525370.5.peg.645 (Q)		ATCC33707
Glycosyltransferase	130	fig|685727.5.peg.4060 (32.74)	fig|525370.5.peg.675 (Q)		ATCC33707
FIG00511468: hypothetical protein	535		fig|525370.5.peg.676 (Q)		ATCC33707
hypothetical protein	112		fig|525370.5.peg.681 (Q)		ATCC33707
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	259		fig|525370.5.peg.751 (Q)		ATCC33707
hypothetical protein	211		fig|525370.5.peg.752 (Q)	fig|1219013.3.peg.4138 (24.56)	ATCC33707
Phenylacetic acid degradation protein PaaD, thioesterase	140		fig|525370.5.peg.754 (Q)		ATCC33707
hypothetical protein	105		fig|525370.5.peg.755 (Q)		ATCC33707
Aldehyde dehydrogenase (EC 1.2.1.3), PaaZ	682		fig|525370.5.peg.756 (Q)		ATCC33707
Transcriptional regulator, TetR family	179		fig|525370.5.peg.757 (Q)		ATCC33707
Phenylacetate-CoA oxygenase, PaaG subunit	317		fig|525370.5.peg.761 (Q)		
Phenylacetate-CoA oxygenase, PaaH subunit	108		fig|525370.5.peg.762 (Q)		
Phenylacetate-CoA oxygenase, PaaI subunit	306		fig|525370.5.peg.763 (Q)		
Phenylacetate-coenzyme A ligase (EC 6.2.1.30) PaaF	433		fig|525370.5.peg.766 (Q)		
hypothetical protein	798	fig|685727.5.peg.1668 (82.28)	fig|525370.5.peg.1078 (Q)		ATCC33707
hypothetical protein	253		fig|525370.5.peg.1079 (Q)		ATCC33707
hypothetical protein	97		fig|525370.5.peg.1080 (Q)		ATCC33707
hypothetical protein	160		fig|525370.5.peg.1081 (Q)		ATCC33707
hypothetical protein	104		fig|525370.5.peg.1082 (Q)		ATCC33707
hypothetical protein	142		fig|525370.5.peg.1083 (Q)		ATCC33707
hypothetical protein	318		fig|525370.5.peg.1085 (Q)		ATCC33707
hypothetical protein	49		fig|525370.5.peg.1086 (Q)		ATCC33707
hypothetical protein	51		fig|525370.5.peg.1087 (Q)		ATCC33707
ATP/GTP binding protein	627		fig|525370.5.peg.1088 (Q)		ATCC33707
hypothetical protein	283		fig|525370.5.peg.1089 (Q)		ATCC33707
hypothetical protein	296		fig|525370.5.peg.1090 (Q)		ATCC33707
hypothetical protein	164		fig|525370.5.peg.1092 (Q)		ATCC33707
hypothetical protein	749		fig|525370.5.peg.1096 (Q)		ATCC33707
hypothetical protein	290		fig|525370.5.peg.1097 (Q)		ATCC33707
hypothetical protein	388		fig|525370.5.peg.1098 (Q)		ATCC33707
hypothetical protein	340		fig|525370.5.peg.1099 (Q)		
hypothetical protein	843		fig|525370.5.peg.1100 (Q)		
FIG00995584: hypothetical protein	656		fig|525370.5.peg.1101 (Q)		
hypothetical protein	917		fig|525370.5.peg.1102 (Q)		
FIG00995267: hypothetical protein	1191		fig|525370.5.peg.1103 (Q)		ATCC33707
FIG00998105: hypothetical protein	922		fig|525370.5.peg.1104 (Q)		ATCC33707

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	97		fig|525370.5.peg.1105 (Q)		ATCC33707
hypothetical protein	78		fig|525370.5.peg.1111 (Q)		ATCC33707
hypothetical protein	120		fig|525370.5.peg.1112 (Q)		ATCC33707
hypothetical protein	201		fig|525370.5.peg.1113 (Q)		ATCC33707
hypothetical protein	98		fig|525370.5.peg.1114 (Q)		ATCC33707
hypothetical protein	45		fig|525370.5.peg.1115 (Q)		ATCC33707
Partial REP13E12 repeat protein	195		fig|525370.5.peg.1224 (Q)		ATCC33707
hypothetical protein	73		fig|525370.5.peg.1425 (Q)		
hypothetical protein	39		fig|525370.5.peg.1441 (Q)		ATCC33707
hypothetical protein	44		fig|525370.5.peg.1444 (Q)		ATCC33707
hypothetical protein	99		fig|525370.5.peg.1599 (Q)		ATCC33707
hypothetical protein	128		fig|525370.5.peg.1600 (Q)		ATCC33707
hypothetical protein	242		fig|525370.5.peg.1721 (Q)		ATCC33707
hypothetical protein	55		fig|525370.5.peg.1722 (Q)		ATCC33707
hypothetical protein	85		fig|525370.5.peg.1723 (Q)		ATCC33707
hypothetical protein	91		fig|525370.5.peg.1724 (Q)		ATCC33707
Phage Gp37Gp68 protein	39		fig|525370.5.peg.1725 (Q)		ATCC33707
hypothetical protein	240		fig|525370.5.peg.1726 (Q)		ATCC33707
hypothetical protein	515		fig|525370.5.peg.1727 (Q)		ATCC33707
hypothetical protein	206		fig|525370.5.peg.1728 (Q)		ATCC33707
putative phage tail	357		fig|525370.5.peg.1729 (Q)		ATCC33707
hypothetical protein	134		fig|525370.5.peg.1730 (Q)		
hypothetical protein	199		fig|525370.5.peg.1732 (Q)		
