

Gene-targeted microfluidic cultivation validated by isolation of a gut bacterium listed in Human Microbiome Project's Most Wanted taxa

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Supporting Text

All chemicals were purchased from commercial sources and used as received unless otherwise stated.

Homemade Reagents

A protocol for making GBSS buffer can be found on the Schmidt Lab website (1). For H₂Oc or PBSc, 0.2% cysteine was added and the solution was sterilely filtered through 0.22 μm membrane. 0.1 M Fe(SCN)₃ solution was sterilely filtered through 0.22 μm membrane (Fisher Scientific) and used as a red dye solution. Tetradecane (Fisher Scientific) was sterilely filtered through 0.22 μm membrane (Fisher Scientific). For assembling SlipChip for depositing PCR reagents, filtered tetradecane was degassed under house vacuum overnight. All plastic consumables and reagents were equilibrated in an anaerobic chamber for more than 24 hours before usage.

Anaerobic Chamber

A Coy lab anaerobic chamber equipped with dehumidifier was used in all anaerobic cultivation experiments. The hydrogen level was maintained at 3–4% and a relative humidity of 30%. The chamber was equipped with recirculating atmosphere filtration system (HePa) to maintain a sterile atmosphere.

Design and Fabrication of SlipChip

SlipChips for chip wash were fabricated as previously reported(2). Photomasks were designed in AutoCAD and ordered from CAD/Art Services, Inc. (Bandon, OR). Soda-lime glass plates with chromium/photoresist and chromium/gold/photoresist coating were purchased from Telic Company (Valencia, CA). The device contained 3,200 microwells for compartmentalization on one plate, and continuous loading channels on the other plate. The depth of wells was 90 μm measured using a profilometer (Dektak 150, Veeco, CA). Through holes were drilled with a 0.035" drill bit (Diamond ball 4F bit, Harvey Tool #74335-C4, Colmar Industrial Supplies, Wheeling, IL) before surface modification. Glass debris from drilling was removed by sonicating the chips in a 1:1 mixture of water and ethanol for more than one hour in a warm water bath. Prior to use, the SlipChips were cleaned with piranha solution, rinsed three times with millipore water followed by 200 proof ethanol, blow dried with nitrogen and silanized with dimethyldichlorosilane using a previously reported protocol (2). An acid piranha solution (caution: this is a corrosive mixture) is used to remove organic contaminants from substrates by mixing 3:1 (v:v) concentrated sulfuric acid (H₂SO₄) with 30% hydrogen peroxide (H₂O₂). Sulfuric Acid (Cat. #A300-212) and 30% Hydrogen peroxide (Cat. #H325-4) can be ordered through Fisher Scientific.

Silanized chips were stored at room temperature in a dessicant box (< 15% humidity, maintained with Drierite). When a glass SlipChip needed to be reused, it was cleaned with Piranha solution first, and then subjected to the same silanization procedure described above.

For the replica-SlipChip, the depth of the features measured by a contact profiler (Dektak 150, Veeco, CA) was 90 μm. The depth was 120 μm for wells, and 60 μm for loading channels of the SlipChip used for depositing PCR reagent wells. The lateral dimensions of cultivation and PCR reagent wells can be measured by photographs from a stereoscope, as shown in the accompanying paper (3).

Performing Chip Wash

The plates of SlipChip were assembled under a layer of tetradecane in a petridish and four binder clips (small binder chips, cat # 429-415, Office Depot) were applied to hold the devices together. The lubricating oil in the loading channel and wells was removed by repeated purging with vacuum for 3 to 5 times at an interval of 1-2 hours between each purging. For anaerobic culture, the SlipChip was placed into the anaerobic chamber for at least 24 hours prior to use. Aqueous solution was loaded onto SlipChip by pipetting, and the device was slipped to form compartments. The solution in the loading channel was removed by purging with a vacuum. In the case of anaerobic cultivation, a gas recirculation pump for atmosphere filtration system was used as a vacuum source. For chip wash experiments with microbial samples, the loading channel can be cleaned by repeated washing with GBSS or PBSc buffer solution to

remove any residual microbial cells and prevent overgrowth of microbes in the loading channel. The continuous loading channels were used as gas exchange channels.

