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Dynamics and diversity of the 'Atopobium cluster' in the human faecal microbiota, and phenotypic characterization of 'Atopobium cluster' isolates

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Abbreviations: GI, gastrointestinal; FISH, fluorescence *in situ* hybridization; DGGE, denaturing gradient gel electrophoresis.

Running title: Polyphasic approach to the characterization of the 'Atopobium cluster' of the human faecal microbiota

The 16S rRNA gene sequences discussed in this study have been deposited in GenBank/EMBL/DDBJ under accession numbers KP233239–KP233454.

Supplementary material is available with the online version of this article.

ABSTRACT

This study monitored the dynamics and diversity of the human faecal ‘*Atopobium* cluster’ over a 3-month period using a polyphasic approach. Fresh faecal samples were collected fortnightly from 13 healthy donors (6 males and 7 females) aged between 26 and 61 years. Fluorescence *in situ* hybridization was used to enumerate total (EUB338mix) and ‘*Atopobium* cluster’ (ATO291) bacteria, with counts ranging between 1.12×10^{11} and 9.95×10^{11} , and 1.03×10^9 and 1.16×10^{11} cells (g dry weight faeces)⁻¹, respectively. The ‘*Atopobium* cluster’ population represented 0.2–22 % of the total bacteria, with proportions donor-dependent. Denaturing gradient gel electrophoresis (DGGE) using ‘*Atopobium* cluster’-specific primers demonstrated faecal populations of these bacteria were relatively stable, with bands identified as *Collinsella aerofaciens*, *Collinsella intestinalis*/*Collinsella stercoris*, *Collinsella tanakaei*, *Coriobacteriaceae* sp. PEAV3-3, *Eggerthella lenta*, *Gordonibacter pamelaeae*, *Olsenella profusa*, *Olsenella uli* and *Paraeggerthella hongkongensis* in the DGGE profiles of individuals. Colony PCR was used to identify ‘*Atopobium* cluster’ bacteria isolated from faeces ($n = 224$ isolates). 16S rRNA gene sequence analysis of isolates demonstrated *Collinsella aerofaciens* represented the predominant (88 % of isolates) member of the ‘*Atopobium* cluster’ found in human faeces, being found in nine individuals. *Eggerthella lenta* was identified in three individuals (3.6 % of isolates). Isolates of *Collinsella tanakaei*, an ‘*Enorma*’ sp. and representatives of novel species belonging to the ‘*Atopobium* cluster’ were also identified in the study. Phenotypic characterization of the isolates demonstrated their highly saccharolytic nature and heterogeneous phenotypic profiles, and 97 % of the isolates displayed lipase activity.

INTRODUCTION

Representatives of four main phyla of bacteria predominate in the human gastrointestinal (GI) tract, with most 16S rRNA gene sequence based surveys reporting *Firmicutes* as the most abundant bacteria, followed by *Bacteroidetes*, *Actinobacteria* and *Proteobacteria* (Rajilić-Stojanović *et al.*, 2007; Zoetendal *et al.*, 2008; Vrieze *et al.*, 2010). Much is known about the diversity of the *Firmicutes*, *Bacteroidetes*, *Proteobacteria* and the genus *Bifidobacterium* (*Actinobacteria*) within the GI tract. Even though more reliable cell-based quantification methods such as FISH indicate they are numerically more predominant than the bifidobacteria in human faeces, representing ~8 % of the total bacteria, little is known about the diversity and metabolic abilities of *Actinobacteria* belonging to the class *Coriobacteriia* (Harmsen *et al.*, 2000; Rigottier-Gois *et al.*, 2003; Lay *et al.*, 2005; Child *et al.*, 2006). However, *Collinsella aerofaciens* is part of the core gut microbiome of healthy and obese adults (Turnbaugh *et al.*, 2009; Qin *et al.*, 2010), and *Adlercreutzia* and *Slackia* species have been associated with equol production in the human GI tract (Maruo *et al.*, 2008; Jin *et al.*, 2010).

Recent studies have suggested an association of members of the *Coriobacteriia* (Gupta *et al.*, 2013) with host obesity, lipid and drug metabolism, cholesterol and triglyceride levels and immunological improvement (Zhang *et al.*, 2009; Hoyles, 2009; Haiser *et al.*, 2013; Lahti *et al.*, 2013; Claus *et al.*, 2011; Martínez *et al.*, 2009, 2013). However, representation of these bacteria in faecal samples has been low in next-generation sequence libraries compared with their representation as determined by quantitative PCR (qPCR) and FISH (Matsuki *et al.*, 2004; Harmsen *et al.*, 2000; Harmsen *et al.*, 2002). It is well known that *Actinobacteria*, specifically bifidobacteria, are under-represented or remain undetected in PCR-based studies, with factors such as selection of DNA extraction method, PCR primers and cycling conditions affecting their representation in clone libraries (Wilson & Blitchington, 1996; Suau *et al.*, 1999; Koenig *et al.*, 2011; Maukonen *et al.*, 2012; Sim *et al.*, 2012). *Actinobacteria* are particularly sensitive to these factors because of their hydrophobic cell walls and the high G+C content of their DNA (up to 67 mol %). Consequently, we adopted a polyphasic approach to characterize members of the ‘*Atopobium* cluster’ within the human faecal

microbiota. Faecal samples were collected from donors over a 3-month period and ‘*Atopobium* cluster’ populations monitored using fluorescence *in situ* hybridization (FISH) (ATO291) and cluster-specific denaturing gradient gel electrophoresis (DGGE; Hoyles, 2009). Identities of bacteria represented by different bands in DGGE profiles were confirmed by cloning and DNA sequencing. In addition, faecal bacteria were cultivated from each donor on fastidious anaerobe agar containing Tween 80 (FAA^{T80}) and ‘*Atopobium* cluster’ bacteria identified using colony PCR. The identities of isolates were confirmed using 16S rRNA gene sequence analysis, and the isolates were also characterized phenotypically. Therefore, the work presented herein represents the most thorough characterization of the human faecal ‘*Atopobium* cluster’ population conducted to date.

METHODS

Processing of samples

Fresh faecal samples were collected on site, fortnightly from 13 healthy donors (6 males and 7 females) aged between 26 and 61 years (**Table 1**) over a 3-month period. All donors provided samples freely and gave oral consent for microbiological analyses to be performed on their faeces. None of the donors had received antibiotic treatment in the 6 months prior to or during the study. No other exclusion criteria were enforced. The samples were collected in stomacher bags (Seward) and immediately placed in an anaerobic cabinet (MACS1000, 80:10:10, N₂:CO₂:H₂; Don Whitley Scientific, UK) and kneaded manually. Approximately 1–2 g of sample was transferred into a pre-weighed microcentrifuge tube for faecal dry weight analysis. A further 5–10 g portion was transferred to a fresh stomacher bag and a 1:9 (w/w) faecal homogenate prepared in pre-reduced phosphate-buffered saline (PBS, 0.1 M, pH 7.2; Oxoid) by manual kneading (Hoyles & McCartney, 2009). Aliquots (4 × 375 µl) of the faecal homogenate were transferred into microcentrifuge tubes for processing for FISH analysis. Additional aliquots (2 × 1 ml) were washed twice in sterile PBS (centrifugation speed 13,000 *g* for 10 min) and stored in PBS/glycerol (1:1, v/v) at -20 °C until DNA extraction. An aliquot of the homogenate from one sample per donor was used to prepare a dilution

series (10^{-1} – 10^{-7}) in anaerobic half-strength peptone water (Oxoid Ltd), for isolation of bacteria on FAA^{T80} as described below.

FISH

Samples were processed for FISH according to Martín-Peláez *et al.* (2008). Probes ATO291 (probeBase accession no. pB-00943; name S⁻-Ato-0291-a-A-17; 5'-GGTCGGTCTCTCAACCC-3'; Harmsen *et al.*, 2000) and EUB338mix [(pB-0159; S-D-Bact-0338-a-A-18; 5'-GCTGCCTCCCGTAGGAGT-3'), (pB-0160; S⁻-BactP-0338-a-A-18; 5'-GCAGCCACCCGTAGGTGT-3'), (pB-0161; S⁻-BactV-0338-a-A-18; 5'-GCTGCCACCCGTAGGTGT-3'); Daims *et al.*, 1999] were used to enumerate 'Atopobium cluster' and total bacteria, respectively. Slides were examined under a Nikon E400 Eclipse epifluorescence microscope. DAPI-stained cells were visualized using a DM 400 filter and hybridized cells using a DM 575 filter. Cells were counted for 15 fields of view and counts (g dry weight faeces)⁻¹ calculated using the equation adapted from Hoyles & McCartney (2009).

$$\text{Cells (g dry weight faeces)}^{-1} = DF \times ACC \times 6732.42 \times DF_{\text{sample}} \times (\text{wet/dry weight}),$$

where DF is the dilution factor [$(300/375 = 0.8) \times 50$ (20 μ l applied to well) $\times 10$ (1/10 faecal homogenate) = 400], ACC is the average cell count, 6732.42 refers to the area of the well divided by the area of the field of view and DF_{sample} refers to the dilution of sample used (e.g. between 5 $\times$ and 2000 $\times$, probe-dependent).

DGGE

'Atopobium cluster'-specific DGGE was performed on all samples, using a modified version of the method of Hoyles (2009). The faecal pellets stored in PBS/glycerol at -20 °C were washed twice (centrifugation speed 13,000 g for 10 min) in PBS prior to DNA extraction using the FastDNA® Spin Kit (MP Biomedicals). The quality of DNA was examined by gel electrophoresis [1 % (w/v) agarose gel containing ethidium bromide (0.4 mg ml⁻¹; Sigma Aldrich) in 1 $\times$ TAE buffer

(diluted from stock 50× TAE; Fisher Scientific) viewed under UV light]. DNA concentration was measured by using a Nanodrop Spectrophotometer ND-1000 (Labtech, UK). DNA (5 ng µl⁻¹) was then used for ‘*Atopobium* cluster’-specific PCR-DGGE as described below.

The ‘*Atopobium* cluster’-specific 16S rRNA gene-targeted primers of Matsuki *et al.* (2004) were employed, but with a GC clamp attached to primer c-Atopo-F [GCc-Atopo-F, 5'-CGCCCGCCGCGCGCGGCGGGCGGGGCGGGGGCACGGGGGGGGGTTGAGAGACCGACC-3' (Hoyles, 2009); c-Atopo-R, 5'-GGACGTCTTCTTCGRGGC-3']. Reaction mixtures (50 µl) contained 10 µl of 5× GoTaq® Flexi Buffer (Promega), 5 µl of dNTPs (12.5 mM each; Promega), 2 µl of MgCl₂ (25 mM; Promega), 1 µl of each primer (20 pmol; Sigma Genosys), 1 µl of *Taq* polymerase (1.25 U; Promega), and 1 µl DNA. Amplification was performed using a MJ mini Personal Thermal Cycler (Bio-Rad). PCR conditions were as follows: one cycle of heating at 95 °C for 5 min, followed by 35 cycles of 95 °C for 30 s, 55 °C for 30 s and 72 °C for 1 min, and a final extension at 72 °C for 7 min. PCR products were examined by using agarose gel electrophoresis and stored at -20 °C.

DGGE was carried out on the V20-HCDC DGGE system (BDH). PCR products (5 µl of each) and an in-house DGGE ladder (comprising amplified DNA from strains listed below) were run directly on polyacrylamide gels with gradients (50–70 %) that were formed with 8 % (w/v) acrylamide stock solutions [40 % acrylamide/bis solution, 37.5:1 (2.6 % C); Bio-Rad] containing 2 % (v/v) glycerol (BDH), and which contained 0 and 100 % denaturant [(7 M PlusOne urea; Pharmacia Biotech) and 40 % (w/v) PlusOne formamide (Amersham Biosciences)]. Electrophoresis was run in 0.5× TAE buffer (diluted from 50× TAE; Fisher Scientific) at a constant voltage of 100 V and a temperature of 60 °C for 16 h. Following electrophoresis, the gels were silver-stained according to the method of Sanguinetti *et al.* (1994) with minor modifications. Gels were scanned at 600 dpi and the images analyzed using GelCompar II (Applied Mathematics, Belgium).

The DGGE ladder was compiled using DNA from the following strains of bacteria:
Atopobium minutum CCUG 31167^T, *Collinsella aerofaciens* CCUG 28087^T, *Collinsella stercoris*

CCUG 45295^T, *Coriobacteriaceae* sp. PEAV3-3 (Hoyles, 2009), *Cryptobacterium curtum* CCUG 55773^T, *Eggerthella lenta* DSM 2243^T, *Gordonibacter pamelaee* CCUG 55131^T, *Olsenella profusa* CCUG 45371^T and *Olsenella uli* CCUG 31166^T.

Identification of predominant bands in ‘*Atopobium* cluster’-specific DGGE profiles

Cloning and sequencing of the faecal ‘*Atopobium* cluster’-specific PCR products (from one sample for each donor) was performed. PCR products were purified using the QIA quick® PCR purification kit (Qiagen) (with cleaned products eluted in 30 µl of EB buffer) and stored at -20 °C prior to cloning using StrataClone PCR cloning kits (Agilent Technologies UK Limited). Eight white or light-blue colonies were randomly selected from each cloning experiment and cultured overnight in LB broths containing ampicillin (10 mg ml⁻¹) at 37 °C. Plasmids were extracted from broth cultures using QIAprep® Spin Miniprep Kit (Qiagen), checked using agarose gel electrophoresis and stored at -20 °C. ‘*Atopobium* cluster’-specific PCR-DGGE was performed using plasmid DNA as template, to determine which band from the donor’s DGGE profile each contained, and plasmid DNA for one representative of each distinctive insert per donor was sequenced by Source Bioscience (LifeSciences, UK) using primer T7 promoter F (5′-TAATACGACTCACTATAGGG-3′). Insert sequences were cropped from the plasmid sequences using 4Peaks (Version 1.7.1; 4Peaks by A. Griekspoor and Tom Groothuis, mekentosj.com) and compared with 16S rRNA gene sequences in EzTaxon-e (Kim *et al.*, 2012) to determine closest relatives.

Isolation of predominant faecal ‘*Atopobium* cluster’ population

The 10⁻⁴–10⁻⁷ dilutions prepared in half-strength peptone water were plated in triplicate on pre-reduced FAA (BIOTECS Laboratories Ltd) supplemented with 5 % laked horse blood (Oxoid Ltd) and Tween 80 (0.5 g l⁻¹; Fisher Scientific) (FAA^{T80}) and incubated anaerobically (MACS1000; Don Whitley Scientific, UK) for 5 days prior to enumeration of bacteria on the dilution plate containing discrete colonies (20–200 colonies). Approximately 160 colonies were randomly selected (or all

colonies if less than 160 on the plate) from one of these three plates, subcultured onto gridded, pre-reduced FAA^{T80} and grown to purity.

Colony PCR to determine ‘*Atopobium* cluster’ isolates

‘*Atopobium* cluster’-specific PCR was performed using a crude colony PCR method to identify which of the isolates were members of the ‘*Atopobium* cluster’ population. Briefly, a single colony was suspended in 10 µl of filter-sterilized H₂O using a sterile toothpick. The cell suspension was microwaved at high temperature for 30 s (Panasonic NN-T221MBBPQ) and used as DNA template for ‘*Atopobium* cluster’-specific PCR using the primers of Matsuki *et al.* (2004). In-house strains were used as negative (*Megasphaera* sp. MRSV3-10, *Sutterella wadsworthensis* FAAV1-5 and *Prevotella buccae* PEAV1-8; Hoyles, 2009) and positive (*Collinsella aerofaciens* FAAV2-5 and FAAV3-9; Hoyles, 2009) controls for ‘*Atopobium* cluster’-specific PCR. Amplification products were examined by agarose gel electrophoresis. Isolates which gave positive colony PCR results were subcultured on FAA^{T80} prior to storage on cryogenic beads (ProLab diagnostics) at -70 °C.

Identification of ‘*Atopobium* cluster’ isolates

Isolates were grown anaerobically on FAA^{T80} prior to DNA extraction using InstaGeneTM Matrix (Bio-Rad). DNA was stored at -20 °C until use. PCR amplification and clean up of 16S rRNA genes was performed as described by Hoyles *et al.* (2004), with sequencing outsourced to Source BioScience. Almost-complete sequences were compared with those in EzTaxon-e to determine closest relatives. Sequences were proofread against those of the type strains of nearest relatives in Geneious Pro 4.6.1 (<http://www.geneious.com>). Alignments were performed to determine sequence similarity between the different isolates and type strains of species. A multiple-sequence alignment was created using ClustalW, and was corrected manually to omit gaps at the 5′ and 3′ ends from further analyses. Phylogenetic (neighbour-joining) analysis was done as described by Hoyles *et al.* (2004).

The identities of isolates tentatively identified as *Collinsella intestinalis* or *Collinsella stercoris* on the basis of 16S rRNA gene sequence analysis were confirmed using the primers of Kageyama & Benno (2000). The PCR programme we used differed from that given in the original publication; using a MJ mini Personal Thermal Cycler, the following programme was used: 94 °C for 5 min, followed by 25 cycles of 94 °C for 60 s, 58 °C for 60 s and 72 °C for 60 s (there was no final elongation step). Sequences were checked for chimeras using Bellerophon 3 (Huber *et al.*, 2004).