hypothetical protein	375		fig|525370.5.peg.1733 (Q)		
hypothetical protein	480		fig|525370.5.peg.1734 (Q)	fig|1219013.3.peg.4933 (21.38)	
hypothetical protein	290		fig|525370.5.peg.1735 (Q)		
tail length tape measure protein	1610		fig|525370.5.peg.1736 (Q)	fig|1219013.3.peg.4935 (25.45)	ATCC33707
hypothetical protein	121		fig|525370.5.peg.1737 (Q)		ATCC33707
hypothetical protein	148		fig|525370.5.peg.1738 (Q)		ATCC33707
phage major tail protein	186		fig|525370.5.peg.1739 (Q)		ATCC33707
hypothetical protein	126		fig|525370.5.peg.1740 (Q)		ATCC33707
hypothetical protein	68		fig|525370.5.peg.1741 (Q)		
hypothetical protein	78		fig|525370.5.peg.1742 (Q)		
hypothetical protein	120		fig|525370.5.peg.1743 (Q)		
hypothetical protein	139		fig|525370.5.peg.1744 (Q)		
hypothetical protein	152		fig|525370.5.peg.1745 (Q)		
hypothetical protein	308		fig|525370.5.peg.1746 (Q)		ATCC33707
hypothetical protein	137		fig|525370.5.peg.1747 (Q)		ATCC33707
hypothetical protein	422		fig|525370.5.peg.1749 (Q)		ATCC33707
phage terminase, large subunit, putative	490		fig|525370.5.peg.1750 (Q)		ATCC33707
hypothetical protein	116		fig|525370.5.peg.1751 (Q)		ATCC33707
hypothetical protein	46		fig|525370.5.peg.1752 (Q)		ATCC33707
hypothetical protein	107		fig|525370.5.peg.1753 (Q)		ATCC33707
hypothetical protein	86		fig|525370.5.peg.1754 (Q)		ATCC33707
hypothetical protein	66		fig|525370.5.peg.1755 (Q)		ATCC33707
hypothetical protein	126		fig|525370.5.peg.1756 (Q)		ATCC33707
hypothetical protein	222		fig|525370.5.peg.1757 (Q)	fig|1219013.3.peg.4952 (31.48)	ATCC33707
hypothetical protein	65		fig|525370.5.peg.1758 (Q)		ATCC33707
hypothetical protein	149		fig|525370.5.peg.1759 (Q)		ATCC33707
hypothetical protein	143		fig|525370.5.peg.1760 (Q)		ATCC33707
hypothetical protein	92		fig|525370.5.peg.1761 (Q)		ATCC33707
hypothetical protein	59		fig|525370.5.peg.1762 (Q)		ATCC33707
hypothetical protein	129		fig|525370.5.peg.1763 (Q)		ATCC33707
hypothetical protein	112		fig|525370.5.peg.1764 (Q)		
hypothetical protein	104		fig|525370.5.peg.1766 (Q)		
hypothetical protein	88		fig|525370.5.peg.1767 (Q)		
hypothetical protein	174		fig|525370.5.peg.1768 (Q)		
Cell division protein FtsK	378		fig|525370.5.peg.1770 (Q)	fig|1219013.3.peg.2065 (54.84)	
hypothetical protein	332		fig|525370.5.peg.1771 (Q)		ATCC33707
hypothetical protein	53		fig|525370.5.peg.1772 (Q)		ATCC33707
hypothetical protein	83		fig|525370.5.peg.1773 (Q)		ATCC33707
hypothetical protein	92		fig|525370.5.peg.1774 (Q)		ATCC33707
hypothetical protein	102		fig|525370.5.peg.1775 (Q)		ATCC33707
hypothetical protein	124		fig|525370.5.peg.1776 (Q)		ATCC33707
hypothetical protein	177		fig|525370.5.peg.1777 (Q)		ATCC33707
hypothetical protein	68		fig|525370.5.peg.1778 (Q)		ATCC33707

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	79		fig|525370.5.peg.1779 (Q)		ATCC33707
hypothetical protein	328		fig|525370.5.peg.1887 (Q)	fig|1219013.3.peg.2816 (96.15)	
hypothetical protein	46		fig|525370.5.peg.1888 (Q)		
hypothetical protein	50		fig|525370.5.peg.1898 (Q)		ATCC33707
hypothetical protein	242		fig|525370.5.peg.2073 (Q)		
hypothetical protein	59		fig|525370.5.peg.2089 (Q)		
hypothetical protein	49		fig|525370.5.peg.2105 (Q)		ATCC33707
hypothetical protein	76		fig|525370.5.peg.2106 (Q)		ATCC33707
hypothetical protein	71		fig|525370.5.peg.2107 (Q)		ATCC33707
hypothetical protein	258		fig|525370.5.peg.2108 (Q)		ATCC33707
hypothetical protein	43		fig|525370.5.peg.2109 (Q)		ATCC33707
hypothetical protein	42		fig|525370.5.peg.2110 (Q)		ATCC33707
hypothetical protein	66		fig|525370.5.peg.2111 (Q)		ATCC33707
hypothetical protein	45		fig|525370.5.peg.2112 (Q)		ATCC33707
hypothetical protein	60		fig|525370.5.peg.2113 (Q)		ATCC33707
hypothetical protein	65		fig|525370.5.peg.2114 (Q)		ATCC33707
hypothetical protein	249		fig|525370.5.peg.2117 (Q)		ATCC33707
hypothetical protein	43		fig|525370.5.peg.2118 (Q)		ATCC33707
hypothetical protein	59		fig|525370.5.peg.2119 (Q)		ATCC33707
hypothetical protein	72		fig|525370.5.peg.2120 (Q)		ATCC33707
