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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, N_2:CO_2:H_2; 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).

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

where DF is the dilution factor [(300/375 = 0.8) × 50 (20 μl applied to well) × 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× and 2000×, 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× 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 $MgCl_2$ (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 pamelaeae* 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 H_2O 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 InstaGene™ 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 pamelaeae* 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 pamelaeae*, *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 form 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 pamelaeae* 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 aerofaciencs* 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 resuscitatable (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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REFERENCES

Arumugam, M., Raes, J., Pelletier, E., Le Paslier, D., Yamada, T., Mende, D. R., Fernandes, G. R., Tap, J., Bruls, T. & 75 other authors. (2011). Enterotypes of the human gut microbiome. *Nature* **473**, 174–180.

Child, M. W., Kennedy, A., Walker, A. W., Bahrami, B., Macfarlane, S. & Macfarlane, G. T. (2006). Studies on the effect of system retention time on bacterial populations colonizing a three-stage continuous culture model of the human large gut using FISH techniques. *FEMS Microbiol Ecol* **55**, 299–310.

Claus, S. P., Ellero, S. L., Berger, B., Krause, L., Bruttin, A., Molina, J., Paris, A., Want, E. J., de Waziers, I. & 11 other authors. (2011). Colonization-induced host-gut microbial metabolic interaction. *MBio* **2**, e00271–10.

Daims, H., Brühl, A., Amann, R., Schleifer, K. H. & Wagner, M. (1999). The domain-specific probe EUB338 is insufficient for the detection of all Bacteria: Development and evaluation of a more comprehensive probe set. *Syst Appl Microbiol* **22**, 434–444.

Eggerth, A. H. (1935). The gram-positive non-spore-bearing anaerobic bacilli of human feces. *J Bacteriol* **30**, 277–299.

Gupta, R. S., Chen, W. J., Adeolu, M. & Chai, Y. (2013). Molecular signatures for the class *Coriobacteriia* and its different clades; proposal for division of the class *Coriobacteriia* into the emended order *Coriobacteriales*, containing the emended family *Coriobacteriaceae* and *Atopobiaceae* fam. nov., and *Eggerthellales* ord. nov., containing the family *Eggerthellaceae* fam. nov. *Int J Syst Evol Microbiol* **63**, 3379–3397.

Haiser, H. J., Gootenberg, D. B., Chatman, K., Sirasani, G., Balskus, E. P. & Turnbaugh, P. J. (2013). Predicting and manipulating cardiac drug inactivation by the human gut bacterium *Eggerthella lenta*. *Science* **341**, 295–298.

Harmsen, H. J. M., Wildeboer-Veloo, A. C. M., Grijpstra, J., Knol, J., Degener, J. E. & Welling, G. W. (2000). Development of 16S rRNA-based probes for the *Coriobacterium* group and the *Atopobium* cluster and their application for enumeration of *Coriobacteriaceae* in human feces from volunteers of different age groups. *Appl Environ Microbiol* **66**, 4523–4527.

Harmsen, H. J., Raangs, G. C., He, T., Degener, J. E. & Welling, G. W. (2002). Extensive set of 16S rRNA-based probes for detection of bacteria in human feces. *Appl Environ Microbiol* **68**, 2982–2990.

Holdeman, L. V., Good, I. J. & Moore, W. E. (1976). Human fecal flora: variation in bacterial composition within individuals and a possible effect of emotional stress. *Appl Environ Microbiol* **31**, 359–375.

Hoyles, L. (2009). *In vitro examination of the effect of orlistat on the ability of the faecal microbiota to utilize dietary lipids.* PhD thesis, University of Reading, UK.

Hoyles, L. & McCartney, A. L. (2009). What do we mean when we refer to *Bacteroidetes* populations in the human gastrointestinal microbiota? *FEMS Microbiol Lett* **299**, 175–183.

Hoyles, L., Collins, M. D., Falsen, E., Nikolaitchouk, N. & McCartney, A. L. (2004). Transfer of members of the genus *Falcivibrio* to the genus *Mobiluncus*, and emended description of the genus *Mobiluncus*. *Syst Appl Microbiol* **27**, 72–83.

Hoyles, L., Clear, J. A. & McCartney, A. L. (2013). Use of denaturing gradient gel electrophoresis to detect Actinobacteria associated with the human faecal microbiota. *Anaerobe* **22**, 90–96.

Huber, T., Faulkner, G. & Hugenholtz, P. (2004). Bellerophon: a program to detect chimeric sequences in multiple sequence alignments. *Bioinformatics* 20, 2317–2319.

Jin, J. S., Kitahara, M., Sakamoto, M., Hattori, M. & Benno, Y. (2010). *Slackia equolifaciens* sp. nov., a human intestinal bacterium capable of producing equol. *Int J Syst Evol Microbiol* **60**, 1721–1724.

Kageyama, A. & Benno, Y. (2000). Emendation of genus *Collinsella* and proposal of *Collinsella stercoris* sp. nov. and *Collinsella intestinalis* sp. nov. *Int J Syst Evol Microbiol* **50**, 1767–1774.

Kageyama, A., Benno, Y. & Nakase, T. (1999a). Phylogenetic and phenotypic evidence for the transfer of *Eubacterium aerofaciens* to the genus *Collinsella* as *Collinsella aerofaciens* gen. nov., comb. nov. *Int J Syst Bacteriol* **49**, 557–565.

Kageyama, A., Benno, Y. & Nakase, T. (1999b). Phylogenetic evidence for transfer of *Eubacterium lentum* to the genus *Eggerthella* as *Eggerthella lenta* gen. nov., comb. nov. *Int J Syst Bacteriol* **49**, 1725–1732.