Phenotypic characterization of ‘*Atopobium* cluster’ isolates

The carbohydrate fermentation capabilities of the faecal ‘*Atopobium* cluster’ isolates were examined using API 20 A (bioMérieux, UK) strips for anaerobes, following the manufacturer’s instructions. It is important to note that ALL steps of strip preparation and inoculation were carried out in the anaerobic cabinet. Briefly, isolates were grown anaerobically in cooked meat medium for 2 days and 200 µl of broth culture used to grow a bacterial lawn on duplicate pre-reduced Columbia blood agar (Oxoid Ltd) supplemented with 5 % laked horse blood (Oxoid Ltd) plates (incubated overnight at 37 °C, anaerobically). Cells were harvested in the anaerobic cabinet with sterile swabs and inoculated into API 20 A medium. While the instructions state the turbidity of cultures should be ≥ 3 McFarland standard, it was not always possible to visualise culture turbidity [namely, *Eggerthella lenta* and closely related isolates (*Eggerthella lenta* DSM 2243^T, D3-3, D3-6, D3-8, D3-65, D3-96, D6-71, D9-63 and D11-98)]; in such cases, the complete bacterial lawns from both plates were used to produce strip inoculum. Following inoculation, the API 20 A strips were incubated anaerobically for 48 h and results recorded as: -, negative; +w, weak positive; +, positive.

RESULTS AND DISCUSSION

Fresh faecal samples were collected fortnightly from 13 healthy adults for 3 months, and molecular- and cultivation-based methods were used to characterize the diversity and dynamics of the ‘*Atopobium* cluster’ population of the human faecal microbiota. FISH was used to enumerate total

bacteria (probes EUB338mix) and the ‘*Atopobium* cluster’ (probe ATO291). ‘*Atopobium* cluster’-specific DGGE (Hoyles, 2009) was used to profile this community within the faecal microbiota, and cloning and sequencing of DNA within bands was used to identify bacteria. Cultivation work was performed on one faecal sample for each subject to investigate the predominant culturable members of the faecal ‘*Atopobium* cluster’ of humans.

FISH analysis of faecal ‘*Atopobium* cluster’ population

When first described, probe ATO291 targeted a paraphyletic group of bacteria that were classified within the family *Coriobacteriaceae*, but neither *Slackia* nor *Denitrobacterium* spp. were detected by the probe (Harmsen *et al.*, 2000). The bacteria targeted by this group were referred to as the ‘*Atopobium* cluster’. Since the publication of the paper describing ATO291, a number of novel species within this cluster (and the *Coriobacteriaceae* as a whole) have been described. In a recent molecular-signature-based study, Gupta *et al.* (2013) redefined the taxonomy of the coriobacteria, proposing the class *Coriobacteriia*, orders *Coriobacteriales* and *Eggerthellales*, and families *Atopobiaceae*, *Eggerthellaceae* and *Coriobacteriaceae*. Details of the coverage of probe ATO291 within the new taxonomic framework can be found in **Fig. 1**. Species/sequences targeted by the probe (and forward DGGE primer) can be found in Supplementary Table 1.

The human faecal ‘*Atopobium* cluster’ populations ranged between 1.03×10^9 (9.01 as $\log_{10}$) and 1.16×10^{11} (11.06 as $\log_{10}$) cells (g dry weight faeces)⁻¹ (**Fig. 2**), and counts of total bacteria (EUB338mix) ranged between 1.12×10^{11} (11.05 as $\log_{10}$) and 9.95×10^{11} (12.08 as $\log_{10}$) cells (g dry weight faeces)⁻¹, consistent with previously published data (Harmsen *et al.*, 2000; Hoyles & McCartney, 2009). Overall, ATO291 counts were fairly stable for all individuals over 3 months (**Table 1; Supplementary Table 2**), with slightly more fluctuation seen in the proportion the ‘*Atopobium* cluster’ made up of the total microbiota (**Supplementary Table 3**). Donors 3 and 13 had lower ATO291 counts than the other subjects, with the ‘*Atopobium* cluster’ representing <0.5 % of the total microbiota for Donor 13. Inter-individual variation was observed in the relative abundance of the

‘*Atopobium* cluster’ bacteria in the faecal microbiota, similarly to Harmsen *et al.* (2000); with averages herein ranging from ~0.2 % (D13) to ~22 % (D2) of the total microbiota. In addition, inter-individual variability in the ‘*Atopobium* cluster’ abundance (relative to their mean) was greater for some individuals (e.g. D4, D7, D12) in this study than others (e.g. D5, D9). Overall, the data herein provide further evidence that the ‘*Atopobium* cluster’ is a predominant member of the healthy faecal microbiota of most humans in the developed world (averaging between 3 and 10 %; 9/13 subjects in this study), highly abundant in a substantial minority of people (3/13 subjects in this study) and almost absent in a small minority.

DGGE analysis of the faecal ‘*Atopobium* cluster’ population

The sequences of the forward and reverse DGGE primers were searched against bacterial and archaeal sequences within Greengenes 13_5. These analyses confirmed that the primers targeted members of the *Coriobacteriia* as described in **Fig. 1**, plus a few sequences distantly related to *Slackia* and *Enterorhabdus* spp., and probably representing novel genera within the *Coriobacteriia* (Supplementary Table 6). Details of how the species/sequences targeted by the DGGE primers were determined and their identities can be found in Supplementary Information and Supplementary Tables 1 and 4–6. In addition, the taxonomic assignments of the Greengenes sequences have been updated for the sequences targeted by the DGGE primers. It should be noted that Greengenes 13_5 does not adequately assign members of the genus *Olsenella* (compare Supplementary Tables 5 and 6), regardless of whether the taxonomy follows that used by Greengenes 13_5 or of Gupta *et al.* (2013).

‘*Atopobium* cluster’-specific PCR-DGGE was successfully performed for all samples, with the exception of those collected from Donor 13 (who had the lowest ATO291 counts, representing <0.3 % of faecal microbiota throughout). Overall, distinctive banding profiles were seen for each individual, containing 2–8 dominant bands per profile (**Fig. 3**). Donor 7 and Donor 8 (partners) had similar DGGE profiles (**Supplementary Figure 1**). Their DGGE profiles were found to be similar for faecal *Actinobacteria* (excluding *Coriobacteriia*) in a previous study (Hoyles *et al.*, 2013).

‘*Atopobium* cluster’-specific PCR-DGGE profiles were relatively stable for each individual across the 3-month study (**Supplementary Figure 2**). The dominant band of the profiles for most subjects corresponded with *Collinsella aerofaciens* in our in-house ladder (but not for D3 and D12), in agreement with previous reports that *Collinsella aerofaciens* is part of the core microbiome of adult humans (Turnbaugh *et al.*, 2009; Qin *et al.*, 2010). Bands corresponding to *Collinsella stercoris*/*Collinsella intestinalis*, *Coriobacteriaceae* sp. PEAV3-3, *Cryptobacterium curtum*, *Eggerthella lenta*, *Gordonibacter pamelaee* and *Olsenella profusa* in the ladder were also seen in some profiles, as well as bands not corresponding with bands in the ladder (some of which were common between different donors) (**Fig. 3**).

Sequencing of clones confirmed that those bands in faecal DGGE profiles corresponding with bands in the ladder were of the same species (**Table 2**); for example, all clones displaying DGGE profiles with a band corresponding to *Collinsella aerofaciens* band in the ladder had ‘best hit’ with *Collinsella aerofaciens*. As well as the bands corresponding to *Collinsella aerofaciens* in the ladder being identified as *Collinsella aerofaciens*, three other clones with banding profiles not corresponding to any of the bands in the ladder (**Fig. 3**: bands 3, 11 and 14*) were revealed as *Collinsella aerofaciens* (99–99.5 % sequence similarity). All other bands for which clones were available represented members of the ‘*Atopobium* cluster’, including *Collinsella tanakaei*, *Eggerthella lenta*, *Gordonibacter pamelaee*, *Paraeggerthella hongkongensis*, *Olsenella profusa* and *Olsenella uli* (**Table 2**). Interestingly, the clones corresponding to bands 25* and 31 (**Fig. 3**), which were associated with (positioned slightly above) the lower band of the *Atopobium minutum* in the ladder were revealed to be *Paraeggerthella hongkongensis*. The failure to detect members of the genus *Atopobium* in this study is consistent with previous findings, corroborating the suggestion that the genus *Atopobium* is not among the core or predominant members of the human gut microbiota.

Bands corresponding to all members of the ‘*Atopobium* cluster’ which have previously been isolated from human faeces [namely, *Collinsella*, *Cryptobacterium*, *Eggerthella*, *Gordonibacter* and *Olsenella* (Kageyama & Benno, 2000; Lau *et al.*, 2004a; Hoyles, 2009; Arumugam *et al.*, 2011)], or

seen in recent microarray data (Wang *et al.*, 2004; Rajilić-Stojanović *et al.*, 2009) were observed in DGGE profiles in this study. Wang *et al.* (2004) reported up to 40 bacterial species from the predominant human faecal microbiota, including *Collinsella* and *Eggerthella* species. In addition, Rajilić-Stojanović *et al.* (2009) demonstrated, using a phylogenetic microarray (HITchip), that the actinobacterial component of the gut microbiome of European, American and Japanese subjects comprised *Bifidobacterium*, *Collinsella*, *Eggerthella* and *Gordonibacter* species.

Paraeggerthella hongkongensis has previously only been associated with bacteraemia (Lau *et al.*, 2004a). However, it would appear that, similar to *Eggerthella lenta*, *Paraeggerthella hongkongensis* is an opportunistic pathogen of GI origin, being detected in the DGGE profiles of Donor 8 and Donor 10. *Olsenella uli* and *Olsenella profusa* are members of the human oral microbiota, and have been associated with periodontal infections, gingivitis and dental caries (Munson *et al.*, 2004). We detected the species, respectively, in the DGGE profiles of Donor 6 and Donor 5. Upon identifying *Olsenella uli*-associated bacteraemia in a patient with acute cholangitis but no evidence of dental disease, Lau *et al.* (2004b) suggested that the bacterium responsible for the infection was of GI origin. There are currently only two reports of the isolation of *Gordonibacter pamelaiae* in the literature: one strain was isolated from the sigmoid region of the colon of a 33-year-old male patient suffering from acute Crohn's disease (Würdemann *et al.*, 2009); the other was isolated in pure culture from an 82-year-old patient with disseminated rectosigmoid carcinoma with fresh blood and mucus in his stool (Woo *et al.*, 2010). We detected the species in the DGGE profiles of six of our donors (**Table 1**).

Characterization of the culturable faecal 'Atopobium cluster' population

Collinsella aerofaciens and *Eggerthella lenta* are reportedly easy to isolate from human faeces (even without 'selective' medium/conditions), implying not only that they are common commensals but also dominant members of the microbiota (otherwise they would be diluted out). However, to date, the vast majority of *Eggerthella lenta* isolates available from culture collections are

of clinical rather than faecal origin, with the bacterium considered an opportunistic pathogen of GI origin (Lau *et al.*, 2004a, b).

There is no known ‘selective’ medium for isolating members of the ‘*Atopobium* cluster’, although addition of 0.5 % Tween 80 in medium has been reported to increase the growth of *Collinsella aerofaciens* (Harmsen *et al.*, 2000) and FAA contains arginine (which *Eggerthella lenta* has a requirement for) so FAA^{T80} was employed in this study. Counts of total bacteria obtained from anaerobic cultivation work on FAA^{T80} plates ranged between 1.11×10^9 and 2.83×10^{10} cells (g dry weight faeces)⁻¹ (**Table 1**; compared with 1.12×10^{11} and 9.95×10^{11} from FISH data). Between 120 and 160 colonies were subcultured from the FAA^{T80} dilution plate with discrete colonies for each sample (one per donor). Of the 1514 isolates that grew, 283 displayed positive colony PCR results (including faint/weak products; 59 isolates) using ‘*Atopobium* cluster’-specific primers and were further characterized (**Table 1**). Partial 16S rRNA gene sequencing [~600 nt; identities determined using EzTaxon-e] revealed that the majority of isolates producing faint/weak ‘*Atopobium* cluster’-specific PCR were not members of the class *Coriobacteriia* (data not included); these included the two isolates from Donor 13 (from whom no ‘*Atopobium*-cluster’ isolates were obtained).

Almost-complete 16S rRNA gene sequencing (~1440 nt) of the 224 isolates confirmed as belonging to the ‘*Atopobium* cluster’ (by partial sequencing) was performed and revealed that the majority (196/224) of ‘*Atopobium*-cluster’ isolates were *Collinsella aerofaciens* (**Table 3**), consistent with the findings of the DGGE data (namely, predominant band corresponding to the *Collinsella aerofaciens* band in the reference). Furthermore, 56 isolates of *Collinsella aerofaciens* were isolated from Donor 2, who had the highest ATO291 count and predominance (~22 % of the total microbiota; **Supplementary Table 2**). However, no *Collinsella aerofaciens* isolates were recovered from donors 3, 4 and 12 (**Table 3**). Again this corroborated the findings of DGGE for these donors; the DGGE profiles of Donor 3 and Donor 12 lacked a band corresponding to *Collinsella aerofaciens* (reference), and said band was co-dominant with other bands in Donor 4’s DGGE profile. The remaining 28

‘*Atopobium* cluster’ isolates represented *Collinsella*, *Eggerthella*, ‘*Enorma*’, *Olsenella* and novel species.

The *Collinsella aerofaciens* isolates recovered in this study shared between 98.3 and 100 % 16S rRNA gene sequence similarity with each other and the type strain. Kageyama *et al.* (1999a) sequenced three strains of *Collinsella aerofaciens* (including the type strain) and found they shared 96.6–97.8 % sequence similarity. DNA–DNA hybridization data showed they had >72 % reassociation, indicating that the strains belonged to the same species. Given the sequence similarity of our isolates to the sequence of the type strain of *Collinsella aerofaciens*, we believe that we have recovered 196 *Collinsella aerofaciens* isolates from the faeces of nine healthy humans.

Phenotypic characterization of *Collinsella aerofaciens* strains isolated from human faecal samples has revealed great diversity in the metabolic capabilities of different strains (Moore & Holdeman, 1974; Holdeman *et al.*, 1976; Kageyama *et al.*, 1999a). Moore & Holdeman (1974) classified three groups of *Collinsella aerofaciens* based on acid production from sucrose and/or cellobiose fermentation. Kageyama *et al.* (1999a) extended this, demonstrating four groups of *Collinsella aerofaciens* based on carbohydrate fermentation patterns of 181 faecal isolates. In addition, these four groups were further divided into 16 sub-groups in relation to fermentation of aesculin, salicin and amygdalin. Subsequently, Harmsen *et al.* (2000) reported another sub-group of *Collinsella aerofaciens*, able to produce acid from arabinose, erythritol, maltose, ribose, starch, trehalose and xylose. As discussed below, our phenotypic data have extended the diversity observed within *Collinsella aerofaciens*. It is possible that such phenotypic diversity within a single species may reflect biological adaptability within specific populations of the microbiota, and may explain why *Collinsella aerofaciens* has been shown to be a core member of the human gut microbiota.

Previous studies have relied on characterizing one or two isolates recovered from multiple donors, whereas our study has characterized multiple isolates from the same donors. All 193 faecal *Collinsella aerofaciens* isolates characterized phenotypically in this study (D5-122, D10-142 and D11-45 did not resuscitate from cryogenic storage) produced acid from D-glucose, D-lactose and D-

mannose fermentation, did not produce acid from glycerol or D-rhamnose fermentation, and were negative for indole utilization and production of urease and catalase (**Table 4**). Variation was seen in the phenotypic characteristics of the isolates for the other tested substrates, although most *Collinsella aerofaciens* isolates also produced acid from D-saccharose (7/193 isolates were negative) and D-maltose (2/193 isolates were negative), and did not produce acid from D-mannitol (3/193 isolates were positive), D-xylose (4/193 isolates were positive), L-arabinose (3/193 isolates were positive), D-melezitose (3/193 isolates were positive) and D-sorbitol (3/193 isolates were positive). The faecal *Collinsella aerofaciens* isolates were classified into 18 different groups (with sub-groups displaying weak positive reactions for one or more test) based on their biochemical characteristics (**Table 4**). Eight of the groups classified in this study were distinct from the groups previously described (Kageyama *et al.*, 1999a) based on demonstration of acid production from one or more of: L-arabinose, D-mannitol, D-melezitose, D-sorbitol and D-xylose or no acid produced from D-maltose. No Group IV fermentation profiles (Kageyama *et al.*, 1999a) were seen from our faecal *Collinsella aerofaciens* isolates. However, isolates with biochemical profiles corresponding to Groups IA, IE/IF (amygdalin is not included in API 20 A), IIF/IIG (no amygdalin data) and III were observed. The API 20 A data for *Collinsella aerofaciens* CCUG 28087^T included weak acid production from D-raffinose, which is inconsistent with previously published work (Kageyama *et al.*, 1999a; Nagai *et al.*, 2010). Unlike Nagai *et al.* (2010), who also used API 20 A tests to determine fermentation profiles (rather than the conventional culture methods employed by Kageyama and colleagues), we found the type strain of *Collinsella aerofaciens*, CCUG 28087^T, did not produce acid from salicin.