hypothetical protein	143		fig|525370.5.peg.2121 (Q)		ATCC33707
hypothetical protein	120		fig|525370.5.peg.2122 (Q)		ATCC33707
hypothetical protein	152		fig|525370.5.peg.2123 (Q)		ATCC33707
hypothetical protein	51		fig|525370.5.peg.2124 (Q)		ATCC33707
hypothetical protein	40		fig|525370.5.peg.2125 (Q)		ATCC33707
hypothetical protein	130		fig|525370.5.peg.2127 (Q)		ATCC33707
hypothetical protein	58		fig|525370.5.peg.2128 (Q)		ATCC33707
hypothetical protein	56		fig|525370.5.peg.2129 (Q)		ATCC33707
hypothetical protein	113		fig|525370.5.peg.2130 (Q)		ATCC33707
Phage terminase	515		fig|525370.5.peg.2131 (Q)		ATCC33707
hypothetical protein	424		fig|525370.5.peg.2132 (Q)		ATCC33707
hypothetical protein	476		fig|525370.5.peg.2133 (Q)		ATCC33707
dehydrogenase / Cytidine deaminase (EC 3.5.4.5)	147		fig|525370.5.peg.2134 (Q)		
hypothetical protein	314		fig|525370.5.peg.2135 (Q)		
hypothetical protein	129		fig|525370.5.peg.2136 (Q)		
hypothetical protein	124		fig|525370.5.peg.2137 (Q)		
hypothetical protein	110		fig|525370.5.peg.2138 (Q)		ATCC33707
Sigma 54-dependent transcriptional activator	94		fig|525370.5.peg.2139 (Q)		ATCC33707
hypothetical protein	133		fig|525370.5.peg.2140 (Q)		ATCC33707
hypothetical protein	268		fig|525370.5.peg.2141 (Q)		ATCC33707
hypothetical protein	88		fig|525370.5.peg.2142 (Q)		ATCC33707
hypothetical protein	38		fig|525370.5.peg.2143 (Q)		ATCC33707
hypothetical protein	98		fig|525370.5.peg.2144 (Q)		ATCC33707
hypothetical protein	149		fig|525370.5.peg.2145 (Q)		ATCC33707
hypothetical protein	151		fig|525370.5.peg.2146 (Q)		ATCC33707
hypothetical protein	1178		fig|525370.5.peg.2147 (Q)	fig|1219013.3.peg.4935 (33.5)	ATCC33707
hypothetical protein	112		fig|525370.5.peg.2150 (Q)		ATCC33707
hypothetical protein	123		fig|525370.5.peg.2152 (Q)		ATCC33707
hypothetical protein	92		fig|525370.5.peg.2153 (Q)		ATCC33707
hypothetical protein	62		fig|525370.5.peg.2154 (Q)		ATCC33707
hypothetical protein	118		fig|525370.5.peg.2155 (Q)		ATCC33707
hypothetical protein	288		fig|525370.5.peg.2156 (Q)		ATCC33707
hypothetical protein	112		fig|525370.5.peg.2157 (Q)		ATCC33707
hypothetical protein	111		fig|525370.5.peg.2158 (Q)		ATCC33707
hypothetical protein	115		fig|525370.5.peg.2159 (Q)		ATCC33707
hypothetical protein	329		fig|525370.5.peg.2160 (Q)		ATCC33707
hypothetical protein	73		fig|525370.5.peg.2161 (Q)		ATCC33707
hypothetical protein	72		fig|525370.5.peg.2162 (Q)		ATCC33707
hypothetical protein	53		fig|525370.5.peg.2163 (Q)		ATCC33707
hypothetical protein	40		fig|525370.5.peg.2164 (Q)		ATCC33707
Integrase-like protein	275		fig|525370.5.peg.2165 (Q)		ATCC33707
hypothetical protein	38		fig|525370.5.peg.2166 (Q)		ATCC33707
hypothetical protein	249		fig|525370.5.peg.2167 (Q)		ATCC33707
hypothetical protein	54		fig|525370.5.peg.2168 (Q)		ATCC33707
hypothetical protein	119		fig|525370.5.peg.2169 (Q)		ATCC33707
hypothetical protein	67		fig|525370.5.peg.2298 (Q)		

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	330		fig|525370.5.peg.2559 (Q)		ATCC33707
hypothetical protein	52		fig|525370.5.peg.2598 (Q)		ATCC33707
hypothetical protein	58		fig|525370.5.peg.2640 (Q)		ATCC33707
Arsenical pump-driving ATPase (EC 3.6.3.16)	380		fig|525370.5.peg.2730 (Q)	fig|1219013.3.peg.532 (100)	
hypothetical protein	82		fig|525370.5.peg.2971 (Q)		
hypothetical protein	79		fig|525370.5.peg.3033 (Q)		
hypothetical protein	61		fig|525370.5.peg.3517 (Q)		
Acyl dehydratase	128		fig|525370.5.peg.3541 (Q)		
FIG00827952: hypothetical protein	420		fig|525370.5.peg.3544 (Q)		
hypothetical protein	52		fig|525370.5.peg.3659 (Q)		
hypothetical protein	38		fig|525370.5.peg.3771 (Q)		ATCC33707
hypothetical protein	38		fig|525370.5.peg.3875 (Q)		
hypothetical protein	164		fig|525370.5.peg.3918 (Q)		
hypothetical protein	80		fig|525370.5.peg.4018 (Q)		ATCC33707
hypothetical protein	619		fig|525370.5.peg.4388 (Q)		
hypothetical protein	44		fig|525370.5.peg.4466 (Q)		
Mobile element protein	285		fig|525370.5.peg.4685 (Q)		