Kim, O. S., Cho, Y. J., Lee, K., Yoon, S. H., Kim, M., Na, H., Park, S. C., Jeon, Y. S., Lee, J. H. & 3 other authors. (2012). Introducing EzTaxon-e: a prokaryotic 16s rRNA gene sequence database with phylotypes that represent uncultured species. *Int J Syst Evol Microbiol* **62**, 716–721.

Koenig, J. E., Spor, A., Scalfone, N., Fricker, A. D., Stombaugh, J., Knight, R., Angenent, L. T. & Ley, R. E. (2011). Succession of microbial consortia in the developing infant gut microbiome. *Proc Natl Acad Sci U S A* **108 (Suppl 1)**, 4578–4585.

Lahti, L., Salonen, A., Kekkonen, R. A., Salojarvi, J., Jalanka-Tuovinen, J., Palva, A., Oresic, M. & de Vos, W. M. (2013). Associations between the human intestinal microbiota, *Lactobacillus rhamnosus* GG and serum lipids indicated by integrated analysis of high-throughput profiling data. *PeerJ*, **1**, e32.

Lau, S. K., Woo, P. C., Woo, G. K., Fung, A. M., Wong, M. K., Chan, K. M., Tam, D. M. & Yuen, K. Y. (2004a). *Eggerthella hongkongensis* sp. nov. and *Eggerthella sinensis* sp. nov., two novel *Eggerthella* species, account for half of the cases of *Eggerthella bacteremia*. *Diagn Microbiol Infect Dis* **49**, 255–263.

Lau, S. K., Woo, P. C., Fung, A. M., Chan, K. M., Woo, G. K. & Yuen, K. Y. (2004b). Anaerobic, non-sporulating, Gram-positive bacilli bacteraemia characterized by 16S rRNA gene sequencing. *J Med Microbiol* **53**, 1247–1253.

Lay, C., Rigottier-Gois, L., Holmstrøm, K., Rajilic, M., Vaughan, E. E., de Vos, W. M., Collins, M. D., Thiel, R., Namsolleck, P. & 2 other authors. (2005). Colonic microbiota signatures across five northern European countries. *Appl Environ Microbiol* **71**, 4153–4155.

Martínez, I., Lattimer, J. M., Hubach, K. L., Case, J. A., Yang, J., Weber, C. G., Louk, J. A., Rose, D. J., Kyureghian, G. & 3 other authors. (2013). Gut microbiome composition is linked to whole grain-induced immunological improvements. *ISME J* **7**, 269–280.

Martínez, I., Wallace, G., Zhang, C., Legge, R., Benson, A. K., Carr, T. P., Moriyama, E. N. & Walter, J. (2009). Diet-induced metabolic improvements in a hamster model of hypercholesterolemia are strongly linked to alterations of the gut microbiota. *Appl Environ Microbiol* **75**, 4175–4184.

Martín-Peláez, S., Gibson, G. R., Martín-Orúe, S. M., Klinder, A., Rastall, R. A., La Ragione, R. M., Woodward, M. J. & Costabile, A. (2008). *In vitro* fermentation of carbohydrates by porcine faecal inocula and their influence on *Salmonella* Typhimurium growth in batch culture systems. *FEMS Microbiol Ecol* **66**, 608–619.

Maruo, T., Sakamoto, M., Ito, C., Toda, T. & Benno, Y. (2008). *Adlercreutzia equolifaciens* gen. nov., sp. nov., an equol-producing bacterium isolated from human faeces, and emended description of the genus *Eggerthella*. *Int J Syst Evol Microbiol* **58**, 1221–1227.

Matsuki, T., Watanabe, K., Fujimoto, J., Takada, T. & Tanaka, R. (2004). Use of 16S rRNA gene-targeted group-specific primers for real-time PCR analysis of predominant bacteria in human feces. *Appl Environ Microbiol* **70**, 7220–7228.

Maukonen, J., Simões, C. & Saarela, M. (2012). The currently used commercial DNA-extraction methods give different results of clostridial and actinobacterial populations derived from human fecal samples. *FEMS Microbiol Ecol* **79**, 697–708.

Mishra, A. K., Hugon, P., Lagier, J.-C., Nguyen, T.-T., Couderc, C., Raoult, D. & Fournier, P.-E. (2013). Non contiguous-finished genome sequence and description of *Enorma massiliensis* gen. nov., sp. nov., a new member of the family *Coriobacteriaceae*. *Stand Genomic Sci* **8**, 290–305.

Moore, W. E. C., Cato, E. P. & Holdeman, L. V. (1971). *Eubacterium lentum* (Eggerth) Prévot 1938: emendation of description and designation of neotype strain. *Int J Syst Bacteriol* **21**, 299–303.

Moore, W. E. & Holdeman, L. V. (1974). Human fecal flora: the normal flora of 20 Japanese-Hawaiians. *Appl Microbiol* **27**, 961–979.

Munson, M. A., Banerjee, A., Watson, T. F. & Wade, W. G. (2004). Molecular analysis of the microflora associated with dental caries. *J Clin Microbiol* **42**, 3023–3029.

Nagai, F., Watanabe, Y. & Morotomi, M. (2010). *Slackia piriformis* sp. nov. and *Collinsella tanakaei* sp. nov., new members of the family *Coriobacteriaceae*, isolated from human faeces. *Int J Syst Evol Microbiol* **60**, 2639–2646.