The majority of our faecal *Collinsella aerofaciens* isolates (111/193) displayed biochemical characteristics of group 8 and its sub-groups. A further 27 *Collinsella aerofaciens* isolates displayed group 7's phenotypic profile, which differed from group 8 only in relation to gelatin hydrolysis (group 8 hydrolysing gelatin and group 7 not). Interestingly, '*Enorma*' sp. D12-104 showed the same phenotypic profile as group 10. Overall, big differences in phenotypic profiles of *Collinsella aerofaciens* were seen within and between donors' isolates (**Table 4**).

Isolate D4-142 was most closely related to the type strain of *Collinsella tanakaei* (99.9 % 16S rRNA gene sequence similarity). API 20 A data for *Collinsella tanakaei* D4-142 was distinctly different from that published for the type strain *Collinsella tanakaei* YIT 12063^T, with acid produced by D4-142 from L-arabinose and weak positives for acid production from D-mannitol, D-xylose, D-melezitose, D-raffinose and D-sorbitol. In addition, D4-142 displayed the ability to hydrolyse gelatin, which was also inconsistent with the published description for *Collinsella tanakaei* (Nagai *et al.*, 2010). Differences between the phenotypes of our isolate and that of Nagai *et al.* (2010) could be due to how we incubated the API strips. We did all phenotypic work in the anaerobic cabinet, whereas Nagai *et al.* (2010) do not state how they incubated their API strips. It is possible that our isolate represents a different species from the type strain of *Collinsella tanakaei*: only DNA–DNA hybridization or whole-genome sequencing could address this. However, it should be noted that the species description of Nagai *et al.* (2010) is based on a sole isolate. Phenotypic heterogeneity within species of the genus *Collinsella* – and discussed herein for *Collinsella aerofaciens* – is well documented. Only the isolation and characterization of more isolates of *Collinsella tanakaei* will provide a full picture of the metabolic capabilities of this bacterium. *Collinsella tanakaei* was only isolated from Donor 4 (a healthy Thai female), and DGGE clones identified as most closely related to *Collinsella tanakaei* were also found for this individual and for Donor 12 (a healthy Malaysian male). The only previous reports on the isolation of *Collinsella tanakaei* from faeces have been from two healthy Japanese males (Nagai *et al.*, 2010) and a healthy Chinese female (Hoyles, 2009). This suggests there may be a geographical/ethnicity factor (e.g. diet/environment/genetics) associated with the presence of *Collinsella tanakaei* in the faecal microbiota (with all individuals so far reported to harbour *Collinsella tanakaei* having countries of origin in Eastern/South East Asia). However, further work would be required to support/refute this hypothesis.

Isolates D3-5, D3-11, D3-44, D3-70, D3-91, D3-123, D3-130, D3-140, D3-141, D3-150, D3-152, D11-10, D11-70 and D11-102 shared 99.0–100 % 16S rRNA gene sequence similarity. These 14 isolates were most closely related to *Collinsella stercoris* and *Collinsella intestinalis* (97.5–97.8 %

and 97.9–98.5 % sequence similarity, respectively). The 14 isolates could not be differentiated from *Collinsella intestinalis* and *Collinsella stercoris* using the ‘*Atopobium* cluster’-specific DGGE approach, as the sequence of the region amplified by the primer set GCC-Atopo-F/Atopo-R was identical in both species and the faecal isolates. Consequently, using the discriminatory PCR method of Kageyama & Benno (2000), we were able to show that the isolates from Donor 3 were *Collinsella intestinalis*, while those from Donor 11 were *Collinsella stercoris* (data not shown). Variation was seen in the phenotypic profiles of the 14 isolates. All produced acid from D-glucose, D-lactose and D-mannose, did not produce acid from D-mannitol, glycerol, D-melezitose, D-sorbitol or D-rhamnose, and were negative for indole utilization and production of urease and catalase. The majority (13/14) of isolates also produced acid from D-maltose, but did not produce acid from D-xylose or D-arabinose. They could not be differentiated from *Collinsella stercoris* and *Collinsella intestinalis* on the basis of the limited number of phenotypic traits tested in this study. Although both *Collinsella stercoris* and *Collinsella intestinalis* are reported to not produce acid from raffinose (Kageyama & Benno, 2000; Nagai *et al.*, 2010), we found that the type strain of *Collinsella intestinalis* was weakly positive for this trait. Our 14 isolates were variable in this trait (the three *Collinsella stercoris* isolates [D11-10, D11-70 and D11-102] and *Collinsella intestinalis* isolates D3-5 and D3-11 were negative, D3-152 was weakly positive and the remaining seven *Collinsella intestinalis* isolates were positive).

Eight isolates belonging or closely related to the genus *Eggerthella* were isolated from four different donors. Seven (D3-3, D3-6, D3-8, D3-65, D3-96, D6-71 and D9-63) were identified as *Eggerthella lenta* (98.7–99.7 % sequence similarity). The eighth isolate (D11-98) was thought to represent a novel genus within the family *Eggerthellaceae* (**Fig. 1**), sharing only 93.1 and 95.1 % 16S rRNA gene sequence similarity with the sequences of the type strains of *Eggerthella sinensis* and *Eggerthella lenta*, respectively. Consequently, it is referred to as *Eggerthellaceae* sp. D11 from hereon, and its characterization will be described elsewhere.

However, it is noteworthy that our *Eggerthella* API 20 A data clearly indicated that, with the exception of the type strain, all strains were saccharolytic. These findings contradict previously

published data, including the species description of *Eggerthella lenta*, which suggest that *Eggerthella lenta* is generally unreactive in typical phenotypic laboratory tests and asaccharolytic (Eggerth, 1935; Moore *et al.*, 1971; Kageyama *et al.*, 1999b; Wade *et al.*, 1999). This most likely reflects the fact that all steps of the phenotypic characterization work performed in this study were carried out in an anaerobic cabinet, as opposed to manipulations being done on the laboratory bench and incubations in anaerobic gas jars (which take up to 1 h to reduce the atmospheric conditions if using gas-generating sachets). Phenotypic tests were carried out on three separate occasions to confirm our results, and produced identical results each time (data not shown).

The 16S rRNA gene sequence of isolate D12-104 shared 98.6 % sequence similarity with that of the type and only strain of '*Enorma massiliensis*', recovered from the faeces of a morbidly obese 26-year-old woman (Mishra *et al.*, 2013). Based on the results of an *in silico* analysis, the 16S rRNA gene sequences of '*Enorma massiliensis*' and D12-104 are identical within the region covered by the '*Atopobium* cluster'-specific DGGE primers (data not shown). D12-104's phenotypic profile differed from that of '*Enorma massiliensis*' in that D12-104 produced acid from D-glucose, D-lactose, D-saccharose, D-maltose, salicin, D-cellobiose, D-mannose and D-trehalose (weakly positive) and was able to utilize aesculin. Using API 50 CH (bioMérieux) to characterize the type and only strain of '*Enorma massiliensis*', Mishra *et al.* (2013) reported no fermentation or assimilation by the bacterium, although they observed fermentation of D-mannose and D-raffinose using API Rapid ID 32 A (bioMérieux), whereas we used API 20 A to characterize D12-104. Using the relaxed level of 16S rRNA sequence similarity proposed by Stackebrandt & Ebers (2006) [i.e. <98.7 % sequence similarity rather than ≤ 97 % (Stackebrandt & Goebel, 1994)] for species delineation, we consider D12-104 may represent a novel species of the genus '*Enorma*', but further work (multi-locus sequence analysis or DNA–DNA hybridization and full phenotypic characterization with comparable methods) would be required to confirm this. For this reason, our isolate is referred to as '*Enorma*' sp. D12-104 from hereon. It is interesting to note that this was the only isolate belonging to the '*Atopobium* cluster' recovered from Donor 12's faecal sample.

Isolates D6-2, D6-73 and D6-32 (hereon referred to as *Olsenella* sp. D6), recovered from Donor 6, shared 99.8–99.9 % 16S rRNA gene sequence similarity with each other, and 93.2–94.0 % with *Olsenella profusa*, *Olsenella uli* and *Olsenella umbonata*. No phenotypic data were available for the isolates as they could not be resuscitated from cryogenic beads. An additional *Olsenella* isolate (D6-110) was isolated from Donor 6: its 16S rRNA gene sequence was highly heterogeneous (i.e. very messy sequence containing numerous ambiguous base calls) and requires cloning to confirm its assignment to *Olsenella* sp. D6. Again, there were no phenotypic data available for this isolate as it could not be resuscitated from cryogenic beads after storage. The colonies of all the *Olsenella* isolates recovered on FAA^{T80} were barely visible, suggesting that this medium did not adequately fulfil their nutritional requirements and the cultures were not ‘fit enough’ to survive storage. Therefore, it is clear that we need to gain a better understanding of the nutritional requirements of members of this genus if we wish to isolate and maintain strains of this genus in future studies.

While some may consider it old-fashioned or out-of-date to include cultivation work in studies investigating the human gastrointestinal microbiota, it is still an important and valid avenue of research. Indeed, isolates such as those obtained herein are essential for mechanistic studies and/or confirmation of assertions from metagenomic analyses suggesting functionally important members of the microbiota and possible health-related associations. Even though there is no known ‘selective’ media for members of the class *Coriobacteriia*, our cultivation work readily isolated members of the ‘*Atopobium* cluster’ from human faecal samples, including isolation of novel species, and demonstrated greater phenotypic diversity of *Collinsella aerofaciens* within and between individuals than previously reported.

Uncultured representatives of the class *Coriobacteriia* have been correlated with host lipid metabolism in human (Lahti *et al.*, 2013) and animal (Martínez *et al.*, 2009, 2013; Claus *et al.*, 2011) studies, and Hoyles (2009) suggested that *Collinsella aerofaciens* plays a role in lipid metabolism within the large intestine. As such, the resuscitable (217/224) faecal ‘*Atopobium* cluster’ isolates were assayed for lipase activity using olive oil/rhodamine B agar as described by Hoyles (2009), with

Staphylococcus aureus (positive) and *Escherichia coli* (negative) used as controls. All seven faecal *Eggerthella lenta* isolates from this study, as well as *Eggerthellaceae* sp. D11, 192/193 *Collinsella aerofaciens* isolates (D8-146 being the exception), *Collinsella tanakaei* D4-142, all three *Collinsella stercoris* isolates and 7/11 *Collinsella intestinalis* isolates (D3-11, D3-70, D3-91 and D3-141 were negative) displayed lipase activity. However, whether this lipolytic activity takes place *in vivo* and/or contributes to host lipid metabolism is unknown and warrants further investigation.

SUMMARY

The ‘*Atopobium* cluster’ is a dominant member of the faecal microbiota of healthy humans [making up around 8 % of the microbiota (0.2–22 %)], yet relatively little has been published on the composition of this bacterial population. A polyphasic approach, combining molecular methods and cultivation work, was used during a longitudinal study to evaluate the diversity and dynamics of the faecal ‘*Atopobium* cluster’ population of healthy humans. Overall, the faecal ‘*Atopobium* cluster’ was relatively stable in healthy humans (both numerically and composition-wise) over a 3-month period, with greater diversity seen than previously recognized for this group of bacteria in this niche. *Collinsella aerofaciens* was shown to be the predominant member of the faecal ‘*Atopobium* cluster’ in healthy humans according to both ‘*Atopobium* cluster’-specific DGGE profiles and cultivation work, although individuals with lower levels of these bacteria as determined by FISH analysis appeared to lack *Collinsella aerofaciens*. There was great inter- and intra-individual variability with respect to the phenotypic characteristics of *Collinsella aerofaciens* isolates recovered from donors, suggesting that within individuals the contribution of this bacterium to the metabolic activity of the microbiota is multifaceted.

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 715

Table 1. Composition and numerics of the ‘*Atopobium* cluster’ population of healthy humans as determined by DGGE, FISH and cultivation analyses

Donor	Age (years)	Gender	Nationality	ATO291 counts [log ₁₀ cells (g dry weight faeces) ⁻¹]*	Species detected in ‘ <i>Atopobium</i> cluster’-specific DGGE†‡	Bacterial counts [log ₁₀ CFU (g dry weight faeces) ⁻¹]	Number of colonies	Positive colony PCR‡	‘ <i>Atopobium</i> cluster’§
1	26	Female	Japanese	10.43–10.77	<u><i>Collinsella aerofaciens</i></u> , <u><i>Eggerthella lenta</i></u>	9.97	82	9	9
2	33	Female	Thai	10.84–11.06	<u><i>Collinsella aerofaciens</i></u> , <u><i>Collinsella intestinalis</i></u> / <u><i>Collinsella stercoris</i></u> , <i>Coriobacteriaceae</i> sp. PEAV3-3	9.98	138	69	56
3	27	Female	British	9.53–9.96	<u><i>Collinsella intestinalis</i></u> / <u><i>Collinsella stercoris</i></u> , <u><i>Eggerthella lenta</i></u>	9.54	122	21	16
4	36	Female	Thai	10.31–10.64	<u><i>Collinsella aerofaciens</i></u> , <u><i>Collinsella intestinalis</i></u> / <u><i>Collinsella stercoris</i></u> , <u><i>Collinsella tanakaei</i></u> , <u><i>Eggerthella lenta</i></u>	10.05	131	2	1
5	28	Male	Mexican	10.29–10.66	<u><i>Collinsella aerofaciens</i></u> , <u><i>Collinsella stercoris</i></u> / <u><i>Collinsella intestinalis</i></u> , <u><i>Gordonibacter pamelaee</i></u> , <u><i>Olsenella profusa</i></u>	10.08	69	5	3
6	31	Female	Turkish	10.14–10.60	<u><i>Collinsella aerofaciens</i></u> , <u><i>Gordonibacter pamelaee</i></u> , <u><i>Olsenella uli</i></u>	9.36	121	25	21
7	42	Female	New Zealand	10.34–10.73	<u><i>Collinsella aerofaciens</i></u> , <u><i>Eggerthella lenta</i></u>	9.43	135	36	29
8	37	Female	British	10.36–10.59	<u><i>Collinsella aerofaciens</i></u> , <u><i>Cryptobacterium curtum</i></u> , <u><i>Eggerthella lenta</i></u> , <u><i>Gordonibacter pamelaee</i></u> , <u><i>Paraeggerthella hongkongensis</i></u>	9.26	135	7	7
9	36	Male	Italian	10.49–10.81	<u><i>Collinsella aerofaciens</i></u> , <i>Coriobacteriaceae</i> sp. PEAV3-3, <u><i>Eggerthella lenta</i></u>	10.08	88	13	9
10	34	Male	Greek	10.57–10.80	<u><i>Collinsella aerofaciens</i></u> , <u><i>Gordonibacter pamelaee</i></u> , <u><i>Paraeggerthella hongkongensis</i></u>	10.45	121	40	30
11	61	Male	British	9.89–10.36	<u><i>Collinsella aerofaciens</i></u> , <u><i>Gordonibacter pamelaee</i></u>	9.48	117	53	42
12	30	Male	Malaysian	10.27–10.55	<u><i>Collinsella tanakaei</i></u> , <u><i>Eggerthella lenta</i></u> , <u><i>Gordonibacter pamelaee</i></u>	10.00	127	1	1
13	31	Male	Greek	9.01–9.34	No DGGE performed (no amplification by ‘ <i>Atopobium</i> cluster’-specific PCR)	9.05	128	2	0

*Data are presented as range across six samples taken over a 3-month period.

†Based on presence of bands in DGGE profile corresponding to bands in the in-house ladder and sequencing of clones corresponding to numbered bands in **Fig. 3**.

Species revealed by sequencing data are underlined.

‡‘*Atopobium* cluster’-specific PCR; isolates producing PCR product of the expected size (including faint amplicons) were included in further analysis.

§Identification based on partial (~600 nt) 16S rRNA gene sequence; *Coriobacteriia* isolates were then further characterized by almost complete (~1440 nt)

16S rRNA gene sequencing.