PBS buffer was loaded into the channel to remove the gas phase, and can be used for repeated washing in the case of microbial samples. The SlipChip was designed to collect the chip wash solution with a single outlet (Fig. S1). To collect the solution, 90 μL PBS buffer was injected into the SlipChip using an Eppendorf pipettor and collected into an Eppendorf pipette tip (1-200 μL , cat. No. 02-717-141, Fisher Scientific) and transferred into an Eppendorf tube. This process was repeated for three times. 90 μL tetradecane was loaded into the SlipChip to further remove the diluted aqueous solution. The solution was also transferred from the pipette tip into the Eppendorf tube.

It is important to keep the lubricating oil in the device from drainage during incubation at elevated temperature or for long-term culture. Loss of lubricating oil in the gap between the two glass plates causes cross-contamination among the confined wells, and cannot be used in the chip wash experiment because the washing buffer would flow through the gap and not into the collection outlet. To prevent loss of oil from the device, a piece of Kimwipe was briefly saturated with 1:1 (vol) mixture of water and tetradecane and then placed inside a Petri dish. The SlipChip was then placed into the Petri dish and Parafilm was used to seal the Petri dish. The Petri dish was then incubated at the desired temperature for microbial culture.

***E. coli* Preparation**

The green fluorescent protein (GFP)-labeled *E. coli* RP 437 were obtained as a gift from Guillaume Lambert at Princeton University. *E. coli* RP 437 was purchased from CGSC (catalog #: 12122) and transformed with DsRed plasmid.

E. coli cells labeled with DsRed fluorescent proteins were enriched with 50 $\mu\text{g mL}^{-1}$ of Ampicillin in LB at 37 $^{\circ}\text{C}$ overnight (12 hours) in a rotary shaking incubator (SI-600 Lab Companion, Jeio Tech) at 200 rpm. Overnight culture was then diluted 100-fold and cultured with 10 $\mu\text{g mL}^{-1}$ of Ampicillin and 40 $\mu\text{mol L}^{-1}$ IPTG in LB media for 3 hrs. Cells from 1 mL culture were then pelleted at 3000 $\times\text{g}$ for 5 min and washed 3 times with 1 mL of ice cold 1 \times PBS buffer before use.

Quantifying the Recovery Efficiency of Chip Wash

To quantitatively test the recovery efficiency of this method, an aqueous solution of 200 nM Alexa Fluor 488 hydrazide (Invitrogen) in PBS buffer was injected into the device and subsequently collected by chip wash method, normalized to a volume of 500 μL , and quantified using a fluorospectrometer (Thermo scientific). 0.45 nM, 0.9 nM, 1.8 nM, 3.6 nM and 7.2 nM of Alexa Fluor 488 hydrazide solutions in PBS buffer were used to obtain a calibration curve. The loading volume of the device was calculated to be 18 μL . Therefore, the concentration of the recovered solution was divided by the concentration of 7.2 nM Alexa Fluor 488 hydrazide to calculate the recovery efficiency.

E. coli cells labeled with DsRed fluorescent proteins were prepared as described above, loaded onto SlipChip and collected immediately using chip wash method. The chip wash solution was normalized to a volume of 500 μL . 18 μL of the same solution was diluted to 500 μL and used as a control. The cells from chip wash solutions as well as the control solution were quantified using INCYTO C-Chip (DHC-N01) under Leica DMI6000 microscope (Leica Microsystems) with a 20 \times /0.4NA Leica objective, TX2 filter and a Hamamatsu ORCA-ER camera with 1 \times coupler with an exposure time of 200 ms. Images were acquired and analyzed by using Metamorph imaging system version 6.3r1 (Universal Imaging). Recovery efficiency was calculated by dividing cell number in the recovered solution by the cell number in the control solution.