Qin, J., Li, R., Raes, J., Arumugam, M., Burgdorf, K. S., Manichanh, C., Nielsen, T., Pons, N., Levenez, F. & 44 other authors. (2010). A human gut microbial gene catalogue established by metagenomic sequencing. *Nature,* **464**, 59–65.

Rajilić-Stojanović, M., Heilig, H. G., Molenaar, D., Kajander, K., Surakka, A., Smidt, H. & de Vos, W. M. (2009). Development and application of the human intestinal tract chip, a phylogenetic microarray: analysis of universally conserved phylotypes in the abundant microbiota of young and elderly adults. *Environ Microbiol* **11**, 1736–1751.

Rajilić-Stojanović, M., Smidt, H. & de Vos, W. M. (2007). Diversity of the human gastrointestinal tract microbiota revisited. *Environ Microbiol* **9**, 2125–2136.

Rigottier-Gois, L., Bourhis, A. G., Gramet, G., Rochet, V. & Doré, J. (2003). Fluorescent hybridisation combined with flow cytometry and hybridisation of total RNA to analyse the composition of microbial communities in human faeces using 16S rRNA probes. *FEMS Microbiol Ecol* **43**, 237–245.

Sanguinetti, C. J., Dias Neto, E. & Simpson, A. J. (1994). Rapid silver staining and recovery of PCR products separated on polyacrylamide gels. *Biotechniques* **17**, 914–921.

Sim, K., Cox, M. J., Wopereis, H., Martin, R., Knol, J., Li, M. S., Cookson, W. O., Moffatt, M. F. & Kroll, J. S. (2012). Improved detection of bifidobacteria with optimised 16S rRNA-gene based pyrosequencing. *PLoS One* **7**, e32543.

Stackebrandt, E. & Ebers, J. (2006). Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* **33**, 152–155.

Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.

Suau, A., Bonnet, R., Sutren, M., Godon, J. J., Gibson, G. R., Collins, M. D. & Doré, J. (1999). Direct analysis of genes encoding 16S rRNA from complex communities reveals many novel molecular species within the human gut. *Appl Environ Microbiol* **65**, 4799–4807.

Thorasin, T. (2013). *Investigation and characterization of the* 'Atopobium *cluster' of the human faecal microbiota.* PhD thesis, University of Reading, UK.

Turnbaugh, P. J., Hamady, M., Yatsunenko, T., Cantarel, B. L., Duncan, A., Ley, R. E., Sogin, M. L., Jones, W. J., Roe, B. A. & 6 other authors. (2009). A core gut microbiome in obese and lean twins. *Nature,* **457**, 480–484.

Vrieze, A., Holleman, F., Zoetendal, E. G., de Vos, W. M., Hoekstra, J. B. & Nieuwdorp, M. (2010). The environment within: how gut microbiota may influence metabolism and body composition. *Diabetologia* **53**, 606–613.

Wade, W. G., Downes, J., Dymock, D., Hiom, S. J., Weightman, A. J., Dewhirst, F. E., Paster, B. J., Tzellas, N. & Coleman, B. (1999). The family *Coriobacteriaceae*: reclassification of *Eubacterium exiguum* (Poco *et al.* 1996) and *Peptostreptococcus heliotrinreducens* (Lanigan 1976) as *Slackia exigua* gen. nov., comb. nov. and *Slackia heliotrinireducens* gen. nov., comb. nov., and *Eubacterium lentum* (Prevot 1938) as *Eggerthella lenta* gen. nov., comb. nov. *Int J Syst Bacteriol* **49**, 595–600.

Wang, R. F., Beggs, M. L., Erickson, B. D. & Cerniglia, C. E. (2004). DNA microarray analysis of predominant human intestinal bacteria in fecal samples. *Mol Cell Probes* **18**, 223–234.

Wilson, K. H. & Blitchington, R. B. (1996). Human colonic biota studied by ribosomal DNA sequence analysis. *Appl Environ Microbiol* **62**, 2273–2278.

Woo, P. C., Teng, J. L., Lam, K. K., Tse, C. W., Leung, K. W., Leung, A. W., Lau, S. K. & Yuen, K. Y. (2010). First report of *Gordonibacter pamelaeae* bacteremia. *J Clin Microbiol* **48**, 319–322.

Würdemann, D., Tindall, B. J., Pukall, R., Lünsdorf, H., Strömpl, C., Namuth, T., Nahrstedt, H., Wos-Oxley, M., Ott, S. & 3 other authors. (2009). *Gordonibacter pamelaeae* gen. nov., sp. nov., a new member of the *Coriobacteriaceae* isolated from a patient with Crohn's disease, and reclassification of *Eggerthella hongkongensis* Lau *et al.* 2006 as *Paraeggerthella hongkongensis* gen. nov., comb. nov. *Int J Syst Evol Microbiol* **59**, 1405–1415.

Zhang, H., DiBaise, J. K., Zuccolo, A., Kudrna, D., Braidotti, M., Yu, Y., Parameswaran, P., Crowell, M. D., Wing, R. & 2 other authors. (2009). Human gut microbiota in obesity and after gastric bypass. *Proc Natl Acad Sci U S A* **106**, 2365–2370.

Zoetendal, E. G., Rajilic-Stojanovic, M. & de Vos, W. M. (2008). High-throughput diversity and functionality analysis of the gastrointestinal tract microbiota. *Gut* **57**, 1605–1615.