Table 2. Details of species identified via sequencing of clones corresponding to the bands numbered in Fig. 3

Band	'Best hit' (GenBank accession no./sequence similarity)	No. of clones	Sequence length (nt)
1	<i>Eggerthella lenta</i> (AEXRO1000021/99.5 %)	2	190
2	<i>Collinsella aerofaciens</i> (AAVJ02000013/100 %)	4	190
3	<i>Collinsella aerofaciens</i> (AAVJ02000013/99.5 %)	1	190
4	<i>Collinsella aerofaciens</i> (AAVJ02000013/100 %)	6	190
5	<i>Collinsella intestinalis</i> (ABXH02000037/100 %)	1	190
6	<i>Eggerthella lenta</i> (AEXRO1000021/99.5 %)	2	190
7	<i>Collinsella intestinalis</i> (ABXH02000037/100 %)	2	190
8	<i>Eggerthella lenta</i> (AEXRO1000021/99.0 %)	1	190
9*	<i>Collinsella tanakaei</i> (AB490807/99.0 %)	2	190
10	<i>Gordonibacter pamelaiae</i> (FP929047/97.9 %)	1	189
11	<i>Collinsella aerofaciens</i> (AAVJ02000013/99.5 %)	1	190
12	<i>Collinsella aerofaciens</i> (AAVJ02000013/100 %)	1	190
13	<i>Collinsella intestinalis</i> (ABXH02000037/100 %)	1	190
14*	<i>Collinsella aerofaciens</i> (AAVJ02000013/99.0 %)	1	190
15*	<i>Olsenella profusa</i> (AF292374/97.5 %)	2	196
16*	<i>Olsenella profusa</i> (AF292374/96.9 %)	1	190
17	<i>Gordonibacter pamelaiae</i> (FP929047/97.3 %)	1	191
18	<i>Collinsella aerofaciens</i> (AAVJ02000013/100 %)	3	190
19*	<i>Olsenella uli</i> (CP002106/98.5 %)	2	196
20	<i>Eggerthella lenta</i> (AEXRO1000021/97.9 %)	1	191
21	<i>Collinsella aerofaciens</i> (AAVJ02000013/100 %)	5	190
22	<i>Gordonibacter pamelaiae</i> (FP929047/97.4 %)	1	189
23	<i>Eggerthella lenta</i> (AEXRO1000021/97.4 %)	1	191
24	<i>Collinsella aerofaciens</i> (AAVJ02000013/99.5 %)	4	190
25*	<i>Paraeggerthella hongkongensis</i> (AY288517/94.2 %)	1	191
26*	<i>Paraeggerthella hongkongensis</i> (AY288517/93.7 %)	1	191
27	<i>Gordonibacter pamelaiae</i> (FP929047/97.4 %)	1	189
28	<i>Gordonibacter pamelaiae</i> (FP929047/97.4 %)	1	189
29*	<i>Gordonibacter pamelaiae</i> (FP929047/97.4 %)	2	189
30	<i>Collinsella aerofaciens</i> (AAVJ02000013/100 %)	2	190
31	<i>Paraeggerthella hongkongensis</i> (AY288517/94.2 %)	1	191
32	<i>Gordonibacter pamelaiae</i> (FP929047/97.9 %)	6	189
33	<i>Collinsella tanakaei</i> (AB490807/97.9 %)	1	189
34	<i>Collinsella tanakaei</i> (AB490807/97.4 %)	7	189

*Multiple bands in DGGE profiles of clones.

Table 3. ‘*Atopobium* cluster’ isolates cultivated from human faeces during this study

Donor	Species Identification*	Isolates†	Number
1	<i>Collinsella aerofaciens</i>	33, 34, 35, 59, 87, 95, 129, 146, 152	9
2	<i>Collinsella aerofaciens</i>	46, 52, 57, 58, 59, 61, 62, 63, 65, 66, 67, 68, 69, 70, 72 , 73, 74, 75, 76, 79, 83, 84, 88, 89, 91, 92, <u>93</u> , 94, 96, 97, 98, 99, 105, 107, 108, 109, 117, 120, 122, 124, 125, 127, 129, 130, 136, 140, 143, 144, 149, 150, 152, 154, 157, 158, 159, 160	56
3	<i>Collinsella intestinalis</i> ‡	5, 11, 44, 70, 91, 123, 130, 140, 141, 150, 152	11
4	<i>Eggerthella lenta</i>	3, 6, 8, 65, 96	5
5	<i>Collinsella tanakaei</i>	142	1
6	<i>Collinsella aerofaciens</i>	67, 75, 122	3
7	<i>Collinsella aerofaciens</i>	3, 4, 5, 9, 12, 15, 34, 39, 77, 80, 95, 98, 113, 130, 147, 155	16
8	<i>Eggerthella lenta</i>	71	1
9	<i>Olsenella</i> sp. D6	2, 32, 73, 110	4
10	<i>Collinsella aerofaciens</i>	49, 50, 52, 53, 57, 61, 62, 64, 71, 73, 74, 82, 83, 87, 88, 89, 103, 104, 110, 113, 116, 119, 121, 122, 126, 135, <u>136</u> , 154, 158	29
11	<i>Collinsella aerofaciens</i>	40, 41 , 61, 75, 118, 124, 146	7
12	<i>Collinsella aerofaciens</i>	74, 76, 82, 101, 108, 111, 136, 142	8
13	<i>Eggerthella lenta</i>	63	1
14	<i>Collinsella aerofaciens</i>	3, 7, 8, 11, 14, 15, 16, 18, 23, 24, 26, 34, 39, 40, 43, 45, 48, 55, 72, 76, 79, 98, 99, 119, 120, 129, 130, 135, 139, <u>142</u>	30
15	<i>Collinsella aerofaciens</i>	2, 6, 7, 8, 9, 12, 13, 15, 18, 19, 25, 28, 29, 30, 39, <u>41</u> , 45 , 47, <u>54</u> , 55, 56, 58, 61, 68, 74, 78, 81, 84, 108, 112, 117, 122, <u>124</u> , 129, <u>145</u> , 154, 156, 157	38
16	<i>Collinsella stercoris</i> ‡	10, 70, 102	3
17	<i>Eggerthellaceae</i> sp. D11	98	1
18	‘ <i>Enorma</i> ’ sp. D12	104	1

*Based on almost complete (~1440 nt) 16S rRNA gene sequencing.

†Based on partial 16S rRNA gene sequencing: ~600 nt initial sequencing data for bolded isolates [as these isolates require cloning to obtain almost complete sequences; not included in **Fig. 3**]; 1250–1327 nt for underlined isolates (due to drop-off in sequence reads and/or potential heterogeneities at the start of the 16S rRNA gene sequence).

‡Identification based on discriminatory PCR method of Kageyama & Benno (2000).

Table 4. Biochemical characteristics of *Collinsella aerofaciens* isolates recovered in this study from the faeces of healthy humans

All produced acid from D-glucose and D-lactose, but not glycerol nor L-rhamnose. All indole-, urease- and catalase-negative.

Group*	Isolates†	Man	Sac	Mal	Sal	Xyl	Ara	Cel	Mne	MIz	Raf	Sor	Tre	Gel	Esc
1	D1: 34; 35; 59; 87; 146; 152	-	-	+	+	-	-	+	+	-	-	-	-	+	+
1a	D1: 95	-	-	+	+	-	-	+	+	-	-	-	-	+w	+
2	D6: 12	-	+	+	-	-	-	-	+	-	-	-	-	-	-
3	D6: 3; 5; 9; 15; 34; 39; 95; 98; 113; 147; 155; D8: 41; 75; 146	-	+	+	-	-	-	-	+	-	-	-	-	+	-
3a	D6: 4; D8: 40; 61	-	+	+	-	-	-	-	+	-	-	-	-	+w	-
4	D6: 77	-	+	+	-	-	-	-	+	-	-	-	+	+	-
5	D6: 130	-	+	+	-	-	-	-	+	-	+	+	-	+	-
6	D7: 87	-	+	+	-	-	-	+w	+	-	-	-	-	+w	-
7	D2: 59; 61; 63; 68; 94; 96; 144; 149; 159; 160; D7: 104; 121; 135; D10: 7; 14; 24; 26; 40; 43; 72; 76; 98; D11: 6; 7; 12; 29; 78	-	+	+	+	-	-	+	+	-	-	-	-	-	+
8	D2: 46; 62; 65; 67; 70; 72; 74; 75; 76; 83; 84; 88; 89; 91; 93; 97; 98; 99; 105; 107; 108; 109; 117; 120; 122; 124; 127; 129; 130; 136; 140; 143; 150; 152; 154; 157; 158; D5: 67; 75; D7: 49; 53; 57; 61; 62; 64; 82; 83; 89; 103; 110; 116; 122; 126; 154; 158; D8: 118; 124; D9: 76; 82; 101; 111; D10: 11; 15; 16; 18; 23; 34; 45; 48; 55; 119; 129; 139; D11: 2; 8; 13; 15; 30; 41; 47; 55; 58; 68; 74; 81; 84; 108; 117; 122; 124; 129; 145	-	+	+	+	-	-	+	+	-	-	-	-	+	+
8a	D2: 58; 66; 69; 73; 125; D7: 50; 52; 119; D10: 8; 120; D11: 157	-	+	+	+	-	-	+	+	-	-	-	-	+w	+
8b	D10: 3	-	+	+	+	-	-	+w	+w	-	-	-	-	+	+
8c	D10: 99	-	+	+	+	-	-	+	+w	-	-	-	-	+	+
8d	D11: 19; 25; 28	-	+	+w	+	-	-	+	+	-	-	-	-	+	+
8e	D11: 54; 56; 61	-	+	+w	+w	-	-	+	+	-	-	-	-	+	+
9	D7: 74; 88; D9: 74	-	+	+	+	-	-	+	+	-	-	-	+	+	+
9a	D9: 136; 142; D11: 18; 112; 154; 156	-	+	+	+	-	-	+	+	-	-	-	+w	+	+
9b	D10: 39	-	+	+	+w	-	-	+	+	-	-	-	+w	+	+
10	D9: 108; D10: 79	-	+	+	+	-	-	+	+	-	-	-	+w	-	+
11	D1: 33; 129; D7: 71; 136	-	+	+	+	-	-	+	+	-	+	-	-	+	+
11a	D2: 79	-	+	+	+	-	-	+	+	-	+	-	-	+w	+
11b	D10: 135	-	+	+	+	-	-	+	+w	-	+	-	-	+	+

Group*	Isolates†	Man	Sac	Mal	Sal	Xyl	Ara	Cel	Mne	Mlz	Raf	Sor	Tre	Gel	Esc
11c	D7: 73	-	+	+	+w	-	-	+w	+	-	+	-	-	+	+
12	D10: 130	-	+	+	+	-	-	+	+	+	-	-	-	+	+
13	D2: 57	-	+	+	+	-	+	+	+	-	-	-	-	-	+
14	D2: 52	-	+	+	+	+	+	+	+	-	+	-	-	+	+
15	D11: 9; 39	-	+	-	+w	-	-	+	+	-	-	-	-	+	+
16	D2: 92	+	+	+	+	+w	-	+	+	-	-	-	-	+	+
17	D7: 113	+	+	+	+	+w	-	+	+	-	+	+	+	+	+
18	D6: 80	+w	+	+	+	+	+	+	+	+w	+	+	+w	+	+
<i>Collinsella aerofaciens</i> CCUG 28087 ^T		-	+	+	-	-	-	-	+	-	+w	-	-	+w	-
<i>Collinsella aerofaciens</i> 4-MRS 4		-	+	+	-	-	-	+	+	-	+	-	-	+	+

*Sub-groups indicated by lettering represented weak positive reactions for one or more test.

†*Collinsella aerofaciens* strains D5-122, D10-142 and D11-45 did not resuscitate from cryogenic storage, so phenotypic data presented is from 193/196 faecal *Collinsella aerofaciens* isolates. API 20 A strip test: acid production from D-mannitol (Man), D-saccharose (Sac), D-maltose (Mal), salicin (Sal), D-xylose (Xyl), L-arabinose (Ara), D-cellobiose (Cel), D-mannose (Mne), D-melezitose (Mlz), D-raffinose (Raf), D-sorbitol (Sor), D-trehalose (Tre); gelatin hydrolysis (Gel); and ability to utilize esculin (Esc). +, Positive reaction; +w, weak positive reaction; -, negative reaction.

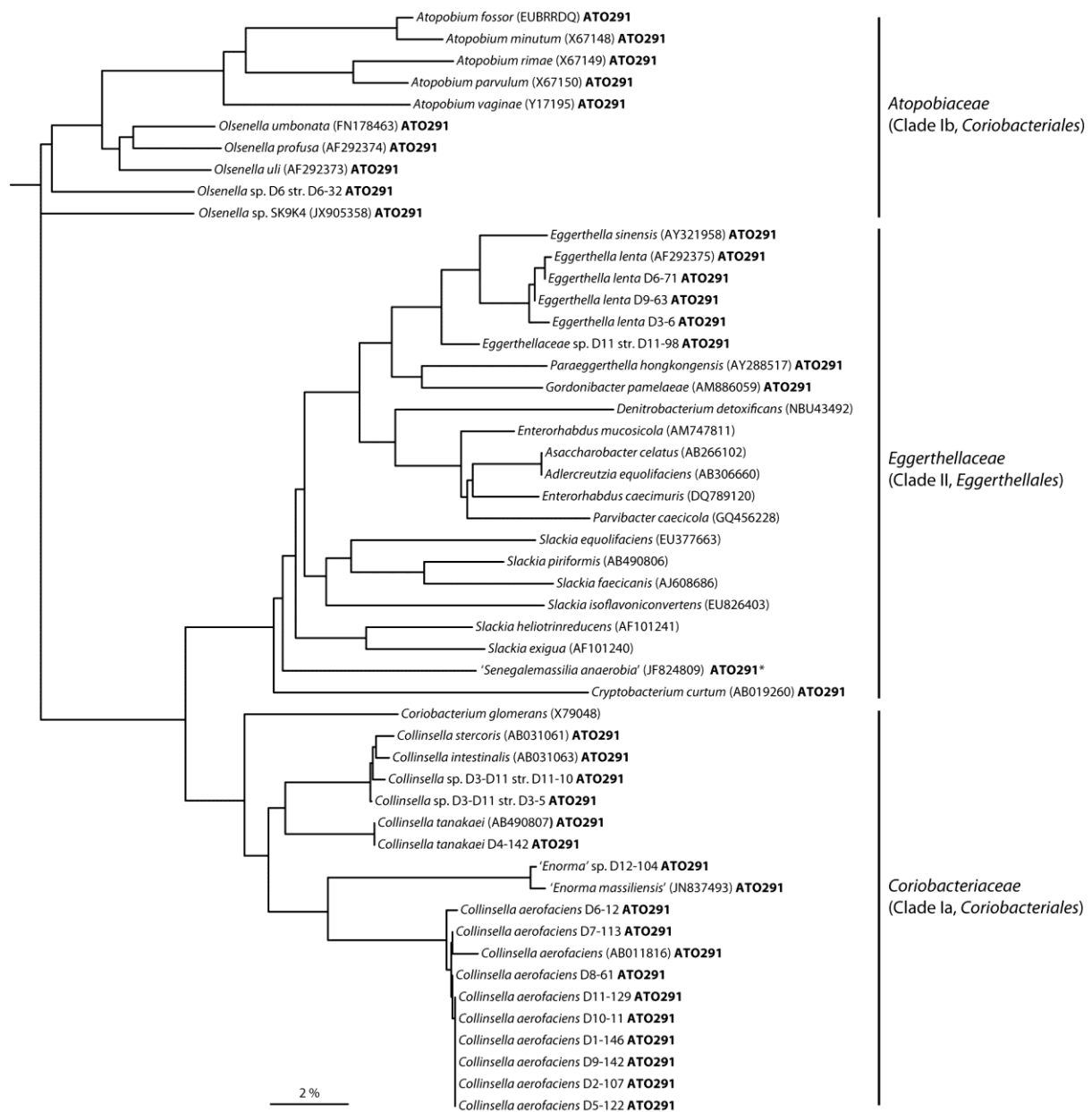


Fig. 1. Phylogenetic tree of the class *Coriobacteriia* and related bacteria isolated from human faeces.

Taxonomic classifications are as described by Gupta *et al.* (2013). The 16S rRNA gene sequence of one isolate of each species detected from each donor is shown (at least 1400 nt sequenced for each isolate). Sequences for species shown with accession numbers are those of the type strain, with the exception of *Olsenella* sp. SK9K4, which is equivalent to *Coriobacteriaceae* sp. PEAV3-3.

GenBank/EMBL/DBJ accession numbers of the isolates recovered in this study can be found in Supplementary Table 7. **ATO291**, detected by probe ATO291 (confirmed by FISH) and ‘*Atopobium* cluster’-specific DGGE; **ATO291***, detected by probe ATO291 (100 % identity with sequence; the pure culture was not checked). Bar, sequence similarity.

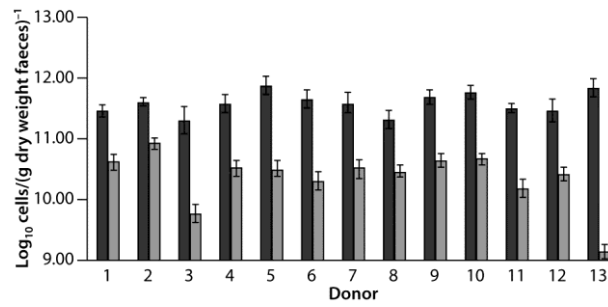


Fig. 2. Estimated number of total and ‘*Atopobium* cluster’ bacteria present in the faeces (per g dry weight) of healthy human adults ($n = 13$) as determined by using FISH analyses. Data are presented as the mean values $\pm$ standard deviation of six faecal samples collected fortnightly from each subject over a 3-month period. Dark-grey bars, total bacteria (probes EUB338mix); light-grey bars, ‘*Atopobium* cluster’ (probe ATO291).