transposase for IS3517	109		fig|525370.5.peg.4686 (Q)		
hypothetical protein	49		fig|525370.5.peg.4845 (Q)		
2,3-dihydroxybiphenyl 1,2-dioxygenase	293	fig|685727.5.peg.72 (100)	fig|525370.5.peg.4851 (Q)		
hypothetical protein	62		fig|525370.5.peg.4873 (Q)		
rRNA small subunit 7-methylguanosine (m7G) methyltransferase GidB	226	fig|685727.5.peg.4735 (95.52)	fig|525370.5.peg.4928 (Q)		ATCC33707-103S
hypothetical protein	54		fig|525370.5.peg.4839 (97.3)	fig|1219013.3.peg.76 (Q)	
hypothetical protein	109			fig|1219013.3.peg.177 (Q)	C7
Glycerol-3-phosphate regulon repressor, DeoR family	277		fig|525370.5.peg.2517 (99.64)	fig|1219013.3.peg.258 (Q)	ATCC33707-C7
hypothetical protein	71		fig|525370.5.peg.2514 (98.57)	fig|1219013.3.peg.261 (Q)	ATCC33707-C7
Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)	394		fig|525370.5.peg.2513 (100)	fig|1219013.3.peg.262 (Q)	ATCC33707-C7
Integrase	287		fig|525370.5.peg.1780 (28.82)	fig|1219013.3.peg.304 (Q)	C7
hypothetical protein	290			fig|1219013.3.peg.305 (Q)	C7
hypothetical protein	346			fig|1219013.3.peg.306 (Q)	C7
hypothetical protein	52			fig|1219013.3.peg.307 (Q)	C7
hypothetical protein	54			fig|1219013.3.peg.308 (Q)	C7
hypothetical protein	114			fig|1219013.3.peg.309 (Q)	C7
hypothetical protein	156			fig|1219013.3.peg.310 (Q)	C7
hypothetical protein	205			fig|1219013.3.peg.311 (Q)	C7
hypothetical protein	51			fig|1219013.3.peg.312 (Q)	C7
hypothetical protein	257			fig|1219013.3.peg.314 (Q)	C7
Transcriptional regulator	351			fig|1219013.3.peg.315 (Q)	C7
hypothetical protein	136			fig|1219013.3.peg.316 (Q)	C7
hypothetical protein	332			fig|1219013.3.peg.317 (Q)	C7
hypothetical protein	305			fig|1219013.3.peg.318 (Q)	C7
hypothetical protein	133			fig|1219013.3.peg.319 (Q)	C7
hypothetical protein	80			fig|1219013.3.peg.320 (Q)	C7
hypothetical protein	66			fig|1219013.3.peg.321 (Q)	C7
hypothetical protein	66			fig|1219013.3.peg.322 (Q)	C7
hypothetical protein	156			fig|1219013.3.peg.334 (Q)	
hypothetical protein	101		fig|525370.5.peg.3516 (97)	fig|1219013.3.peg.335 (Q)	
hypothetical protein	194		fig|525370.5.peg.794 (96.02)	fig|1219013.3.peg.435 (Q)	ATCC33707-C7
Putative polysaccharide deacetylase	294		fig|525370.5.peg.790 (99.66)	fig|1219013.3.peg.439 (Q)	ATCC33707-C7
L-asparaginase (EC 3.5.1.1)	337		fig|525370.5.peg.789 (100)	fig|1219013.3.peg.440 (Q)	
hypothetical protein	163			fig|1219013.3.peg.494 (Q)	
hypothetical protein	65			fig|1219013.3.peg.506 (Q)	
hypothetical protein	91			fig|1219013.3.peg.530 (Q)	
WhiB-type transcription regulator	53			fig|1219013.3.peg.531 (Q)	
Arsenical pump-driving ATPase (EC 3.6.3.16)	347		fig|525370.5.peg.2729 (100)	fig|1219013.3.peg.533 (Q)	
FIG011121: hypothetical protein	44		fig|525370.5.peg.2728 (100)	fig|1219013.3.peg.534 (Q)	
Enoyl-CoA hydratase (EC 4.2.1.17)	269		fig|525370.5.peg.2695 (100)	fig|1219013.3.peg.566 (Q)	
hypothetical protein	369		fig|525370.5.peg.2693 (100)	fig|1219013.3.peg.568 (Q)	
hypothetical protein	350		fig|525370.5.peg.2687 (100)	fig|1219013.3.peg.574 (Q)	ATCC33707-C7
hypothetical protein	131		fig|525370.5.peg.2681 (97.69)	fig|1219013.3.peg.580 (Q)	C7
Transcriptional regulator, IclR family	273		fig|525370.5.peg.2674 (99.26)	fig|1219013.3.peg.587 (Q)	
hypothetical protein	170		fig|525370.5.peg.2667 (98.82)	fig|1219013.3.peg.594 (Q)	ATCC33707-C7
Beta-mannanase-like protein	329		fig|525370.5.peg.2627 (98.78)	fig|1219013.3.peg.633 (Q)	
Cellulose synthase catalytic subunit	658		fig|525370.5.peg.2625 (99.24)	fig|1219013.3.peg.635 (Q)	
hypothetical protein	146		fig|525370.5.peg.2623 (99.31)	fig|1219013.3.peg.637 (Q)	

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
FIG00994841: hypothetical protein	90		fig|525370.5.peg.2460 (100)	fig|1219013.3.peg.675 (Q)	
hypothetical protein	51		fig|525370.5.peg.2410 (94)	fig|1219013.3.peg.725 (Q)	C7
hypothetical protein	121			fig|1219013.3.peg.766 (Q)	
hypothetical protein	73		fig|525370.5.peg.2349 (94.44)	fig|1219013.3.peg.787 (Q)	