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 ‘*Atopobium* cluster’-specific DGGE†‡**	**Bacterial counts [$\log_{10}$ CFU (g dry weight faeces)$^{-1}$]**	**Number of colonies**	**Positive colony PCR‡**	**‘*Atopobium* cluster’§**
1	26	Female	Japanese	10.43–10.77	*Collinsella aerofaciens*, *Eggerthella lenta*	9.97	82	9	9
2	33	Female	Thai	10.84–11.06	*Collinsella aerofaciens*, *Collinsella intestinalis*/*Collinsella stercoris*, *Coriobacteriaceae* sp. PEAV3-3	9.98	138	69	56
3	27	Female	British	9.53–9.96	*Collinsella intestinalis/Collinsella stercoris*, *Eggerthella lenta*	9.54	122	21	16
4	36	Female	Thai	10.31–10.64	*Collinsella aerofaciens*, *Collinsella intestinalis*/*Collinsella stercoris*, *Collinsella tanakaei*, *Eggerthella lenta*	10.05	131	2	1
5	28	Male	Mexican	10.29–10.66	*Collinsella aerofaciens*, *Collinsella stercoris/Collinsella intestinalis*, *Gordonibacter pamelaeae*, *Olsenella profusa*	10.08	69	5	3
6	31	Female	Turkish	10.14–10.60	*Collinsella aerofaciens*, *Gordonibacter pamelaeae*, *Olsenella uli*	9.36	121	25	21
7	42	Female	New Zealand	10.34–10.73	*Collinsella aerofaciens*, *Eggerthella lenta*	9.43	135	36	29
8	37	Female	British	10.36–10.59	*Collinsella aerofaciens*, *Cryptobacterium curtum*, *Eggerthella lenta*, *Gordonibacter pamelaeae*, *Paraeggerthella hongkongensis*	9.26	135	7	7
9	36	Male	Italian	10.49–10.81	*Collinsella aerofaciens*, *Coriobacteriaceae* sp. PEAV3-3, *Eggerthella lenta*	10.08	88	13	9
10	34	Male	Greek	10.57–10.80	*Collinsella aerofaciens*, *Gordonibacter pamelaeae*, *Paraeggerthella hongkongensis*	10.45	121	40	30
11	61	Male	British	9.89–10.36	*Collinsella aerofaciens*, *Gordonibacter pamelaeae*	9.48	117	53	42
12	30	Male	Malaysian	10.27–10.55	*Collinsella tanakaei*, *Eggerthella lenta*, *Gordonibacter pamelaeae*	10.00	127	1	1
13	31	Male	Greek	9.01–9.34	No DGGE performed (no amplification by ‘*Atopobium* 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	*Eggerthella lenta* (AEXRO1000021/99.5 %)	2	190
2	*Collinsella aerofaciens* (AAVJ02000013/100 %)	4	190
3	*Collinsella aerofaciens* (AAVJ02000013/99.5 %)	1	190
4	*Collinsella aerofaciens* (AAVJ02000013/100 %)	6	190
5	*Collinsella intestinalis* (ABXH02000037/100 %)	1	190
6	*Eggerthella lenta* (AEXRO1000021/99.5 %)	2	190
7	*Collinsella intestinalis* (ABXH02000037/100 %)	2	190
8	*Eggerthella lenta* (AEXRO1000021/99.0 %)	1	190
9*	*Collinsella tanakaei* (AB490807/99.0 %)	2	190
10	*Gordonibacter pamelaeae* (FP929047/97.9 %)	1	189
11	*Collinsella aerofaciens* (AAVJ02000013/99.5 %)	1	190
12	*Collinsella aerofaciens* (AAVJ02000013/100 %)	1	190
13	*Collinsella intestinalis* (ABXH02000037/100 %)	1	190
14*	*Collinsella aerofaciens* (AAVJ02000013/99.0 %)	1	190
15*	*Olsenella profusa* (AF292374/97.5 %)	2	196
16*	*Olsenella profusa* (AF292374/96.9 %)	1	190
17	*Gordonibacter pamelaeae* (FP929047/97.3 %)	1	191
18	*Collinsella aerofaciens* (AAVJ02000013/100 %)	3	190
19*	*Olsenella uli* (CP002106/98.5 %)	2	196
20	*Eggerthella lenta* (AEXRO1000021/97.9 %)	1	191
21	*Collinsella aerofaciens* (AAVJ02000013/100 %)	5	190
22	*Gordonibacter pamelaeae* (FP929047/97.4 %)	1	189
23	*Eggerthella lenta* (AEXRO1000021/97.4 %)	1	191
24	*Collinsella aerofaciens* (AAVJ02000013/99.5 %)	4	190
25*	*Paraeggerthella hongkongensis* (AY288517/94.2 %)	1	191
26*	*Paraeggerthella hongkongensis* (AY288517/93.7 %)	1	191
27	*Gordonibacter pamelaeae* (FP929047/97.4 %)	1	189
28	*Gordonibacter pamelaeae* (FP929047/97.4 %)	1	189
29*	*Gordonibacter pamelaeae* (FP929047/97.4 %)	2	189
30	*Collinsella aerofaciens* (AAVJ02000013/100 %)	2	190
31	*Paraeggerthella hongkongensis* (AY288517/94.2 %)	1	191
32	*Gordonibacter pamelaeae* (FP929047/97.9 %)	6	189
33	*Collinsella tanakaei* (AB490807/97.9 %)	1	189
34	*Collinsella tanakaei* (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	*Collinsella aerofaciens*	33, 34, 35, 59, 87, 95, 129, 146, 152	9
2	*Collinsella aerofaciens*	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, 93, 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	*Collinsella intestinalis*‡	5, 11, 44, 70, 91, 123, 130, 140, 141, 150, 152	11
	Eggerthella lenta	3, 6, 8, 65, 96	5
4	*Collinsella tanakaei*	142	1
5	*Collinsella aerofaciens*	67, 75, 122	3
6	*Collinsella aerofaciens*	3, 4, 5, 9, 12, 15, 34, 39, 77, 80, 95, 98, 113, 130, 147, 155	16
	Eggerthella lenta	71	1
	Olsenella sp. D6	2, 32, 73, **110**	4
7	*Collinsella aerofaciens*	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, 136, 154, 158	29
8	*Collinsella aerofaciens*	40, **41**, 61, 75, 118, 124, 146	7
9	*Collinsella aerofaciens*	74, 76, 82, 101, 108, 111, 136, 142	8
	Eggerthella lenta	63	1
10	*Collinsella aerofaciens*	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, 142	30
11	*Collinsella aerofaciens*	2, 6, **7**, 8, 9, 12, 13, 15, 18, 19, 25, 28, 29, 30, 39, 41, **45**, 47, 54, 55, 56, 58, 61, 68, 74, 78, 81, 84, 108, 112, 117, 122, 124, 129, 145, 154, 156, 157	38
	Collinsella stercoris‡	10, 70, 102	3
	Eggerthellaceae sp. D11	98	1
12	‘*Enorma*’ 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**	**Mlz**	**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	+	+
***Collinsella aerofaciens* CCUG 28087^T**		-	+	+	-	-	-	-	+	-	+w	-	-	+w	-
***Collinsella aerofaciens* 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.