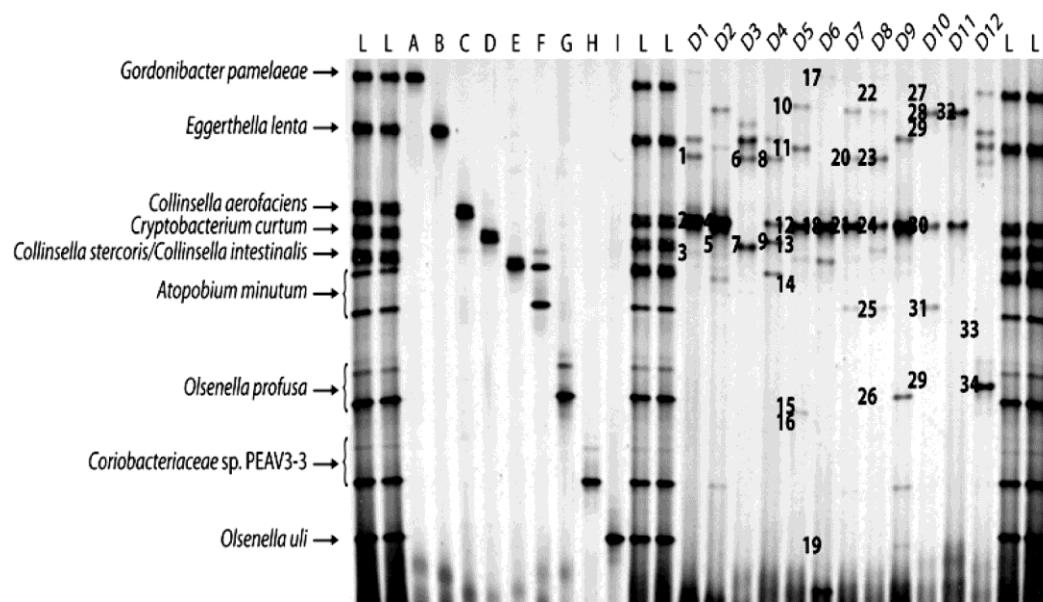
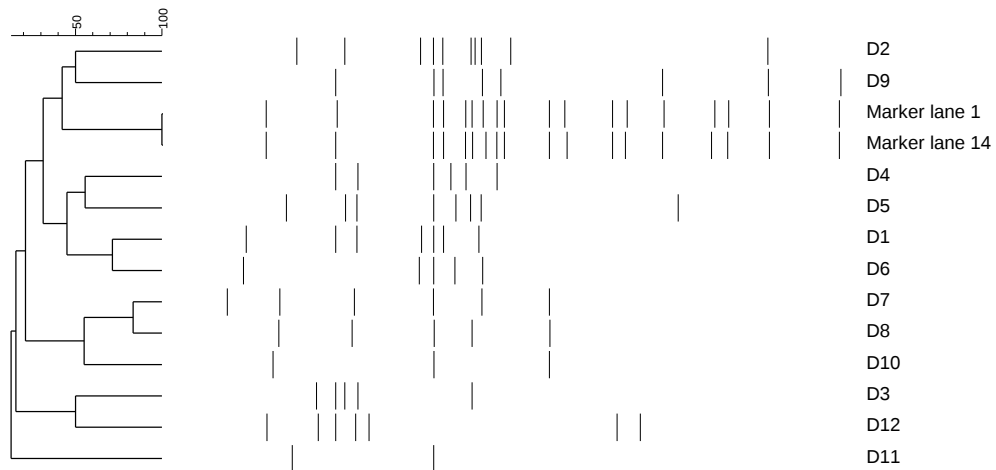


Fig. 3. Use of targeted DGGE to characterize the diversity of the faecal ‘*Atopobium* cluster’ population of healthy human adults ($n = 12$; D1 to D12). DNA was extracted from faecal samples collected fortnightly from each subject over a 3-month period (a representative for each volunteer is presented). PCR-DGGE was performed as described in Methods. L, in-house ladder created using the following strains: (A) *Gordonibacter pamelaeae* CCUG 55131^T, (B) *Eggerthella lenta* DSM 2243^T, (C) *Collinsella aerofaciens* CCUG 28087^T, (D) *Cryptobacterium curtum* CCUG 55773^T, (E) *Collinsella stercoris* CCUG 45295^T, (F) *Atopobium minutum* CCUG 31167^T, (G) *Olsenella profusa* CCUG 45371^T, (H) *Coriobacteriaceae* sp. PEAV3-3 and (I) *Olsenella uli* CCUG 31166^T. Numbers indicate bands corresponding to clones that were identified via sequencing, details in Table 2.

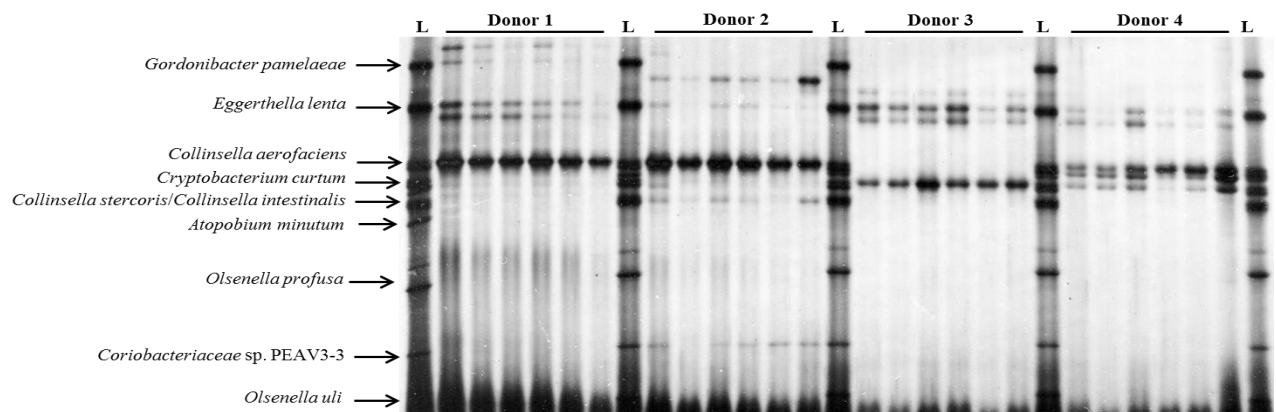
Supplementary information for Thorasin *et al.*

Determination of species/sequences targeted by the '*Atopobium* cluster'-specific DGGE primers

Targets of the forward (c-Atopo-F, 5' to 3': GGGTTGAGAGACCGACC) and reverse (c-Atopo-R, 5' to 3': GGACGTCTTCTTCGRGGC; R = A|G) DGGE primers (without the GC clamp) were checked against archaeal and bacterial sequences ($n = 203452$) within Greengenes 13_5. The Greengenes dataset represented sequences used to cluster sequences at 99 % sequence similarity within 16S rRNA gene-based studies using, for example, QIIME. Sequence GGGTTGAGAGACCGACC was used to search for targets of the forward primer, while CCTGCAGAAGAAGC[T|C]CCG was used to search for targets of the reverse primer. The forward primer hit 361/203452 sequences (Supplementary Table 1), while the reverse primer hit 1253/203452 sequences (Supplementary Table 4). The forward/reverse primers hit 280/203452 sequences contain matches to both primers (Supplementary Table 5). Of the 280 sequences that were targeted by the primers, all targeted the *Coriobacteriia*. Although Greengenes sequence 297503 was listed as belonging to the order *Clostridiales*, a BLAST search confirmed that its nearest relatives were species of the genus *Collinsella* (86 % identity to *Collinsella aerofaciens*). Supplementary Table 6 contains information for the sequences with the taxonomic classification corrected from that presented by Greengenes. The identities of all 280 matching sequences were checked using ENA Sequence Search (<http://www.ebi.ac.uk/ena/search>).



Supplementary Figure 1. Analysis of DGGE profiles for donors 1–12, based on the image shown in Fig. 3. The gel was scanned at 600 dpi and saved as a TIFF file. The image was imported into GelCompar II (Applied Mathematics). Bands were assigned manually and by comparison with the original gel. Jaccard/UPGMA was used to examine the similarity of banding profiles across donors.



Supplementary Figure 2. Investigation of the diversity and temporal stability of the ‘*Atopobium* cluster’ in the faeces of healthy human adults using cluster-specific DGGE, data presented for 4 of 13 volunteers (and are representative of temporal stability observed for all subjects). DNA was extracted from faecal samples collected fortnightly from each subject over a three-month period. PCR-DGGE was performed as described in Methods. Gels were run on 50–70 % gradients. L, in-house ladder created using the following strains: *Gordonibacter pamelaee* CCUG 55131^T, *Eggerthella lenta* DSM 2243^T, *Collinsella aerofaciens* CCUG 28087^T, *Cryptobacterium curtum* CCUG 55773^T, *Collinsella stercoris* CCUG 45295^T, *Atopobium minutum* CCUG 31167^T, *Olsenella profusa* CCUG 45371^T, *Coriobacteriaceae* sp. PEA3-3 and *Olsenella uli* CCUG 31166^T.

Supplementary Table 1. Greengenes species/sequences targeted by probe ATO291 and the forward DGGE primer

[illegible]

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
4432463	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4438008	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4441081	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4441494	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4441685	k_Bacteria	p_Tenericutes	c_Mollicutes	o_Mycoplasmatales	f_Mycoplasmataceae	g_Mycoplasma	s_
4449251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4451251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
4452299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4454024	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
4455003	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4457632	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4460902	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4460903	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4464591	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4471917	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4473973	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
4475900	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4481613	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4483293	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens

Supplementary Table 2. Numerics of the faecal '*Atopobium* cluster' population of healthy human adults by FISH over a three-month period*

Probe	Week	Donor												
		1	2	3	4	5	6	7	8	9	10	11	12	13
ATO291	1	10.53	10.88	9.81	10.31	10.66	10.43	10.67	10.36	10.71	10.57	10.36	10.27	9.21
	3	10.7	11	9.53	10.51	10.61	10.14	10.4	10.51	10.49	10.59	10.27	10.3	9.03
	5	10.7	11.06	9.88	10.41	10.62	10.26	10.53	10.5	10.64	10.74	9.89	10.5	9.01
	7	10.6	10.97	9.66	10.64	10.29	10.23	10.4	10.5	10.69	10.75	10.27	10.55	9.11
	9	10.43	10.84	9.72	10.63	10.54	10.25	10.34	10.59	10.81	10.61	10.15	10.44	9.34
	11	10.77	10.88	9.96	10.65	10.42	10.6	10.73	10.39	10.53	10.8	10.23	10.42	9.12
	Average	10.62	10.94	9.76	10.52	10.52	10.32	10.51	10.48	10.65	10.68	10.19	10.41	9.14
	SD	0.13	0.09	0.15	0.14	0.14	0.17	0.16	0.08	0.12	0.1	0.16	0.11	0.12
EUB338mix	1	11.34	11.61	11.53	11.8	11.98	11.59	11.78	11.28	11.7	11.86	11.46	11.7	11.9
	3	11.37	11.59	11.05	11.75	11.98	11.44	11.66	11.42	11.53	11.85	11.6	11.37	11.58
	5	11.45	11.61	11.13	11.42	12	11.66	11.36	11.13	11.61	11.86	11.61	11.58	11.98
	7	11.47	11.53	11.18	11.51	11.6	11.63	11.54	11.48	11.84	11.62	11.53	11.23	11.84
	9	11.54	11.7	11.33	11.64	11.89	11.82	11.75	11.24	11.75	11.72	11.44	11.35	11.86
	11	11.59	11.62	11.62	11.43	11.83	11.79	11.49	11.48	11.67	11.69	11.51	11.58	11.93
	Average	11.46	11.61	11.31	11.59	11.88	11.66	11.6	11.34	11.68	11.77	11.53	11.47	11.85
	SD	0.1	0.05	0.23	0.16	0.15	0.14	0.16	0.14	0.11	0.1	0.07	0.18	0.14

*Data are presented as $\log_{10}$ [cells (g dry weight faeces)⁻¹] for each sample ATO291, '*Atopobium* cluster' counts; EUB338mix, total counts.

Supplementary Table 3. Relative abundance of '*Atopobium* cluster' population of healthy human adults*

Week	Donor												
	1	2	3	4	5	6	7	8	9	10	11	12	13
1	15.39	18.57	1.93	3.19	4.71	6.84	7.69	12.11	10.38	5.1	7.89	3.74	0.2
3	21.42	25.7	3.04	5.88	4.32	5.04	5.41	12.28	9.25	5.47	4.64	8.58	0.28
5	17.79	28.78	5.53	9.81	4.16	4.04	14.78	23.43	10.64	7.49	1.9	8.35	0.11
7	13.6	27.72	2.98	13.57	4.93	3.96	7.35	10.57	7	13.38	5.49	20.7	0.19
9	7.67	13.8	2.46	9.64	4.42	2.66	3.92	22.72	11.38	7.91	5.09	12.52	0.3
11	14.96	18.14	2.17	16.53	3.9	6.42	17.4	8.18	7.25	12.82	5.23	6.89	0.15
Mean	15.14	22.12	3.02	9.77	4.41	4.83	9.43	14.88	9.32	8.7	5.04	10.13	0.21
SD	4.57	6.1	1.31	4.87	0.37	1.6	5.41	6.52	1.83	3.59	1.92	5.91	0.07

*Data are presented as percentage ATO291 counts make up of total bacteria (EUB338mix) counts.

Supplementary Table 4. Greengenes species/sequences targeted by the reverse DGGE primer