hypothetical protein	84		fig|525370.5.peg.2301 (94.74)	fig|1219013.3.peg.835 (Q)	
hypothetical protein	147			fig|1219013.3.peg.837 (Q)	
hypothetical protein	64		fig|525370.5.peg.2262 (98.41)	fig|1219013.3.peg.874 (Q)	
hypothetical protein	109		fig|525370.5.peg.2259 (100)	fig|1219013.3.peg.877 (Q)	
hypothetical protein	45		fig|525370.5.peg.2220 (100)	fig|1219013.3.peg.916 (Q)	
hypothetical protein	40		fig|525370.5.peg.2192 (100)	fig|1219013.3.peg.944 (Q)	
hypothetical protein	53			fig|1219013.3.peg.967 (Q)	C7
hypothetical protein	41			fig|1219013.3.peg.968 (Q)	C7
hypothetical protein	40			fig|1219013.3.peg.969 (Q)	C7
hypothetical protein	43			fig|1219013.3.peg.970 (Q)	C7
hypothetical protein	51			fig|1219013.3.peg.999 (Q)	C7
Methyltransferase type 12	252			fig|1219013.3.peg.1001 (Q)	C7
hypothetical protein	38			fig|1219013.3.peg.1097 (Q)	C7
Prophage Lp2 protein 6	374			fig|1219013.3.peg.1189 (Q)	C7
hypothetical protein	73		fig|525370.5.peg.3791 (98.61)	fig|1219013.3.peg.1219 (Q)	
hypothetical protein	38			fig|1219013.3.peg.1227 (Q)	
hypothetical protein	393		fig|525370.5.peg.3707 (98.08)	fig|1219013.3.peg.1306 (Q)	
hypothetical protein	72			fig|1219013.3.peg.1476 (Q)	
hypothetical protein	43			fig|1219013.3.peg.1480 (Q)	
OsmC-like protein	136			fig|1219013.3.peg.1729 (Q)	
hypothetical protein	230			fig|1219013.3.peg.1758 (Q)	C7
hypothetical protein	55			fig|1219013.3.peg.1762 (Q)	C7
hypothetical protein	38			fig|1219013.3.peg.1764 (Q)	C7
hypothetical protein	38			fig|1219013.3.peg.1768 (Q)	C7
hypothetical protein	62			fig|1219013.3.peg.1769 (Q)	C7
hypothetical protein	77			fig|1219013.3.peg.1770 (Q)	C7
YeeC-like protein	402			fig|1219013.3.peg.1771 (Q)	C7
FIG006126: DNA helicase, restriction/modification system component YeeB	657			fig|1219013.3.peg.1772 (Q)	C7
FIG045374: Type II restriction enzyme, methylase subunit YeeA	901			fig|1219013.3.peg.1773 (Q)	C7
hypothetical protein	230			fig|1219013.3.peg.1774 (Q)	C7
hypothetical protein	275			fig|1219013.3.peg.1775 (Q)	C7
hypothetical protein	187			fig|1219013.3.peg.1776 (Q)	C7
Fe-S protein, homolog of lactate dehydrogenase SO1521	107		fig|525370.5.peg.1073 (95.74)	fig|1219013.3.peg.1778 (Q)	C7
hypothetical protein	45			fig|1219013.3.peg.1779 (Q)	C7
hypothetical protein	184			fig|1219013.3.peg.1815 (Q)	C7
hypothetical protein	513			fig|1219013.3.peg.1822 (Q)	C7
hypothetical protein	190			fig|1219013.3.peg.1823 (Q)	C7
hypothetical protein	242			fig|1219013.3.peg.1824 (Q)	C7
hypothetical protein	233			fig|1219013.3.peg.1831 (Q)	
KH domain RNA binding protein YlqC	81		fig|525370.5.peg.946 (100)	fig|1219013.3.peg.1916 (Q)	
hypothetical protein	43			fig|1219013.3.peg.2163 (Q)	
hypothetical protein	40			fig|1219013.3.peg.2285 (Q)	
hypothetical protein	60			fig|1219013.3.peg.2297 (Q)	
hypothetical protein	59			fig|1219013.3.peg.2322 (Q)	
hypothetical protein	58			fig|1219013.3.peg.2417 (Q)	
hypothetical protein	69			fig|1219013.3.peg.2511 (Q)	C7
hypothetical protein	377		fig|525370.5.peg.4061 (37.2)	fig|1219013.3.peg.2531 (Q)	
hypothetical protein	157			fig|1219013.3.peg.2544 (Q)	C7
Protein of unknown function DUF262	606			fig|1219013.3.peg.2545 (Q)	C7
Uncharacterized protein SCO1141	138			fig|1219013.3.peg.2547 (Q)	C7
hypothetical protein	78		fig|525370.5.peg.1796 (98.57)	fig|1219013.3.peg.2556 (Q)	
hypothetical protein	40			fig|1219013.3.peg.2693 (Q)	C7
hypothetical protein	46			fig|1219013.3.peg.2694 (Q)	C7
Glycosyltransferase	334		fig|525370.5.peg.1985 (98.21)	fig|1219013.3.peg.2712 (Q)	
hypothetical protein	71			fig|1219013.3.peg.2722 (Q)	C7
hypothetical protein	74			fig|1219013.3.peg.2732 (Q)	C7
hypothetical protein	120			fig|1219013.3.peg.2733 (Q)	C7
hypothetical protein	133		fig|525370.5.peg.1925 (100)	fig|1219013.3.peg.2776 (Q)	C7
hypothetical protein	38		fig|525370.5.peg.1924 (100)	fig|1219013.3.peg.2777 (Q)	ATCC33707-C7
hypothetical protein	60		fig|525370.5.peg.1907 (98.31)	fig|1219013.3.peg.2794 (Q)	
hypothetical protein	67			fig|1219013.3.peg.2846 (Q)	C7
hypothetical protein	57			fig|1219013.3.peg.2868 (Q)	