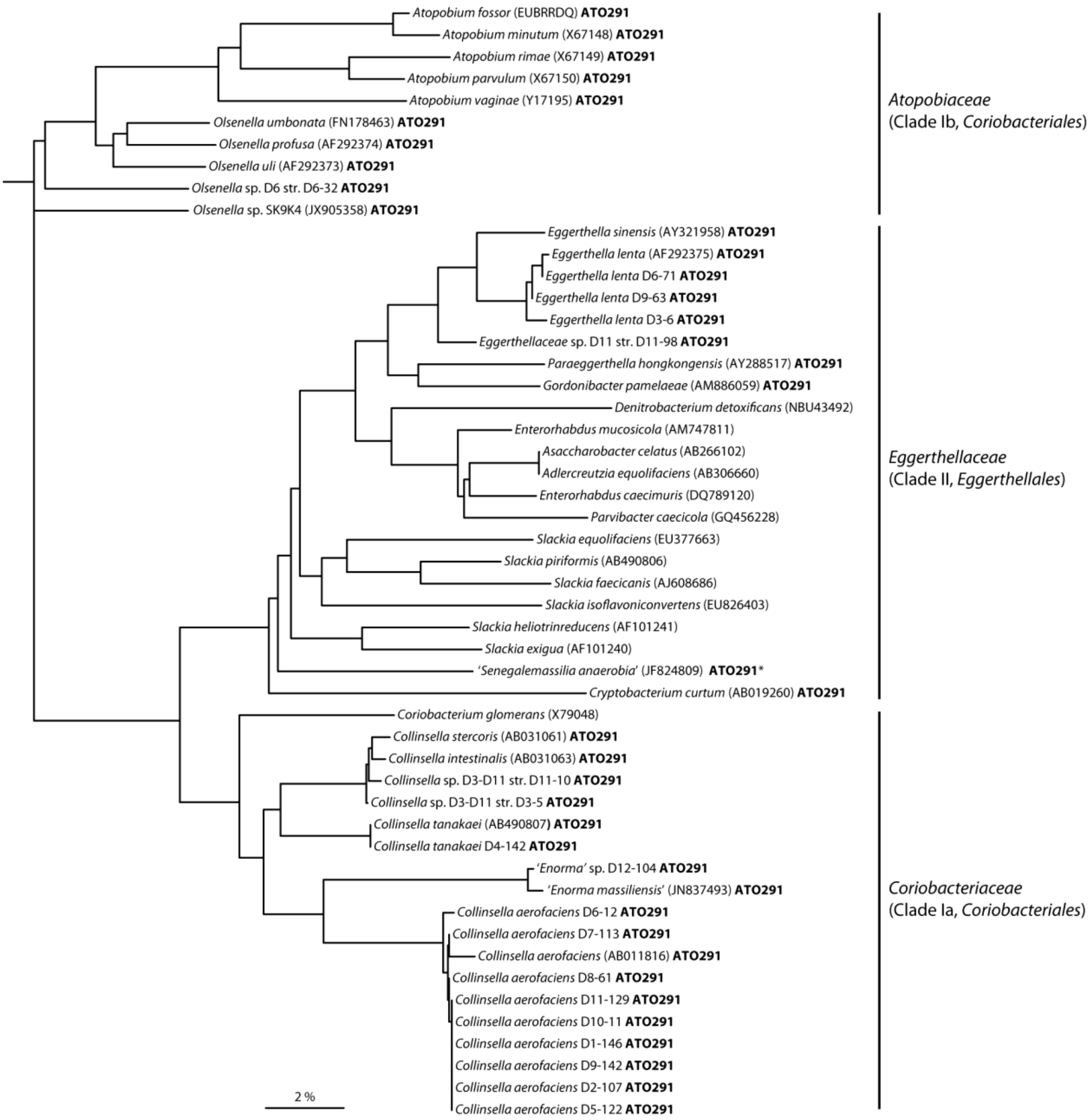


Fig. 1. Phylogenetic tree of the class *Coriobacteriia* and related bacteria isolated from human faeces. Taxonomic classifications are as described by Gupta *et al.* (2013). The 16S rRNA gene sequence of one isolate of each species detected from each donor is shown (at least 1400 nt sequenced for each 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/DDBJ 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.