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
11368	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
11369	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
11376	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
11379	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atropobium	s_
11394	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
11396	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
11399	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
11401	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
11402	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
11418	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
12524	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_parvicella
12527	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_parvicella
12861	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
23706	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
27160	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
32126	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
33773	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Streptomyces	s_
34932	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Streptomyces	s_
36306	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
38784	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
42186	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
42261	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
48649	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
51091	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
52274	k_Bacteria	p_Proteobacteria	c_TA18	o_PHOS-HD29	f_	g_	s_
54353	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
58323	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Ferrimicrobium	s_
60177	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
63126	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
65445	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
65467	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
75442	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
76995	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
78784	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
79134	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
79338	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_	s_
84258	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
87668	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
93202	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium
93368	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
94227	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
94574	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
99332	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
99431	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Actinocatenispora	s_
100157	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
100258	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
100819	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
102750	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
102945	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
103611	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
104871	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
105062	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_	s_
105527	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
107187	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
108547	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Oceanicaulis	s_
110224	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_	g_	s_
111390	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
111607	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
111683	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
111842	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
111907	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
113885	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
121375	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
128109	k_Bacteria	p_Actinobacteria	c_EC1113	o_	f_	g_	s_
128216	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
133137	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_Rhodovibrio	s_
133178	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
133861	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
134095	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
134670	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_	s_
135652	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
135902	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
136127	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
136158	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_Rhodovibrio	s_
136290	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
136338	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
138117	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
138551	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_parvicella
139094	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
139221	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
139390	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_
139478	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
139768	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Maricaulis	s_
140552	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Acidimicrobium	s_
140736	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
144917	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
146867	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
147071	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
147336	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
147381	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
148072	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
149113	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
149820	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
151097	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
151098	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
151523	k_Bacteria	p_Actinobacteria	c_Actinomycetia	o_Actinomycetales	f_	g_	s_
152250	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
153112	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_JdFBGBact	g_	s_
153923	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
153998	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
154804	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
155186	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
156127	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
159635	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
160075	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
160397	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
160500	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
161280	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
161486	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
162736	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_	s_
163566	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
164890	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
166794	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
169464	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
172895	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
172928	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
173965	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
174142	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
174266	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
174445	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
174755	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
174774	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
174893	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
175023	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
175311	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
175316	k_Bacteria	p_Actinobacteria	c_Thermoleophilum	o_Gaellales	f_	g_	s_
175508	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
175909	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
176181	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
177016	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
177108	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
178476	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
178487	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
178735	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
178750	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
178874	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
180031	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_	s_
180680	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
181558	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
181742	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
181998	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
182134	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
182152	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
182804	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
183084	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
183088	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
184924	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
185197	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
185472	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
185553	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
185565	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
186148	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
186703	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
186966	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
187312	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
187490	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
187806	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
188966	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
189294	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
189808	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
189997	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
191327	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
191595	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
191604	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
191627	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
192452	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
192875	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
193279	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
193436	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
193575	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
194306	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
195061	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
195737	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
196014	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
196140	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
197242	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
197899	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
198471	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
198774	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
199358	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
199403	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
199686	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
203809	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
207510	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
209725	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
213344	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
213997	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
215181	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
215999	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
216128	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
216638	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
216694	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
217034	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
217430	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
217558	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
219317	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
219366	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
221771	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Ferrimicrobium	s_
222063	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
222364	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
222905	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
223139	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
224718	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
225385	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
225425	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
225473	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
225849	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
226395	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
226742	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
226762	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
227758	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
228081	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
229856	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
229896	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
230366	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
230578	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
231108	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
231565	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
231940	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
232306	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
232823	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
233075	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
233223	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
233950	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
234329	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
234585	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
235014	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
235305	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
236029	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
238794	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
239057	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
239156	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
240211	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Nocardiaceae	g_Rhodococcus	s_
240287	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
240827	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
241185	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
241521	k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Solirubrobacterales	f_	g_	s_
242820	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
243320	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
243610	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
243632	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
245324	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
245434	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
245550	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
245756	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
246810	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
247128	k_Bacteria	p_BRC1	c_NPL-UPA2	o_	f_	g_	s_
247757	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Attopobium	s_
248619	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
249053	k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Gaellales	f_Gaellaceae	g_	s_
249435	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
249582	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
250987	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
251136	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
251702	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_rimae
253088	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Solirubrobacterales	f_	g_	s_
253177	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Ferrimicrobium	s_
253374	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
253488	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
253636	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
253790	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
254173	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
255515	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
256498	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
256950	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
257176	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
257322	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
257611	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
257631	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
258056	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
258158	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_	f_	g_	s_
258304	k_Bacteria	p_Proteobacteria	c_Zetaproteobacteria	o_Mariprofundales	f_Mariprofundaceae	g_Mariprofundus	s_
259098	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
260011	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
260950	k_Bacteria	p_WS3	c_PRR-12	o_	f_	g_	s_
261411	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
261642	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
262696	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_	s_
263143	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
263495	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
263650	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
263760	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
264066	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
264339	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
264392	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ntu14	g_	s_
264974	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
265106	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
265482	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
265696	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
265891	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
266217	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
266446	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
266555	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
266837	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
267123	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
267805	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
268199	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
269141	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
269986	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
270215	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
270461	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ntu14	g_	s_
270614	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
270925	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
271068	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
271780	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
272478	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
272516	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
273162	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
273527	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
273584	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
273957	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_	s_
275333	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
275974	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
275984	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_	s_
276120	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
276151	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
276378	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
276687	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_koll13	g_	s_
277288	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
277518	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Acidimicrobium	s_
277667	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_Devesia	s_
279158	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
281976	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
286163	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Maricaulis	s_
287514	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
287705	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
288004	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
288683	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
289308	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
289344	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
290161	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
290360	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
290572	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
290804	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
290985	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
291190	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
291811	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
291881	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
292058	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
292165	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
292248	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
292607	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
293392	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
293910	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
294210	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
295329	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
295496	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
295696	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
295768	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
296075	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
296320	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Attopobium	s_
297027	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
297503	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
297831	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
298855	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
300347	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
300353	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Arthrobacter	s_
300355	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
301137	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
301447	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
301512	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
301826	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
302491	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
302545	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
302647	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
303310	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
303349	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
303498	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
303693	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
304619	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
304770	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
305141	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
305536	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
307071	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
307140	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
310028	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
311469	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_	s_
311749	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_	s_
313509	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
313837	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
313977	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
314908	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
315149	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
315191	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
315485	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
317304	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacteriales	f_Caulobacteraceae	g_	s_
317641	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
318076	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
318405	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
318902	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
319727	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
320214	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
320696	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
321979	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
324598	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
325303	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Solirubrobacterales	f_	g_	s_
325353	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_	s_
326055	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
326430	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium	s_hiranonis
327354	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
327805	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
328654	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
329224	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
329414	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
329688	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
331048	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
331142	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
331553	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
333608	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
334327	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
336584	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
336788	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
337954	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
338145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
338553	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
338644	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
340181	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
341374	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
341445	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
343633	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
344332	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
344601	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
344783	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
344828	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
345484	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
346107	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
347368	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
347628	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s
347783	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s
348047	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ntu14	g	s
349529	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
350141	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
350644	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g	s
351639	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
351800	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
352607	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s
352624	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f	g	s
353836	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s
355130	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Maricaulis	s
356028	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
357383	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
357442	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
357619	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
357849	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
358251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
358359	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
358610	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
358743	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
358914	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
359299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s
360377	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
361012	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
361158	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
361370	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
361945	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
362152	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
362875	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
363277	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
363322	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
363539	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
363794	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
364679	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
364815	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
364907	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
365033	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
365181	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
365792	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
366383	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s
366392	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
367068	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s
367565	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
367748	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
367804	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
368175	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
369354	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
370091	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
414949	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s
415315	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s
419024	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s
434040	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
454745	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g	s
461524	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
469663	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
471157	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s
508866	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
509083	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
509223	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
509462	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Roseococcus	s
509553	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
510433	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
510509	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s
510547	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
511151	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
511318	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
511430	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
512041	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
512499	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
512505	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g	s
512880	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
513950	k_Bacteria	p_Actinobacteria	c_OPB41	o	f	g	s
514642	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s
517156	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
518645	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
521058	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
521275	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
521913	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g	s
523889	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
524725	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s
525926	k_Bacteria	p_Actinobacteria	c_PAUC37f	o	f	g	s
529793	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g	s
530138	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
532378	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
532857	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f	g	s
534049	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o	f	g	s
534597	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
534621	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
534913	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
535040	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_AKIW874	g_	s_
535129	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
535859	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
536292	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
536885	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
538386	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
539240	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
539421	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
541919	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
542243	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
542933	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
543272	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_AKIW874	g_	s_
544036	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
544782	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
544880	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
545368	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
545614	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Maricaulis	s_
545876	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
546504	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
547749	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
548077	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
548305	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
548310	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
550020	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
550136	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_	g_	s_
550320	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_koll13	g_	s_
551051	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
551179	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
553502	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
554988	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Coriobacterium	s_
555010	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
555399	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
557132	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
557722	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
558305	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
559265	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
559406	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Actinocatenispora	s_
559533	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
559669	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
559951	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Maricaulis	s_
560981	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
561595	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
562164	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_AKIW874	g_	s_
562659	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
562817	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
563215	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
563304	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
564514	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
564553	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
564648	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
564840	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Actinocatenispora	s_
564848	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
565792	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
566154	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
566309	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
566562	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
566906	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
567166	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
569142	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
569735	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
569953	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
570120	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
570289	k_Bacteria	p_Actinobacteria	c_Nitiliruptoria	o_Nitiliruptorales	f_Nitiliruptoraceae	g_	s_
570851	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Ferrimicrobium	s_
571109	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
571419	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
572680	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
574621	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
574727	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_JdFBGBact	g_	s_
574943	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
574996	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Roseococcus	s_
575252	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
575533	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
576054	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_JdFBGBact	g_	s_
576328	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Roseococcus	s_
576926	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
577150	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
577384	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
577499	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
578143	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
578627	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
580258	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
581082	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
581287	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
581739	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
581799	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
581840	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
581964	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
582069	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
583699	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Micrococcales	f_	g_	s_
583824	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
584272	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
584385	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
584444	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
584744	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
584954	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
586509	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Coriobacterium	s_
587028	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
587336	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_	s_
587753	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
590427	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
590544	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
590637	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
591444	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
591965	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
592779	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
593210	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
593301	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_	s_
593605	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Oceanicaulis	s_
593654	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
593718	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
594018	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
594448	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
611485	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
612137	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
616899	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
617066	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
617216	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
617739	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
617900	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
620364	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
620418	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Roseococcus	s_
624434	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
624830	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
626632	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
631764	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
635683	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
636316	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_	s_
636877	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
638525	k_Bacteria	p_Proteobacteria	c_Zetaproteobacteria	o_Mariprofundales	f_Mariprofundaceae	g_Mariprofundus	s_
639636	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
641189	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
642172	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
646800	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
646962	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
647795	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
651642	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
656093	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_	f_	g_	s_
656652	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
658132	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_parvicella
660038	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
662465	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
665276	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
668735	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
670463	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
672094	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
672222	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
672811	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
674891	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
680769	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
682572	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
688850	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
689125	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
691242	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
706766	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
706876	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
708459	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
710899	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
711271	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
712346	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
714187	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
719440	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
723530	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
724147	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
726166	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_	s_
729346	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
730394	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
732702	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
733386	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
741708	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
742358	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
743897	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
751862	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
754510	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
756681	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
757002	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
759692	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
760409	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
775560	k_Bacteria	p_Acidobacteria	c_PAUC37f	o_	f_	g_	s_
775693	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
778701	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Paracoccus	s_aminovorans
784095	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_	s_
788779	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
789373	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
791123	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
791583	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
797762	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
805645	k_Bacteria	p_Deferribacteres	c_Deferribacteres	o_Deferribacterales	f_V1807b93	g_	s_
805996	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
806107	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
806117	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
807854	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
808174	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
808652	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
809732	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
809823	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
809866	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
810204	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
810350	k_Bacteria	p_WS3	c_PRR-12	o_	f_	g_	s_
810653	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
810895	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
811126	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
811377	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Actinocatenispora	s_
811378	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
812076	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
813793	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
814290	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
814461	k_Bacteria	p_Acidobacteria	c_EC1113	o_	f_	g_	s_
814570	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
814892	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_	f_	g_	s_
815014	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
815057	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
816254	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
816299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
817038	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
817222	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
817706	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
817927	k_Bacteria	p_Actinobacteria	c_Nitrliruptoria	o_Euzebyales	f_Euzebyaceae	g_Euzebya	s_
818032	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
818671	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
819722	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Actinocatenispora	s_
820524	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
821177	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
821331	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
821768	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_lamiaceae	g_	s_
822101	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
823207	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
825086	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Micrococcales	f_	g_	s_
825225	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
826651	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
828291	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
828674	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
829151	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_	g_	s_
829210	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
829662	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
830411	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
830966	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
831377	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
831738	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
832019	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
832690	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
833748	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
834349	k_Bacteria	p_Actinobacteria	c_Nitrliruptoria	o_Nitrliruptorales	f_Nitrliruptoraceae	g_	s_
838452	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
838814	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
838943	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
838982	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
839363	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
840275	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
842580	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
842800	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
849361	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
849924	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
851594	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
851636	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
851667	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atropobium	s_rimae
851788	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
854368	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
855799	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
858535	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
865441	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
868178	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
868209	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
871230	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
872701	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
875867	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
881152	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_	s_
883190	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
883610	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
885942	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
893041	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
901984	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
904872	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Corynebacteriaceae	g_Corynebacterium	s_
910158	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
913263	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
920225	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
921185	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_Gaiellaceae	g_	s_
922149	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
927819	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
930646	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
931098	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
942880	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
942926	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
943249	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
949545	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
953558	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
954818	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
955577	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
957595	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
960217	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Solirubrobacterales	f_	g_	s_
966113	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
968016	k_Bacteria	p_Actinobacteria	c_Nitrospirillum	o_Nitrospirillum	f_Nitrospirillum	g_	s_
971146	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
973233	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
977238	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
977740	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
978614	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
980682	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
984175	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
993841	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1006496	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1006600	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1009388	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1011216	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1012668	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1022659	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1027400	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1034960	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
1042596	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1043005	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1044244	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1046664	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1058281	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
1059328	k_Bacteria	p_Actinobacteria	c_Nitrospirillum	o_Nitrospirillum	f_Nitrospirillum	g_	s_
1060881	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_Rickettsiaceae	g_	s_
1061084	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1062936	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1067940	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1068149	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1068936	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1069082	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1076826	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
1083150	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
1085954	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1088836	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
1090930	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_Gaiellaceae	g_	s_
1097892	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1098356	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
1099581	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1101476	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1101883	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1102346	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1104588	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1105155	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1105744	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1106384	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
1106705	k_Bacteria	p_Proteobacteria	c_Zetaproteobacteria	o_Mariprofundales	f_Mariprofundaceae	g_Mariprofundus	s_
1107294	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_Gaiellaceae	g_	s_
1108232	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1108274	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
1108629	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1109913	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1110606	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
1111016	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
1111090	k_Bacteria	p_Actinobacteria	c_Nitrospirillum	o_Nitrospirillum	f_Nitrospirillum	g_	s_
1111123	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1111157	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1113159	k_Bacteria	p_Proteobacteria	c_Zetaproteobacteria	o_Mariprofundales	f_Mariprofundaceae	g_Mariprofundus	s_
1113175	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
1117044	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1117128	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
1117346	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
1117515	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
1117644	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
1118381	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1119116	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1119470	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1119959	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_	s_
1120543	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1122110	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
1122584	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1122710	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1124237	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
1124877	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Attopobium	s_
1125874	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
1125934	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomyetaceae	g_Streptomyces	s_
1127627	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_Rhodoplanes	s_
1128417	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1129276	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1129672	k_Bacteria	p_LD1	c_	o_	f_	g_	s_
1130173	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomyetaceae	g_Streptomyces	s_
1130688	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_
1131203	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
1131607	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1132453	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
1132609	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1132885	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1132974	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1134003	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1135285	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacteriales	f_Caulobacteraceae	g_	s_
1135388	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_Gaiellaceae	g_	s_
1135893	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_Gaiellaceae	g_	s_
1136606	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
1136657	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1140016	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Actinocatenispora	s_
1140324	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
1140359	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1140775	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1141218	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_
1144101	k_Bacteria	p_Actinobacteria	c_Nitrliruptoria	o_Nitrliruptorales	f_Nitrliruptoraceae	g_	s_
1145012	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1145677	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
1146405	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1147637	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
1147903	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
1517876	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1524893	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1620492	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacteriales	f_Hyphomonadaceae	g_Oceanicaulis	s_
1634660	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Attopobium	s_
1639770	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1639771	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1639775	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
1639776	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1646183	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
1654602	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1669782	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaiellales	f_AK1AB1_02E	g_	s_
1755138	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1811927	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
1822603	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1903534	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
1961378	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
1980062	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacteriales	f_Hyphomonadaceae	g_Maricaulis	s_
2036459	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
2038293	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
2127939	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
2140518	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
2202127	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2202129	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
2209135	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2226600	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
2232355	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
2251911	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
2345835	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2376177	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2383905	k_Bacteria	p_Actinobacteria	c_PAUC37f	o_	f_	g_	s_
2389070	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_koll13	g_	s_
2408242	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
2456523	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
2479454	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
2485755	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
2562091	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
2605340	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2605341	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2625114	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2630197	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2672245	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacteriales	f_Hyphomonadaceae	g_Oceanicaulis	s_
2673132	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ntu14	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
2680441	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2692407	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
2706576	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
2706589	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
2736755	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
2753150	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
2761928	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
2865047	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
2881199	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
2929850	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_	s_
2967250	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Iamiaceae	g_	s_
2985051	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
2990918	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris
3046844	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
3053206	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
3102225	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
3114222	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_AK1AB1_02E	g_	s_
3156801	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_Devosia	s_
3170029	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3186757	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
3187471	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3199469	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Oceanicaulis	s_
3222448	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3231020	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Solirubrobacterales	f_	g_	s_
3258717	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3263959	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
3266281	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3268474	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3294759	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
3297208	k_Bacteria	p_SC4	c_	o_	f_	g_	s_
3342180	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
3348150	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_	f_	g_	s_
3533944	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3589737	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Iamiaceae	g_	s_
3603301	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_	g_	s_
3625698	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
3691870	k_Bacteria	p_Acidobacteria	c_PAUC37f	o_	f_	g_	s_
3706429	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
3712728	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
3713324	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3720783	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
3721067	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_	s_
3735163	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
3756908	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
3791329	k_Bacteria	p_Deferribacteres	c_Deferribacteres	o_Deferribacterales	f_V1B07b93	g_	s_
3842679	k_Bacteria	p_Acidobacteria	c_EC1113	o_	f_	g_	s_
3865727	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
3915437	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3934280	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
3950306	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
3956474	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
3956482	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
3956483	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4027525	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Micrococcus	s_luteus
4093084	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4112170	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4159758	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4215058	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4248170	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
4274154	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4295054	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4295071	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4295907	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4296449	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4298389	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4298421	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_	g_	s_
4299095	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4300558	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium
4300564	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium
4302355	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
4302655	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4303029	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4304843	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4304866	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4305331	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4307934	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4308642	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4308837	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4308910	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4309098	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4309864	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
4310452	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4312115	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4312579	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4312899	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4313430	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4313541	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4313851	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
4313852	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4314391	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4314392	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4314523	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4314528	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4314629	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4314847	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4315228	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_	s_
4317202	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
4317246	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4317437	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4318066	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_koll13	g_	s_
4318134	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4318139	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
4318578	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
4318834	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Acidimicrobium	s_
4319542	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4319571	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4319774	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ZA3409c	g_	s_
4320648	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4321037	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium
4321657	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4322801	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4327618	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4327622	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4328026	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4328029	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4328135	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4328472	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4331596	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4332073	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4332126	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4332143	k_Bacteria	p_WS3	c_PRR-12	o_PBS-III-9	f_	g_	s_
4332235	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4332977	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_	g_	s_
4336218	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4336546	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
4337931	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4338580	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_lamiaceae	g_	s_
4338645	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4339145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4339386	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4339547	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
4339796	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Oceanicaulis	s_
4342881	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4343149	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4344047	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4344610	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4344785	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4345120	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
4345173	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_
4345944	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
4347476	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4348508	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4349583	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4350964	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4351649	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4351681	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4352063	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4353898	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4354458	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4354775	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4355496	k_Bacteria	p_Actinobacteria	c_Nitrospirillum	o_Nitrospirillum	f_Nitrospirillum	g_	s_
4358703	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4359642	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
4360159	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4360813	k_Bacteria	p_Actinobacteria	c_EC1113	o_	f_	g_	s_
4360983	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4361768	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4361862	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4363494	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4364514	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4364718	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4365147	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4366417	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4368101	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4369456	k_Bacteria	p_Actinobacteria	c_Nitrospirillum	o_Nitrospirillum	f_Nitrospirillum	g_	s_
4371083	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4372310	k_Bacteria	p_Actinobacteria	c_Thermoleophilum	o_Gaellales	f_Gaellaceae	g_	s_
4372595	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_lamiaceae	g_	s_
4373837	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4374046	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4375876	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4376095	k_Bacteria	p_Actinobacteria	c_Thermoleophilum	o_Gaellales	f_Gaellaceae	g_	s_
4377578	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
4377579	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
4377581	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
4380333	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
4380670	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4382048	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4383103	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_parvicella
4384124	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4386664	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
4387658	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
4387765	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4388114	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_	g_	s_
4389339	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Oceanicaulis	s_
4389639	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4389970	k_Bacteria	p_Acidobacteria	c_PAUC37f	o_	f_	g_	s_
4390766	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
4391813	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4391823	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_	f_	g_	s_
4393266	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_JdFBGBact	g_	s_
4393345	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_lamiaceae	g_	s_
4393532	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
4395747	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4396016	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Streptomyces	s_
4396361	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_AK1AB1_02E	g_	s_
4399156	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4400048	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4400723	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_	s_
4400904	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4401163	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4402537	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4403259	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4405403	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4406036	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4407079	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_Ferrimicrobium	s_
4408222	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4408484	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4409058	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4409442	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
4409494	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4409907	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Solirubrobacterales	f_	g_	s_
4409917	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
4410916	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4412145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
4412421	k_Bacteria	p_Actinobacteria	c_Nitrospirillum	o_Nitrospirillum	f_Nitrospirillum	g_	s_
4413630	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_	f_	g_	s_
4414336	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4415093	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
4415138	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4415545	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_	s_
4416973	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4417169	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4418477	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4418531	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Roseococcus	s_
4418896	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Acidimicrobiaceae	g_	s_
4419660	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4419948	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_EB1017	g_	s_
4420534	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4421241	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4425448	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4426470	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4426889	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4426893	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4428477	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4429954	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4430334	k_Bacteria	p_Actinobacteria	c_Thermoleophilii	o_Gaellales	f_Gaellaceae	g_	s_
4431106	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4431189	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4431234	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_	g_	s_
4432463	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4433031	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4434910	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4435417	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s_
4435891	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4437557	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4437839	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4438008	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4438412	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4439096	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_	s_
4439229	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_lamiaceae	g_	s_
4440329	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Streptomyces	s_
4441019	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f_	g_	s_
4441081	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4441494	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4444028	k_Bacteria	p_Actinobacteria	c_OPB41	o_	f_	g_	s_
4444043	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_	s_
4448701	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4448709	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_	s_
4449251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4449270	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_	f_	g_	s_
4449485	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_	g_	s_
4449740	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
4451251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atropobium	s
4452299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4452511	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g_Candidatus Microthrix	s_parvicella
4453570	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Slackia	s
4455003	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4457632	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4457992	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_Rickettsiaceae	g	s
4458189	k_Bacteria	p_Acidobacteria	c_PAUC37f	o	f	g	s
4460902	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4460903	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4461101	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_Rickettsiaceae	g	s
4461164	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f	g	s
4463767	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Nocardiodaceae	g	s
4464026	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Micrococcus	s_luteus
4464591	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4464787	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f	g	s
4465218	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Oceanicaulis	s
4465276	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium
4467946	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Microthrixaceae	g	s
4471917	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4472356	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
4474716	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g	s
4475254	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g	s
4475900	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g	s
4476401	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f	g	s
4477120	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f	g	s
4477409	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
4478609	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_biprosthecium
4478656	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o	f	g	s
4479100	k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Gaiellales	f_Gaiellaceae	g	s
4479104	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
4479482	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
4479944	k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_0319-7L14	f	g	s
4481613	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4482823	k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f	g	s
4483293	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens