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	141	fig|685727.5.peg.266 (32)		fig|1219013.3.peg.2873 (Q)	
hypothetical protein	203		fig|525370.5.peg.4357 (99.5)	fig|1219013.3.peg.2924 (Q)	
Oxidoreductase, short-chain dehydrogenase/reductase family (EC 1.1.1.-)	211			fig|1219013.3.peg.2961 (Q)	
hypothetical protein	150			fig|1219013.3.peg.3004 (Q)	
hypothetical protein	85		fig|525370.5.peg.4395 (100)	fig|1219013.3.peg.3026 (Q)	
hypothetical protein	148			fig|1219013.3.peg.3074 (Q)	
hypothetical protein	39			fig|1219013.3.peg.3084 (Q)	C7
hypothetical protein	106		fig|525370.5.peg.3360 (97.12)	fig|1219013.3.peg.3227 (Q)	C7
hypothetical protein	43		fig|525370.5.peg.3348 (100)	fig|1219013.3.peg.3240 (Q)	
hypothetical protein	38			fig|1219013.3.peg.3280 (Q)	
Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) / Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7)	67		fig|525370.5.peg.3297 (98.48)	fig|1219013.3.peg.3292 (Q)	
hypothetical protein	47		fig|525370.5.peg.3287 (95.65)	fig|1219013.3.peg.3302 (Q)	C7
hypothetical protein	70			fig|1219013.3.peg.3342 (Q)	
hypothetical protein	56			fig|1219013.3.peg.3346 (Q)	
hypothetical protein	63			fig|1219013.3.peg.3393 (Q)	C7
possible sugar phosphate isomerase/ epimerase	274		fig|525370.5.peg.3096 (99.63)	fig|1219013.3.peg.3494 (Q)	
FIG00995642: hypothetical protein	365		fig|525370.5.peg.3094 (99.18)	fig|1219013.3.peg.3496 (Q)	
hypothetical protein	38			fig|1219013.3.peg.3626 (Q)	
putative transposase	89		fig|525370.5.peg.2750 (80.23)	fig|1219013.3.peg.3841 (Q)	
putative acyltransferase domain protein	66			fig|1219013.3.peg.3842 (Q)	
hypothetical protein	39			fig|1219013.3.peg.3914 (Q)	
Ferrichrome ABC transporter	322		fig|525370.5.peg.1527 (99.38)	fig|1219013.3.peg.3919 (Q)	
hypothetical protein	48		fig|525370.5.peg.1526 (95.12)	fig|1219013.3.peg.3920 (Q)	
hypothetical protein	50		fig|525370.5.peg.1518 (100)	fig|1219013.3.peg.3928 (Q)	ATCC33707-C7
Adenylate kinase (EC 2.7.4.3)	173			fig|1219013.3.peg.3948 (Q)	
hypothetical protein	248		fig|525370.5.peg.1440 (77.42)	fig|1219013.3.peg.4001 (Q)	ATCC33707-C7
hypothetical protein	38			fig|1219013.3.peg.4007 (Q)	
hypothetical protein	40			fig|1219013.3.peg.4017 (Q)	C7
hypothetical protein	40			fig|1219013.3.peg.4090 (Q)	
hypothetical protein	679		fig|525370.5.peg.1248 (99.56)	fig|1219013.3.peg.4197 (Q)	ATCC33707-C7
hypothetical protein	723			fig|1219013.3.peg.4209 (Q)	
hypothetical protein	76			fig|1219013.3.peg.4212 (Q)	C7
hypothetical protein	457			fig|1219013.3.peg.4213 (Q)	C7
hypothetical protein	75			fig|1219013.3.peg.4214 (Q)	C7
hypothetical protein	380			fig|1219013.3.peg.4215 (Q)	C7
putative glycosyl transferase	336			fig|1219013.3.peg.4216 (Q)	C7
hypothetical protein	73			fig|1219013.3.peg.4219 (Q)	C7
hypothetical protein	222			fig|1219013.3.peg.4221 (Q)	C7
hypothetical protein	39			fig|1219013.3.peg.4246 (Q)	
Believed to be an alternative form of N-formylglutamate deformylase (EC 3.5.1.68), but experimentally invalidated	435		fig|525370.5.peg.619 (97.15)	fig|1219013.3.peg.4270 (Q)	
hypothetical protein	860		fig|525370.5.peg.616 (99.28)	fig|1219013.3.peg.4273 (Q)	
hypothetical protein	229		fig|525370.5.peg.614 (98.68)	fig|1219013.3.peg.4275 (Q)	
ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)	336		fig|525370.5.peg.610 (100)	fig|1219013.3.peg.4279 (Q)	ATCC33707-C7
Transcriptional regulator, IclR family	248		fig|525370.5.peg.609 (99.19)	fig|1219013.3.peg.4280 (Q)	ATCC33707-C7
Gentisate 1,2-dioxygenase (EC 1.13.11.4)	357			fig|1219013.3.peg.4369 (Q)	
FMN reductase (EC 1.5.1.29)	199	fig|685727.5.peg.1276 (27.27)		fig|1219013.3.peg.4371 (Q)	
Transcriptional regulator, IclR family	278		fig|525370.5.peg.2082 (27.54)	fig|1219013.3.peg.4374 (Q)	
hypothetical protein	60			fig|1219013.3.peg.4377 (Q)	
hypothetical protein	48		fig|525370.5.peg.4657 (97.87)	fig|1219013.3.peg.4390 (Q)	
hypothetical protein	102		fig|525370.5.peg.540 (92.08)	fig|1219013.3.peg.4546 (Q)	