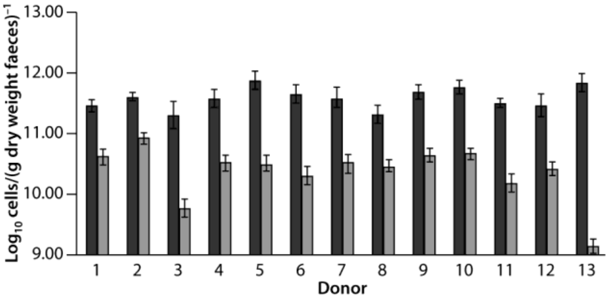


Fig. 2. Estimated number of total and ‘*Atopobium* cluster’ bacteria present in the faeces (per g dry weight) of healthy human adults (*n* = 13) as determined by using FISH analyses. Data are presented as the mean values ± standard deviation of six faecal samples collected fortnightly from each subject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

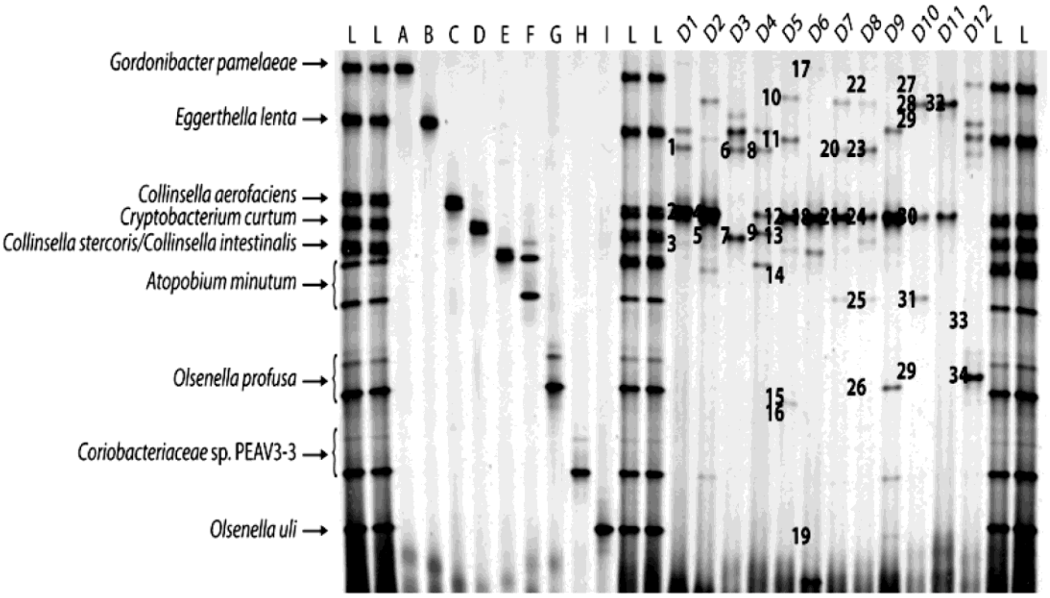


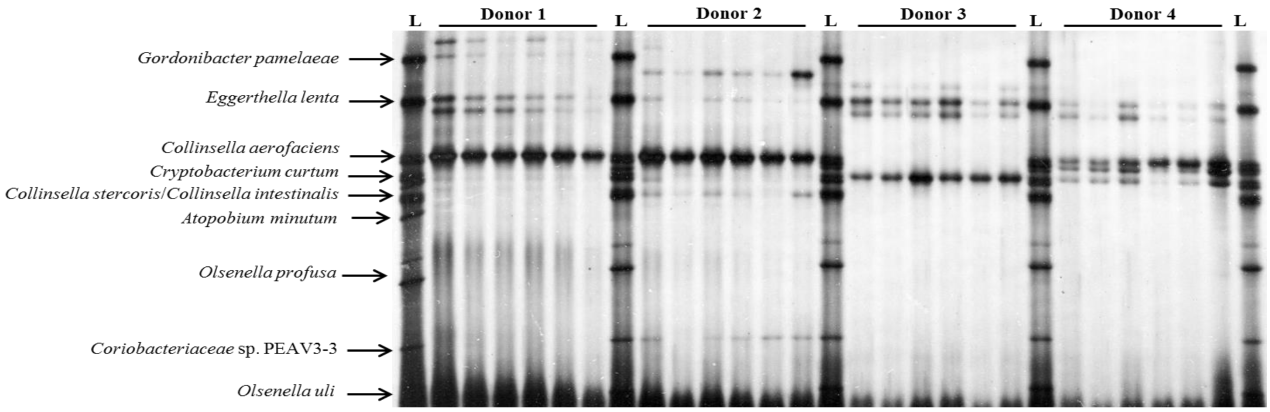
Fig. 3. Use of targeted DGGE to characterize the diversity of the faecal '*Atopobium* cluster' population of healthy human adults (*n* = 12; D1 to D12). DNA was extracted from faecal samples collected fortnightly from each subject over a 3-month period (a representative for each volunteer is presented). 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 pamelaeae* 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. PEAV3-3 and *Olsenella uli* CCUG 31166^T.