Supplementary Table 5. Greengenes species/sequences targeted by the DGGE primers

[illegible]

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
4393532	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
4395747	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4408222	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4409058	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4412145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Eggerthella	s_lenta
4431189	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4432463	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4438008	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4441081	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4441494	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4449251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4451251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_
4452299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4455003	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4457632	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4460902	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4460903	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4464591	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4471917	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4475900	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_
4481613	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens
4483293	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens

Supplementary Table 6. Greengenes species/sequences targeted by the DGGE primers with corrected taxonomic assignments

Red text shows changes made to taxonomic assignments (compare with Supplementary Table 5).

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species	ENA sequence search ID	Accession no.	Identity (%)
11368	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Eubacterium aerofaciens	AB011814	100.00
11369	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Eubacterium aerofaciens	AB011815	100.00
11379	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_fossor	Eubacterium fossor	AB015945	100.00
23706	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella sp. RCA55-58	AB037385	100.00
27160	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWEZ01000030	96.00
32126	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_	Eggerthella sp. 1_3_56FAA	ACWN01000099	90.00
36306	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella sp. RCA55-4	AB031059	100.00
38784	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella sp. RCA56-80	AB037383	100.00
42186	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata lac15	FN178461	98.00
87668	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium vaginae DSM 15829	ADNA01000041	93.00
99332	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella umbonata lac15	FN178461	95.00
100258	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	98.00
111683	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella umbonata lac15	FN178461	95.00
133178	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_	Eggerthella sp. YY7918	AP012211	91.00
136127	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Gordonibacter	s_	Gordonibacter sp. CEBAS 1/15P	HG000667	98.00
136290	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta SECO-Mt75m2	AY937380	100.00
136338	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Paraeggerthella	s_hongkongensis	Eggerthella hongkongensis strain HKU13	AY321961	100.00
139094	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella umbonata lac15	FN178461	95.00
139221	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0004	EU592964	93.00
139478	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella umbonata lac15	FN178461	94.00
146867	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Senegalimassilia	s_	Senegalimassilia anaerobia JC110	CAEM01000062	92.00
147071	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella sp. M55	LK021115	95.00
149820	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium parvulum DNF00906	JRND01000008	91.00
163566	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	95.00
164890	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	95.00
166794	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	98.00
169464	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	95.00
172895	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809 str. F0356	ACVE01000002	96.00
172928	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809 str. F0356	ACVE01000002	95.00
173965	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Adlercreutzia/Asaccharobacter	s_	Adlercreutzia equolifaciens FJC-A10	AB306660	95.00
174266	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	98.00
174755	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	98.00
174774	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	98.00
174893	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	98.00
175023	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	97.00
175508	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Gordonibacter	s_	Gordonibacter sp. CEBAS 1/15P	HG000667	99.00
176181	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0004	EU592964	90.00
177016	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	98.00
177108	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
178487	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella aerofaciens JCM 10786	AB644262	92.00
178750	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
178874	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
180680	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
181558	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
181742	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
182134	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
182152	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
182804	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Senegalimassilia	s_anaerobia	Senegalimassilia anaerobia JC110	HE611021	99.00

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species	ENA sequence search ID	Accession no.	Identity (%)
183088	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
184924	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta SECO-Mt75m2	AY937380	98.00
185197	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
185565	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
186703	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	97.00
186966	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens ATCC 25986	AAVN02000007	98.00
187312	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella sp. MS5	LK021115	98.00
187490	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella aerofaciens JCM 10788	AB644263	93.00
189997	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella aerofaciens JCM 10788	AB644263	93.00
191327	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
191595	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	97.00
191604	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
191627	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
192452	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
193436	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella aerofaciens JCM 10786	AB644262	96.00
193575	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens ATCC 25986	AAVN02000007	97.00
194306	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10774	AB643471	99.00
195737	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10774	AB643471	98.00
196014	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
197899	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
198471	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
199358	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10774	AB643471	99.00
227758	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Enorma	s_	Enorma massiliensis phi	HE978576	96.00
228081	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella aerofaciens ATCC 25986	AAVN02000007	93.00
230578	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
231108	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0004	EU592964	92.00
232823	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
233075	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	96.00
234585	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Enorma	s_	Enorma massiliensis phi	HE978576	96.00
247757	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWE201000030	94.00
251702	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_rimae	Atopobium rimae	AF292371	97.00
263650	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella umbonata lac15	FN178461	96.00
266446	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_uli	Olsenella uli	AF292373	97.00
269986	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. Mou02	KM405314	99.00
273584	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0004	EU592964	95.00
277288	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata lac15	FN178461	99.00
287514	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	97.00
287705	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella tanakaei YIT 12063	ADLS01000035	94.00
288004	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis JCM 10643	AB558489	97.00
288683	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_	Eggerthella lenta DSM 2243	CP001726	90.00
289308	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	97.00
290360	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella stercoris DSM 13279	ABXJ01000150	98.00
290572	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella tanakaei YIT 12063	ADLS01000035	94.00
290985	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella tanakaei YIT 12063	ADLS01000035	95.00
291190	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
291811	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	97.00
292607	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Slackia	s_	Slackia piriformis YIT 12062	JH815198	91.00
294210	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	98.00
295496	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_profusa	Olsenella profusa F0195	AWE201000030	98.00
296075	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	98.00
296320	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium sp. BS2	JDFG01000039	95.00
297503	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_	g_	s_	Collinsella stercoris DSM 13279	DS995480	83.00
298555	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella intestinalis DSM 13280	GG692710	95.00
300347	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	98.00
300355	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
301512	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_	Eggerthella sp. 1_3_56FAA	ACWN01000099	91.00

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species	ENA sequence search ID	Accession no.	Identity (%)
301826	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s	Collinsella tanakaei YIT 12063	ADLS01000035	94.00
302647	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_tanakaei	Collinsella tanakaei YIT 12063	ADLS01000035	97.00
303310	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	98.00
303498	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella sp. oral taxon 809	GU470903	91.00
303693	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_tanakaei	Collinsella tanakaei YIT 12063	ADLS01000035	98.00
307140	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
310028	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s	Enterorhabdus caecimuris B7	ASSY01000008	92.00
313837	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella uli DSM 7084	CP002106	93.00
313977	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
329414	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	97.00
329688	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s	Collinsella intestinalis DSM 13280	GG692710	96.00
331142	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
334327	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella uli DSM 7084	CP002106	92.00
338145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata lac15	FN178461	98.00
341374	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella umbonata lac15	FN178461	96.00
344332	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella umbonata lac15	FN178461	94.00
344601	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s	Collinsella intestinalis DSM 13280	GG692710	95.00
344783	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella uli DSM 7084	CP002106	91.00
346107	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Adlercreutzia/Asaccharobacter	s	Adlercreutzia equolifaciens DSM 19450	AP013105	93.00
350141	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s	Atopobium vaginae DSM 15829	ADNA01000041	93.00
351639	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Senegalimassilia	s	Senegalimassilia anaerobia JC110	CAEM01000062	92.00
352607	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s	Collinsella aerofaciens JCM 10786	AB644262	93.00
357383	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
357442	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
357849	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
358251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
358359	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
358610	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta SECO-Mt75m2	AY937380	98.00
358743	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	96.00
360377	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
361012	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella stercoris DSM 13279	DS995480	100.00
361158	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
361370	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	95.00
361945	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	97.00
362152	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
362875	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	99.00
363322	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	96.00
363539	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	95.00
363794	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
364679	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
364815	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	96.00
364907	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
365033	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	96.00
366392	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella sp. oral taxon 809	GU470903	91.00
367565	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
367748	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
367804	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
368175	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
369354	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella profusa F0195	AWEZ01000030	92.00
370091	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10788	AB644263	99.00
414949	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s	Collinsella tanakaei YIT 12063	ADLS01000035	95.00
415315	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s	Collinsella tanakaei YIT 12063	ADLS01000035	96.00
461524	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s	Olsenella sp. Mou02	KM405314	99.00
469663	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_vaginae	Atopobium vaginae DSM 15829	ACGK02000001	100.00
508866	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Adlercreutzia/Asaccharobacter	s	Adlercreutzia equolifaciens DSM 19450	AP013105	92.00
510509	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s	Atopobium sp. ICM57	HQ616400	95.00

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species	ENA sequence search ID	Accession no.	Identity (%)
514642	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_parvulum	Atopobium parvulum DNF00906	JRND01000008	99.00
521275	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWEZ01000030	96.00
523889	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_profusa	Olsenella profusa F0195	AWEZ01000030	100.00
524725	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_rimae	Atopobium rimae ATCC 49626	ACFE01000007	100.00
530138	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata lac15	FN178461	100.00
539240	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_uli	Olsenella uli DSM 7084	CP002106	97.00
551179	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	94.00
561595	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
566154	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium parvulum JCM 10300	AB558168	95.00
571109	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
571419	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata lac15	FN178461	98.00
572680	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella sp. M55	LK021115	98.00
574621	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
576926	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	96.00
580258	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_	Coriobacteriaceae bacterium SNR48-44	AB752501	90.00
581287	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium parvulum DSM 20469	CP001721	94.00
582069	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium parvulum DSM 20469	CP001721	95.00
584954	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella umbonata lac15	FN178461	96.00
587028	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
587753	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809	GU470903	95.00
617216	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Eggerthellaceae	g_	s_	Eggerthella sp. 1_3_56FAA	ACWN01000099	90.00
617739	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella uli DSM 7084	CP002106	93.00
646800	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWEZ01000030	95.00
706766	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809	GU470903	100.00
723530	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809	GU470903	93.00
724147	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Cryptobacterium	s_curtum	Cryptobacterium curtum	AB019260	100.00
797762	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809	GU470903	93.00
810895	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	99.00
816299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. BS-3	GU045476	100.00
842580	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella stercoris DSM 13279	DS995480	98.00
849361	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta SECO-Mt75m2	AY937380	99.00
851594	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_vaginae	Atopobium vaginae PB189-T1-4	AEDQ01000024	100.00
851636	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens ATCC 25986	AAVN02000007	100.00
851667	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_rimae	Atopobium rimae ATCC 49626	ACFE01000007	100.00
851788	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692711	100.00
858535	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWEZ01000030	94.00
872701	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium sp. HHRM1715	KF537630	99.00
893041	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium sp. oral taxon 810 str. F0209	KE952969	99.00
942880	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_profusa	Olsenella profusa F0195	AWEZ01000030	97.00
980682	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWEZ01000030	94.00
1034960	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1183	AB739700	97.00
1106384	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_uli	Olsenella uli DSM 7084	CP002106	97.00
1110606	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens ATCC 25986	AAVN02000007	98.00
1124877	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_minutum	Atopobium minutum	X67148	100.00
1132453	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_tanakaiei	Collinsella tanakaiei YIT 12063	ADLS01000035	100.00
1140324	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Paraeggerthella	s_hongkongensis	Eggerthella hongkongensis	Y288517	100.00
1141218	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_sinensis	Eggerthella sinensis HKU14	AY321958	100.00
1147903	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella intestinalis DSM 13280	GG692710	95.00
1634660	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_parvulum	Atopobium parvulum DSM 20469	CP001721	100.00
1646183	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Enorma	s_massiliensis	Enorma massiliensis phl	JN837493	100.00
1811927	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
1903534	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_	Atopobium sp. oral taxon 810 str. F0209	KE952969	99.00
2036459	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	98.00
2038293	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Gordonibacter	s_	Gordonibacter sp. CAT-2	KF785806	99.00
2127939	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_	Eggerthella sp. YY7918	AP012211	100.00
2232355	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Paraeggerthella	s_hongkongensis	Eggerthella hongkongensis HKU11	AY321959	99.00