hypothetical protein	233		fig|525370.5.peg.510 (97.5)	fig|1219013.3.peg.4573 (Q)	ATCC33707-C7
hypothetical protein	48			fig|1219013.3.peg.4606 (Q)	C7
hypothetical protein	318		fig|525370.5.peg.401 (99.37)	fig|1219013.3.peg.4686 (Q)	
regulatory protein, TetR	208		fig|525370.5.peg.400 (98.55)	fig|1219013.3.peg.4687 (Q)	
hypothetical protein	39			fig|1219013.3.peg.4711 (Q)	
hypothetical protein	401		fig|525370.5.peg.345 (98.75)	fig|1219013.3.peg.4743 (Q)	
hypothetical protein	222		fig|525370.5.peg.328 (98.19)	fig|1219013.3.peg.4759 (Q)	ATCC33707-C7
hypothetical protein	93			fig|1219013.3.peg.4810 (Q)	
Enoyl-CoA hydratase (EC 4.2.1.17)	213		fig|525370.5.peg.3654 (31.58)	fig|1219013.3.peg.4824 (Q)	C7
phage integrase family protein	398		fig|525370.5.peg.1780 (28.89)	fig|1219013.3.peg.4900 (Q)	C7
hypothetical protein	56			fig|1219013.3.peg.4901 (Q)	C7
hypothetical protein	72			fig|1219013.3.peg.4902 (Q)	C7
hypothetical protein	201			fig|1219013.3.peg.4903 (Q)	C7
hypothetical protein	129			fig|1219013.3.peg.4905 (Q)	C7
hypothetical protein	117			fig|1219013.3.peg.4906 (Q)	C7

Table S1 continued…

Function	Protein Length	103S Feature (blast hit)	ATCC33707 Feature (blast hit)	C7 Feature (blast hit)	HGT
hypothetical protein	110			fig|1219013.3.peg.4907 (Q)	C7
hypothetical protein	134			fig|1219013.3.peg.4908 (Q)	C7
hypothetical protein	332			fig|1219013.3.peg.4909 (Q)	C7
hypothetical protein	123			fig|1219013.3.peg.4910 (Q)	C7
hypothetical protein	97			fig|1219013.3.peg.4911 (Q)	C7
hypothetical protein	47			fig|1219013.3.peg.4924 (Q)	C7
hypothetical protein	364		fig|525370.5.peg.2599 (24.66)	fig|1219013.3.peg.4925 (Q)	ATCC33707
hypothetical protein	146			fig|1219013.3.peg.4926 (Q)	C7
hypothetical protein	138			fig|1219013.3.peg.4927 (Q)	C7
hypothetical protein	220			fig|1219013.3.peg.4928 (Q)	C7
hypothetical protein	107		fig|525370.5.peg.1731 (30.09)	fig|1219013.3.peg.4929 (Q)	C7
hypothetical protein	143			fig|1219013.3.peg.4930 (Q)	C7
hypothetical protein	251		fig|525370.5.peg.2151 (69.96)	fig|1219013.3.peg.4931 (Q)	C7
hypothetical protein	123			fig|1219013.3.peg.4932 (Q)	C7
Phage minor tail protein	548		fig|525370.5.peg.2149 (34.43)	fig|1219013.3.peg.4933 (Q)	ATCC33707-C7
Phage minor tail protein # Gp27	304		fig|525370.5.peg.2148 (29.34)	fig|1219013.3.peg.4934 (Q)	ATCC33707-C7
hypothetical protein	188			fig|1219013.3.peg.4936 (Q)	C7
hypothetical protein	246			fig|1219013.3.peg.4937 (Q)	C7
hypothetical protein	112			fig|1219013.3.peg.4938 (Q)	C7
FIG00545832: hypothetical protein	109			fig|1219013.3.peg.4939 (Q)	C7
hypothetical protein	99			fig|1219013.3.peg.4940 (Q)	C7
hypothetical protein	137			fig|1219013.3.peg.4941 (Q)	C7
hypothetical protein	71			fig|1219013.3.peg.4942 (Q)	C7
hypothetical protein	128			fig|1219013.3.peg.4943 (Q)	C7
hypothetical protein	335			fig|1219013.3.peg.4944 (Q)	C7
hypothetical protein	200			fig|1219013.3.peg.4945 (Q)	C7
hypothetical protein	593			fig|1219013.3.peg.4946 (Q)	C7
hypothetical protein	534			fig|1219013.3.peg.4947 (Q)	C7
hypothetical protein	433			fig|1219013.3.peg.4948 (Q)	C7
hypothetical protein	166			fig|1219013.3.peg.4949 (Q)	C7
hypothetical protein	238			fig|1219013.3.peg.4950 (Q)	C7
hypothetical protein	100			fig|1219013.3.peg.4951 (Q)	C7
hypothetical protein	225		fig|525370.5.peg.2126 (38)	fig|1219013.3.peg.4952 (Q)	ATCC33707-C7
hypothetical protein	111			fig|1219013.3.peg.4953 (Q)	C7
hypothetical protein	71			fig|1219013.3.peg.4954 (Q)	C7
hypothetical protein	124			fig|1219013.3.peg.4955 (Q)	C7
hypothetical protein	205			fig|1219013.3.peg.4957 (Q)	C7
hypothetical protein	43			fig|1219013.3.peg.4958 (Q)	C7
hypothetical protein	116			fig|1219013.3.peg.4959 (Q)	C7
hypothetical protein	107			fig|1219013.3.peg.4960 (Q)	C7
hypothetical protein	63			fig|1219013.3.peg.4961 (Q)	C7
hypothetical protein	121			fig|1219013.3.peg.4962 (Q)	C7
hypothetical protein	41			fig|1219013.3.peg.4963 (Q)	C7
hypothetical protein	117			fig|1219013.3.peg.4964 (Q)	C7
hypothetical protein	90			fig|1219013.3.peg.4965 (Q)	C7