Supplementary Table 1. Greengenes species/sequences targeted by probe ATO291 and the forward 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
11379	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	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__
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__
87668	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
99332	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
100258	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
111683	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
128261	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
133178	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
136127	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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__
139478	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
143800	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
145127	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
147370	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
149443	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
149820	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
163566	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
163696	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__
174266	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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
175508	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
175907	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
176181	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
176828	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
177478	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
178487	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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
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
182045	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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
182617	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__	s__
182804	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
183104	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
184745	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
185416	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
185565	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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__
188594	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
189390	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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
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
191719	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

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
193145	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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
195674	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__	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
196951	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcus	s__
197212	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
199358	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
200827	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
218522	k__Bacteria	p__Tenericutes	c__Mollicutes	o__Mycoplasmatales	f__Mycoplasmataceae	g__Mycoplasma	s__
227758	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
227819	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__
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__
232823	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
232900	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__
234585	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
235262	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Bifidobacteriales	f__Bifidobacteriaceae	g__Bifidobacterium	s__adolescentis
244577	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
247757	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
251702	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__rimae
262384	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__
266446	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
269986	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
272555	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
273584	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
276650	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
277288	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
288809	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__
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__
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
291543	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__	s__
291811	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__stercoris
292607	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
295496	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__Atopobium	s__
297503	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__	g__	s__
299855	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__
300355	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
301038	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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
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__
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__
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
318153	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
326048	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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
331142	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
334327	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
338145	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
341374	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__
346107	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
350141	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
351639	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__
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
357451	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
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__
359721	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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
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__
365212	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
365933	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
366392	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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
370166	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
408604	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
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__
461524	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
461868	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
469663	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
508866	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
510509	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
512048	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
514642	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
515249	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
518574	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
521275	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
527042	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__rimae
528013	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
528412	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
530138	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
531157	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
539240	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
541074	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
541875	k__Bacteria	p__Tenericutes	c__Mollicutes	o__Mycoplasmatales	f__Mycoplasmataceae	g__Mycoplasma	s__
544654	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
551179	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
560141	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
561595	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
565593	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
566154	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
568719	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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
576926	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
580258	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
581287	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
582069	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
584954	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
587028	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
587753	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
593352	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
593556	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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__
646800	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
682726	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
706766	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
797762	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
810895	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
816299	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
841419	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
842580	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__stercoris
842982	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
846649	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
849361	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
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__Atopobium	s__rimae

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
851788	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__stercoris
858535	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
872701	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
893041	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
919665	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
942880	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
968416	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
980682	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1034960	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1085854	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
1106384	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1110606	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
1124877	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
1132453	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
1140324	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1141218	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__
1147903	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
1634660	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
1646183	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1764555	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1811927	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
1903534	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
2163609	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
2176004	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
2232355	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
2251910	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
2251911	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
2259936	k__Bacteria	p__Spirochaetes	c__GN05	o__IF025	f__	g__	s__
2761928	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
2919166	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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
3102225	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
3186757	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3263959	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3294759	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3720783	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
3865727	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3932937	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4125815	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
4274154	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4295071	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4299095	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4302355	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
4302557	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__
4308811	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
4314847	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4317246	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
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
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
4332235	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4336546	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
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__
4343149	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4345173	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
4354775	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4361220	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4361768	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4368101	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4373344	k__Bacteria	p__Tenericutes	c__Mollicutes	o__Mycoplasmatales	f__Mycoplasmataceae	g__Candidatus Hepatoplasma	s__
4380670	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4384124	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4387252	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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
4397092	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
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

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__Atopobium	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Acidobacteria	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__Actinobacteria	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__Thermoleophilia	o__Gaiellales	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__Atopobium	s__
248619	k__Bacteria	p__Actinobacteria	c__MB-A2-108	o__0319-7L14	f__	g__	s__
249053	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Thermoleophilia	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__Devosia	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__Atopobium	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__
299855	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__Caulobacterales	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__Thermoleophilia	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__Acidobacteria	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	g__	s__
593718	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__V1B07b93	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__Nitriliruptoria	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__Iamiaceae	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Atopobium	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__Thermoleophilia	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	g__	s__
922149	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__
927819	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	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__Thermoleophilia	o__Gaiellales	f__AK1AB1_02E	g__	s__
960217	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Solirubrobacterales	f__	g__	s__
966113	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__
968016	k__Bacteria	p__Actinobacteria	c__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Thermoleophilia	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__Thermoleophilia	o__Gaiellales	f__AK1AB1_02E	g__	s__
1090930	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	g__	s__
1097892	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__
1098356	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	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__Thermoleophilia	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Atopobium	s__
1125874	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__ZA3409c	g__	s__
1125934	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Streptomycetaceae	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__Streptomycetaceae	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__Caulobacterales	f__Caulobacteraceae	g__	s__
1135388	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	g__	s__
1135893	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Rhodobacterales	f__Hyphomonadaceae	g__Oceanicaulis	s__
1634660	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	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__Thermoleophilia	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__Rhodobacterales	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__Acidobacteria	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__Rhodobacterales	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__Thermoleophilia	o__Gaiellales	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__Thermoleophilia	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__Thermoleophilia	o__Gaiellales	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__Iamiaceae	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Acidobacteria	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	g__	s__
4371083	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__
4372310	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	g__	s__
4372595	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__Iamiaceae	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Iamiaceae	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__Thermoleophilia	o__Gaiellales	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__Thermoleophilia	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__Nitriliruptoria	o__Nitriliruptorales	f__Nitriliruptoraceae	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__Thermoleophilia	o__Gaiellales	f__Gaiellaceae	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__Iamiaceae	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__Atopobium	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__Nocardioidaceae	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