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species	ENA sequence search ID	Accession no.	Identity (%)
2251911	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta SECO-Mt75m2	AY937380	98.00
2761928	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Cryptobacterium	s_curtum	Cryptobacterium curtum DSM 15641	CP001682	100.00
2985051	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Gordonibacter	s_pamelaeae	Gordonibacter pamelaeae 7-10-1-b	FP929047	100.00
2990918	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_stercoris/intestinalis	Collinsella intestinalis DSM 13280	GG692710	98.00
3102225	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0206	EU592965	95.00
3186757	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens ATCC 25986	AAVN02000007	98.00
3263959	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
3294759	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
3720783	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Paraeggerthella	s_hongkongensis	Eggerthella hongkongensis HKU11	AY321959	97.00
3735163	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809 str. F0356	ACVE01000002	96.00
3756908	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_uli	Olsenella uli DSM 7084	CP002106	100.00
3865727	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
4274154	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
4295071	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	91.00
4299095	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10774	AB643471	99.00
4302355	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_parvulum	Atopobium parvulum JCM 10300	AB558168	98.00
4304866	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000005	92.00
4305331	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	91.00
4307934	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809 str. F0356	ACVE01000002	92.00
4312115	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	93.00
4312579	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4312899	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4313430	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	91.00
4314847	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	98.00
4317246	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4318134	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809	GU470903	94.00
4318139	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	97.00
4321657	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata A2	AJ251324	99.00
4322801	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	97.00
4328026	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	93.00
4328029	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
4332235	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00
4336546	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta DSM 2243	CP001726	98.00
4339145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_	s_	Coriobacteriaceae bacterium GD5	CAPF01000102	100.00
4339386	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4343149	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4345173	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_	Collinsella aerofaciens JCM 7790	AB595135	96.00
4354775	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	99.00
4361768	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. SK9K4	JX905358	99.00
4368101	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_uli	Olsenella uli DSM 7084	CP002106	97.00
4380670	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella profusa F0195	AWEZ01000030	94.00
4384124	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 7790	AB595135	97.00
4393532	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta ZL3	JQ085756	100.00
4395747	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10774	AB643471	99.00
4408222	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	91.00
4409058	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
4412145	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Eggerthella	s_lenta	Eggerthella lenta DSM 2243	CP001726	100.00
4431189	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10774	AB643471	99.00
4432463	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata A2	AJ251324	98.00
4438008	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0004	EU592964	93.00
4441081	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	100.00
4441494	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	91.00
4449251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_	s_	Enterorhabdus caecimuris B7	ASSY01000008	91.00
4451251	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Atopobium	s_parvulum	Atopobium parvulum DNF00906	JRND01000008	98.00
4452299	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. F0206	EU592965	96.00
4455003	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. 1832	AB739701	93.00

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species	ENA sequence search ID	Accession no.	Identity (%)
4457632	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_	Olsenella sp. oral taxon 809 str. F0356	ACVE01000002	96.00
4460902	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4460903	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus mucosicola Mt1B8T	AM747811	92.00
4464591	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4471917	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Eggerthellales	f_Eggerthellaceae	g_Enterorhabdus	s_	Enterorhabdus caecimuris B7	ASSY01000008	92.00
4475900	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Atopobiaceae	g_Olsenella	s_umbonata	Olsenella umbonata A2	AJ251324	98.00
4481613	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10786	AB644262	98.00
4483293	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_aerofaciens	Collinsella aerofaciens JCM 10796	AB644265	98.00

Supplementary Table 7. GenBank/EMBL/DDBJ accession numbers for isolates described in this study

Strain name	GenBank/EMBL/DDBJ accession number	Isolate
D1-129	KP233239	<i>Collinsella aerofaciens</i>
D1-146	KP233240	<i>Collinsella aerofaciens</i>
D1-152	KP233241	<i>Collinsella aerofaciens</i>
D1-33	KP233242	<i>Collinsella aerofaciens</i>
D1-34	KP233243	<i>Collinsella aerofaciens</i>
D1-35	KP233244	<i>Collinsella aerofaciens</i>
D1-59	KP233245	<i>Collinsella aerofaciens</i>
D1-87	KP233246	<i>Collinsella aerofaciens</i>
D1-95	KP233247	<i>Collinsella aerofaciens</i>
D10-11	KP233248	<i>Collinsella aerofaciens</i>
D10-119	KP233249	<i>Collinsella aerofaciens</i>
D10-120	KP233250	<i>Collinsella aerofaciens</i>
D10-129	KP233251	<i>Collinsella aerofaciens</i>
D10-130	KP233252	<i>Collinsella aerofaciens</i>
D10-135	KP233253	<i>Collinsella aerofaciens</i>
D10-139	KP233254	<i>Collinsella aerofaciens</i>
D10-14	KP233255	<i>Collinsella aerofaciens</i>
D10-142	KP233256	<i>Collinsella aerofaciens</i>
D10-15	KP233257	<i>Collinsella aerofaciens</i>
D10-16	KP233258	<i>Collinsella aerofaciens</i>
D10-18	KP233259	<i>Collinsella aerofaciens</i>
D10-23	KP233260	<i>Collinsella aerofaciens</i>
D10-24	KP233261	<i>Collinsella aerofaciens</i>
D10-26	KP233262	<i>Collinsella aerofaciens</i>
D10-3	KP233263	<i>Collinsella aerofaciens</i>
D10-34	KP233264	<i>Collinsella aerofaciens</i>
D10-39	KP233265	<i>Collinsella aerofaciens</i>
D10-40	KP233266	<i>Collinsella aerofaciens</i>
D10-43	KP233267	<i>Collinsella aerofaciens</i>
D10-45	KP233268	<i>Collinsella aerofaciens</i>
D10-48	KP233269	<i>Collinsella aerofaciens</i>
D10-55	KP233270	<i>Collinsella aerofaciens</i>
D10-7	KP233271	<i>Collinsella aerofaciens</i>
D10-72	KP233272	<i>Collinsella aerofaciens</i>
D10-76	KP233273	<i>Collinsella aerofaciens</i>
D10-79	KP233274	<i>Collinsella aerofaciens</i>
D10-8	KP233275	<i>Collinsella aerofaciens</i>
D10-98	KP233276	<i>Collinsella aerofaciens</i>
D10-99	KP233277	<i>Collinsella aerofaciens</i>
D11-10	KP233278	<i>Collinsella stercoris</i>
D11-102	KP233279	<i>Collinsella stercoris</i>
D11-108	KP233280	<i>Collinsella aerofaciens</i>
D11-112	KP233281	<i>Collinsella aerofaciens</i>
D11-117	KP233282	<i>Collinsella aerofaciens</i>
D11-12	KP233283	<i>Collinsella aerofaciens</i>
D11-122	KP233284	<i>Collinsella aerofaciens</i>
D11-124	KP233285	<i>Collinsella aerofaciens</i>
D11-129	KP233286	<i>Collinsella aerofaciens</i>
D11-13	KP233287	<i>Collinsella aerofaciens</i>
D11-145	KP233288	<i>Collinsella aerofaciens</i>
D11-15	KP233289	<i>Collinsella aerofaciens</i>
D11-154	KP233290	<i>Collinsella aerofaciens</i>
D11-156	KP233291	<i>Collinsella aerofaciens</i>
D11-157	KP233292	<i>Collinsella aerofaciens</i>
D11-18	KP233293	<i>Collinsella aerofaciens</i>
D11-19	KP233294	<i>Collinsella aerofaciens</i>
D11-2	KP233295	<i>Collinsella aerofaciens</i>
D11-25	KP233296	<i>Collinsella aerofaciens</i>
D11-28	KP233297	<i>Collinsella aerofaciens</i>
D11-29	KP233298	<i>Collinsella aerofaciens</i>

Strain name	GenBank/EMBL/DBJ accession number	Isolate
D11-30	KP233299	<i>Collinsella aerofaciens</i>
D11-39	KP233300	<i>Collinsella aerofaciens</i>
D11-41	KP233301	<i>Collinsella aerofaciens</i>
D11-47	KP233302	<i>Collinsella aerofaciens</i>
D11-54	KP233303	<i>Collinsella aerofaciens</i>
D11-55	KP233304	<i>Collinsella aerofaciens</i>
D11-56	KP233305	<i>Collinsella aerofaciens</i>
D11-58	KP233306	<i>Collinsella aerofaciens</i>
D11-6	KP233307	<i>Collinsella aerofaciens</i>
D11-61	KP233308	<i>Collinsella aerofaciens</i>
D11-68	KP233309	<i>Collinsella aerofaciens</i>
D11-70	KP233310	<i>Collinsella stercoris</i>
D11-74	KP233311	<i>Collinsella aerofaciens</i>
D11-78	KP233312	<i>Collinsella aerofaciens</i>
D11-8	KP233313	<i>Collinsella aerofaciens</i>
D11-81	KP233314	<i>Collinsella aerofaciens</i>
D11-84	KP233315	<i>Collinsella aerofaciens</i>
D11-9	KP233316	<i>Collinsella aerofaciens</i>
D12-104	KP233317	<i>Enorma</i> sp. D12
D2-105	KP233318	<i>Collinsella aerofaciens</i>
D2-107	KP233319	<i>Collinsella aerofaciens</i>
D2-108	KP233320	<i>Collinsella aerofaciens</i>
D2-109	KP233321	<i>Collinsella aerofaciens</i>
D2-117	KP233322	<i>Collinsella aerofaciens</i>
D2-120	KP233323	<i>Collinsella aerofaciens</i>
D2-122	KP233324	<i>Collinsella aerofaciens</i>
D2-124	KP233325	<i>Collinsella aerofaciens</i>
D2-125	KP233326	<i>Collinsella aerofaciens</i>
D2-127	KP233327	<i>Collinsella aerofaciens</i>
D2-129	KP233328	<i>Collinsella aerofaciens</i>
D2-130	KP233329	<i>Collinsella aerofaciens</i>
D2-136	KP233330	<i>Collinsella aerofaciens</i>
D2-140	KP233331	<i>Collinsella aerofaciens</i>
D2-143	KP233332	<i>Collinsella aerofaciens</i>
D2-144	KP233333	<i>Collinsella aerofaciens</i>
D2-149	KP233334	<i>Collinsella aerofaciens</i>
D2-150	KP233335	<i>Collinsella aerofaciens</i>
D2-152	KP233336	<i>Collinsella aerofaciens</i>
D2-154	KP233337	<i>Collinsella aerofaciens</i>
D2-157	KP233338	<i>Collinsella aerofaciens</i>
D2-158	KP233339	<i>Collinsella aerofaciens</i>
D2-159	KP233340	<i>Collinsella aerofaciens</i>
D2-160	KP233341	<i>Collinsella aerofaciens</i>
D2-46	KP233342	<i>Collinsella aerofaciens</i>
D2-52	KP233343	<i>Collinsella aerofaciens</i>
D2-57	KP233344	<i>Collinsella aerofaciens</i>
D2-58	KP233345	<i>Collinsella aerofaciens</i>
D2-59	KP233346	<i>Collinsella aerofaciens</i>
D2-61	KP233347	<i>Collinsella aerofaciens</i>
D2-62	KP233348	<i>Collinsella aerofaciens</i>
D2-63	KP233349	<i>Collinsella aerofaciens</i>
D2-65	KP233350	<i>Collinsella aerofaciens</i>
D2-67	KP233351	<i>Collinsella aerofaciens</i>
D2-68	KP233352	<i>Collinsella aerofaciens</i>
D2-69	KP233353	<i>Collinsella aerofaciens</i>
D2-70	KP233354	<i>Collinsella aerofaciens</i>
D2-73	KP233355	<i>Collinsella aerofaciens</i>
D2-74	KP233356	<i>Collinsella aerofaciens</i>
D2-75	KP233357	<i>Collinsella aerofaciens</i>
D2-76	KP233358	<i>Collinsella aerofaciens</i>
D2-79	KP233359	<i>Collinsella aerofaciens</i>
D2-83	KP233360	<i>Collinsella aerofaciens</i>
D2-84	KP233361	<i>Collinsella aerofaciens</i>
D2-88	KP233362	<i>Collinsella aerofaciens</i>
D2-89	KP233363	<i>Collinsella aerofaciens</i>
D2-91	KP233364	<i>Collinsella aerofaciens</i>

Strain name	GenBank/EMBL/DBJ accession number	Isolate
D2-92	KP233365	<i>Collinsella aerofaciens</i>
D2-93	KP233366	<i>Collinsella aerofaciens</i>
D2-94	KP233367	<i>Collinsella aerofaciens</i>
D2-96	KP233368	<i>Collinsella aerofaciens</i>
D2-97	KP233369	<i>Collinsella aerofaciens</i>
D2-98	KP233370	<i>Collinsella aerofaciens</i>
D2-99	KP233371	<i>Collinsella aerofaciens</i>
D3-11	KP233372	<i>Collinsella intestinalis</i>
D3-123	KP233373	<i>Collinsella intestinalis</i>
D3-130	KP233374	<i>Collinsella intestinalis</i>
D3-140	KP233375	<i>Collinsella intestinalis</i>
D3-141	KP233376	<i>Collinsella intestinalis</i>
D3-150	KP233377	<i>Collinsella intestinalis</i>
D3-152	KP233378	<i>Collinsella intestinalis</i>
D3-44	KP233379	<i>Collinsella intestinalis</i>
D3-5	KP233380	<i>Collinsella intestinalis</i>
D3-6	KP233381	<i>Eggerthella lenta</i>
D3-65	KP233382	<i>Eggerthella lenta</i>
D3-70	KP233383	<i>Collinsella intestinalis</i>
D3-8	KP233384	<i>Eggerthella lenta</i>
D3-91	KP233385	<i>Collinsella intestinalis</i>
D3-96	KP233386	<i>Eggerthella lenta</i>
D4-142	KP233387	<i>Collinsella tanakaei</i>
D5-122	KP233388	<i>Collinsella aerofaciens</i>
D5-67	KP233389	<i>Collinsella aerofaciens</i>
D5-75	KP233390	<i>Collinsella aerofaciens</i>
D6-113	KP233391	<i>Collinsella aerofaciens</i>
D6-12	KP233392	<i>Collinsella aerofaciens</i>
D6-130	KP233393	<i>Collinsella aerofaciens</i>
D6-147	KP233394	<i>Collinsella aerofaciens</i>
D6-15	KP233395	<i>Collinsella aerofaciens</i>
D6-155	KP233396	<i>Collinsella aerofaciens</i>
D6-2	KP233397	<i>Olsenella</i> sp. D6
D6-3	KP233398	<i>Collinsella aerofaciens</i>
D6-32	KP233399	<i>Olsenella</i> sp. D6
D6-34	KP233400	<i>Collinsella aerofaciens</i>
D6-39	KP233401	<i>Collinsella aerofaciens</i>
D6-4	KP233402	<i>Collinsella aerofaciens</i>
D6-5	KP233403	<i>Collinsella aerofaciens</i>
D6-71	KP233404	<i>Eggerthella lenta</i>
D6-73	KP233405	<i>Olsenella</i> sp. D6
D6-77	KP233406	<i>Collinsella aerofaciens</i>
D6-80	KP233407	<i>Collinsella aerofaciens</i>
D6-9	KP233408	<i>Collinsella aerofaciens</i>
D6-95	KP233409	<i>Collinsella aerofaciens</i>
D6-98	KP233410	<i>Collinsella aerofaciens</i>
D7-103	KP233411	<i>Collinsella aerofaciens</i>
D7-104	KP233412	<i>Collinsella aerofaciens</i>
D7-110	KP233413	<i>Collinsella aerofaciens</i>
D7-113	KP233414	<i>Collinsella aerofaciens</i>
D7-116	KP233415	<i>Collinsella aerofaciens</i>
D7-119	KP233416	<i>Collinsella aerofaciens</i>
D7-121	KP233417	<i>Collinsella aerofaciens</i>
D7-122	KP233418	<i>Collinsella aerofaciens</i>
D7-126	KP233419	<i>Collinsella aerofaciens</i>
D7-135	KP233420	<i>Collinsella aerofaciens</i>
D7-136	KP233421	<i>Collinsella aerofaciens</i>
D7-154	KP233422	<i>Collinsella aerofaciens</i>
D7-158	KP233423	<i>Collinsella aerofaciens</i>
D7-49	KP233424	<i>Collinsella aerofaciens</i>
D7-50	KP233425	<i>Collinsella aerofaciens</i>
D7-52	KP233426	<i>Collinsella aerofaciens</i>
D7-53	KP233427	<i>Collinsella aerofaciens</i>
D7-57	KP233428	<i>Collinsella aerofaciens</i>
D7-61	KP233429	<i>Collinsella aerofaciens</i>
D7-62	KP233430	<i>Collinsella aerofaciens</i>

Strain name	GenBank/EMBL/DBJ accession number	Isolate
D7-64	KP233431	<i>Collinsella aerofaciens</i>
D7-71	KP233432	<i>Collinsella aerofaciens</i>
D7-73	KP233433	<i>Collinsella aerofaciens</i>
D7-74	KP233434	<i>Collinsella aerofaciens</i>
D7-82	KP233435	<i>Collinsella aerofaciens</i>
D7-83	KP233436	<i>Collinsella aerofaciens</i>
D7-87	KP233437	<i>Collinsella aerofaciens</i>
D7-88	KP233438	<i>Collinsella aerofaciens</i>
D7-89	KP233439	<i>Collinsella aerofaciens</i>
D8-118	KP233440	<i>Collinsella aerofaciens</i>
D8-124	KP233441	<i>Collinsella aerofaciens</i>
D8-146	KP233442	<i>Collinsella aerofaciens</i>
D8-40	KP233443	<i>Collinsella aerofaciens</i>
D8-61	KP233444	<i>Collinsella aerofaciens</i>
D8-75	KP233445	<i>Collinsella aerofaciens</i>
D9-101	KP233446	<i>Collinsella aerofaciens</i>
D9-108	KP233447	<i>Collinsella aerofaciens</i>
D9-111	KP233448	<i>Collinsella aerofaciens</i>
D9-136	KP233449	<i>Collinsella aerofaciens</i>
D9-142	KP233450	<i>Collinsella aerofaciens</i>
D9-63	KP233451	<i>Eggerthella lenta</i>
D9-74	KP233452	<i>Collinsella aerofaciens</i>
D9-76	KP233453	<i>Collinsella aerofaciens</i>
D9-82	KP233454	<i>Collinsella aerofaciens</i>