hypothetical protein	165			fig|1219013.3.peg.4966 (Q)	C7
hypothetical protein	122			fig|1219013.3.peg.4967 (Q)	C7
hypothetical protein	92			fig|1219013.3.peg.4968 (Q)	C7
hypothetical protein	99			fig|1219013.3.peg.4969 (Q)	C7
hypothetical protein	281		fig|525370.5.peg.2116 (29.37)	fig|1219013.3.peg.4970 (Q)	ATCC33707-C7
Phage-related protein, predicted endonuclease	312		fig|525370.5.peg.2115 (29.96)	fig|1219013.3.peg.4971 (Q)	ATCC33707-C7
hypothetical protein	91			fig|1219013.3.peg.4972 (Q)	C7
hypothetical protein	68			fig|1219013.3.peg.4973 (Q)	C7
hypothetical protein	98			fig|1219013.3.peg.4974 (Q)	C7
hypothetical protein	102			fig|1219013.3.peg.4975 (Q)	C7
Integrase	352		fig|525370.5.peg.1714 (24.2)	fig|1219013.3.peg.4976 (Q)	ATCC33707

Note: 1. Genes used as the query for blast searches are marked with (Q) whereas the blast score is mentioned with the target features.

2. Two genes of strain 103S, one of ATCC33707 and four C7 genes showed similarities with more than one features in another genome. These genes and their target genes are labelled in green, blue and red, respectively.

3. The last column HGT represents “Horizontal Gene Transfer” and we mentioned the strain IDs where the genes are borne by the genomic islands that are predicted by the program Alien Hunter.

Supplementary Table 2. A list of nonsense SNPs in *R. equi* strains C7 and ATCC33707 using 103S as the reference

103S				C7		ATCC 33707	
Position	Ref. allele	Locus/gene	Product	SNP allele	SNP type	SNP allele	SNP type
717240	C	fig|685727.5.peg.690	CONSERVED 13E12 REPEAT FAMILY PROTEIN			a	nonsense
777219	C	fig|685727.5.peg.749	MCE-family protein Mce1F	a	nonsense		
777362	C	fig|685727.5.peg.749	MCE-family protein Mce1F	t	nonsense		
778256	G	fig|685727.5.peg.751	MCE associated membrane protein	a	nonsense		
832375	C	fig|685727.5.peg.791	putative ABC transporter ATP binding protein	t	nonsense	t	nonsense
953696	C	fig|685727.5.peg.895	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)			t	nonsense
1018281	A	fig|685727.5.peg.965	hypothetical protein	t	nonsense		
1046258	C	fig|685727.5.peg.994	putative esterase	t	nonsense	t	nonsense
1060941	C	fig|685727.5.peg.1008	hypothetical protein			a	nonsense
1086868	G	fig|685727.5.peg.1037	hypothetical protein			a	nonsense
1420888	G	fig|685727.5.peg.1369	YndJ	a	nonsense		
1441851	G	fig|685727.5.peg.1390	hypothetical protein			a	nonsense
1474013	G	fig|685727.5.peg.1422	Pyruvate oxidase (EC 1.2.3.3)	a	nonsense		
1719095	C	fig|685727.5.peg.1649	hypothetical protein	t	nonsense		
1766963	A	fig|685727.5.peg.1671	Ribosyl nicotinamide transporter, PnuC-like	g	nonsense	c	nonsynonymous
1806315	C	fig|685727.5.peg.1711	secreted peptidase			a	nonsense
1939596	G	fig|685727.5.peg.1836	hypothetical protein			t	nonsense
2159015	G	fig|685727.5.peg.2048	oxetanocin A resistance protein			a	nonsense
2593202	C	fig|685727.5.peg.2435	hypothetical protein	t	nonsense		
2646430	C	fig|685727.5.peg.2481	Polyhydroxyalkanoic acid synthase	t	nonsense		
2754494	C	fig|685727.5.peg.2584	Epoxide hydrolase (EC 3.3.2.9)	t	nonsense		
2755296	A	fig|685727.5.peg.2585	FIG01136303: hypothetical protein	g	nonsense	g	nonsense
2777171	C	fig|685727.5.peg.2615	hypothetical protein	t	nonsense		
3092582	C	fig|685727.5.peg.2906	hypothetical protein			a	nonsense
3296283	C	fig|685727.5.peg.3095	hypothetical protein			t	nonsense
3395747	G	fig|685727.5.peg.3187	hypothetical protein			a	nonsense
3735874	G	fig|685727.5.peg.3515	hypothetical protein	a	nonsense	a	nonsense
4133706	C	fig|685727.5.peg.3890	hypothetical protein	t	nonsense	t	nonsense
4160134	C	fig|685727.5.peg.3917	Acetate kinase (EC 2.7.2.1)	t	nonsense	t	nonsense
4300318	G	fig|685727.5.peg.4054	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	a	nonsense		
4350321	C	fig|685727.5.peg.4088	FIG00863843: hypothetical protein	t	nonsense	t	nonsense
4379112	C	fig|685727.5.peg.4112	hypothetical protein			a	nonsense
4959414	C	fig|685727.5.peg.4661	hypothetical protein	g	nonsense		