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
11379	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	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__
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__
87668	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
99332	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
100258	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
111683	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
133178	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
136127	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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__
139478	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	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__
149820	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
174266	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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
175508	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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
178487	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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
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
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__
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
185565	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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__
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
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
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
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
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
199358	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
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__
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__
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__
234585	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
247757	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
251702	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__rimae
263650	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
266446	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
269986	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
273584	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
277288	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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__
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
292607	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
295496	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__Atopobium	s__
297503	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__	g__	s__
299855	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__
300355	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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
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__
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__
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
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
331142	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
334327	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
338145	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
341374	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__
346107	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
350141	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
351639	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__
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
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__
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
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__
366392	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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__
508866	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
510509	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
514642	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
521275	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
530138	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
539240	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
551179	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
561595	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
566154	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
571109	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens

GreenGenes_ID	Domain	Phylum	Class	Order	Family	Genus	Species
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
576926	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
580258	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
581287	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
582069	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
584954	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
587028	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
587753	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
646800	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
706766	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
797762	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
810895	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
816299	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
842580	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__stercoris
849361	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
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__Atopobium	s__rimae
851788	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__stercoris
858535	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
872701	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
893041	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
942880	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
980682	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1034960	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1106384	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1110606	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
1124877	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
1132453	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
1140324	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1141218	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__
1147903	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
1634660	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	s__
1646183	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
1811927	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
1903534	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	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__
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
2761928	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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
3102225	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
3186757	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3263959	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3294759	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
3720783	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
3865727	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4274154	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4295071	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4299095	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4302355	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Atopobium	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__
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__
4314847	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4317246	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	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__
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
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
4332235	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4336546	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella	s__lenta
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__
4343149	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4345173	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__
4354775	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens
4361768	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4368101	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4380670	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__	s__
4384124	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae	g__Collinsella	s__aerofaciens

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. MS5	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	AWEZ01000030	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	AWEZ01000030	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
299855	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. MS5	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__tanakaei	Collinsella tanakaei 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 phI	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	*Collinsella aerofaciens*
D1-146	KP233240	*Collinsella aerofaciens*
D1-152	KP233241	*Collinsella aerofaciens*
D1-33	KP233242	*Collinsella aerofaciens*
D1-34	KP233243	*Collinsella aerofaciens*
D1-35	KP233244	*Collinsella aerofaciens*
D1-59	KP233245	*Collinsella aerofaciens*
D1-87	KP233246	*Collinsella aerofaciens*
D1-95	KP233247	*Collinsella aerofaciens*
D10-11	KP233248	*Collinsella aerofaciens*
D10-119	KP233249	*Collinsella aerofaciens*
D10-120	KP233250	*Collinsella aerofaciens*
D10-129	KP233251	*Collinsella aerofaciens*
D10-130	KP233252	*Collinsella aerofaciens*
D10-135	KP233253	*Collinsella aerofaciens*
D10-139	KP233254	*Collinsella aerofaciens*
D10-14	KP233255	*Collinsella aerofaciens*
D10-142	KP233256	*Collinsella aerofaciens*
D10-15	KP233257	*Collinsella aerofaciens*
D10-16	KP233258	*Collinsella aerofaciens*
D10-18	KP233259	*Collinsella aerofaciens*
D10-23	KP233260	*Collinsella aerofaciens*
D10-24	KP233261	*Collinsella aerofaciens*
D10-26	KP233262	*Collinsella aerofaciens*
D10-3	KP233263	*Collinsella aerofaciens*
D10-34	KP233264	*Collinsella aerofaciens*
D10-39	KP233265	*Collinsella aerofaciens*
D10-40	KP233266	*Collinsella aerofaciens*
D10-43	KP233267	*Collinsella aerofaciens*
D10-45	KP233268	*Collinsella aerofaciens*
D10-48	KP233269	*Collinsella aerofaciens*
D10-55	KP233270	*Collinsella aerofaciens*
D10-7	KP233271	*Collinsella aerofaciens*
D10-72	KP233272	*Collinsella aerofaciens*
D10-76	KP233273	*Collinsella aerofaciens*
D10-79	KP233274	*Collinsella aerofaciens*
D10-8	KP233275	*Collinsella aerofaciens*
D10-98	KP233276	*Collinsella aerofaciens*
D10-99	KP233277	*Collinsella aerofaciens*
D11-10	KP233278	*Collinsella stercoris*
D11-102	KP233279	*Collinsella stercoris*
D11-108	KP233280	*Collinsella aerofaciens*
D11-112	KP233281	*Collinsella aerofaciens*
D11-117	KP233282	*Collinsella aerofaciens*
D11-12	KP233283	*Collinsella aerofaciens*
D11-122	KP233284	*Collinsella aerofaciens*
D11-124	KP233285	*Collinsella aerofaciens*
D11-129	KP233286	*Collinsella aerofaciens*
D11-13	KP233287	*Collinsella aerofaciens*
D11-145	KP233288	*Collinsella aerofaciens*
D11-15	KP233289	*Collinsella aerofaciens*
D11-154	KP233290	*Collinsella aerofaciens*
D11-156	KP233291	*Collinsella aerofaciens*
D11-157	KP233292	*Collinsella aerofaciens*
D11-18	KP233293	*Collinsella aerofaciens*
D11-19	KP233294	*Collinsella aerofaciens*
D11-2	KP233295	*Collinsella aerofaciens*
D11-25	KP233296	*Collinsella aerofaciens*
D11-28	KP233297	*Collinsella aerofaciens*
D11-29	KP233298	*Collinsella aerofaciens*

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

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

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