Reagents and Equipment for PCR

Primers for PCR were ordered from Integrated DNA Technologies (Coralville, IA). SsoFast EvaGreen Supermix (2X) was purchased from Bio-Rad Laboratories (Hercules, CA). Bovine serum albumin solution (BSA) was purchased from Roche Diagnostics (Indianapolis, IN). PCR Mastercycler and in situ adapter were purchased from Eppendorf (Hamburg, Germany).

Using Chip Wash to Monitor Bacterial Growth with a Single Species Model System

E. coli cells labeled with DsRed fluorescent proteins prepared as described above were serially diluted to a final density of $\sim 10^5$ CFU/mL in 10 $\mu\text{g mL}^{-1}$ of Ampicillin and 40 $\mu\text{mol L}^{-1}$ IPTG in LB media or 1 \times PBS buffer that does not support growth of bacteria as a negative control and loaded onto SlipChip. SlipChip was incubated at 37 $^{\circ}\text{C}$ overnight. The solution was collected after cultivation using chip wash. Genomic DNA was purified from chip wash solutions using QiaAmp kit (Qiagen). For calibration, genomic DNA was purified from bulk liquid culture of *E. coli* cells labeled with DsRed fluorescent proteins, quantified by Quanti-it DNA high sensitivity quantification kit (Invitrogen), and serially diluted in AE buffer containing 0.01 mg/mL of BSA. The reaction master mixture for qPCR was prepared by mixing 10 μL of 2X SsoFast EvaGreen Supermix, 1 μL of forward and reverse primer (10 $\mu\text{mol L}^{-1}$), 1 μL of template solution and 8 μL of water (Fisher Scientific, BP 2470-1). qPCR was performed on the Eco real-time PCR machine (Illumina, Inc, San Diego, CA) with 27F(4) (5'-AGAGTTTGATCCTGGCTCAG -3') and 534R (5)-ATTACCGCGGCTGCTGG-3') primers. We observed a 10,000-fold increase in DNA concentration (Fig. S1), suggesting that for this particular model system, non-growing cells contribute to 0.01% of the genetic material recovered from chip wash.

Performing Chip Wash and Plate Wash Experiment with a Two-Species Model System

Cells of *Clostridium scindens* (ATCC 35704) and *Enterococcus faecalis* (ATCC 49532) were separately enriched in Schaedler Anaerobe Broth (Oxoid) at 37°C in an incubator (model# 10-140E, Quincy lab Inc) overnight (~ 16 hours) in an anaerobic chamber (Coylab). The culture was diluted 100 fold and incubated at 37°C for 5 hours (*E. faecalis*) and 8 hours (*C. scindens*). The cells were pelleted at 6000 ×g for 3 minutes and washed with PBS_c for 3 times. Cell numbers of the two species were estimated for loading by cell counting using INCYTO C-Chip (DHC-N01) under Leica DMI6000 microscope (Leica Microsystems) with a 20 x/0.4NA Leica objective. The two species were mixed at 5:1 ratio (*C. scindens*: *E. faecalis*, confirmed by separately plating the two species) in Schaedler Anaerobe Broth at a final density of ~10⁵ CFU/mL, loaded onto SlipChip and incubated at 37°C for 24 hours for growth. Genomic DNA extracted from 18 μL of the same solution containing mixture of cells using QiaAmp kit (Qiagen) was used as non-growth control. To perform plate wash, 4 μL of the same solution containing mixture of cells was plated on Schaedler Anaerobe medium with 2% (wt/vol) noble agar (Fisher Scientific) to achieve a final density of ~300 colonies (counted on day 3 after cultivation when both of the species reached saturation on an agar plate) to reduce interaction between colonies. The cultivar was collected by chip wash and plate wash. Plate wash was performed following a previously described protocol(6) with minor modifications. Cell scrapers (Fisher Scientific) were used to collect cultivar into 1 mL of GBSS buffer. 50 μL of the combined solution was centrifuged at 6000× g for 10 minutes to pellet the cells. Serial dilutions of genomic DNA from macroscale liquid culture of the two species quantified by Quanti-it DNA high sensitivity quantification kit (Invitrogen) were used to calibrate the qPCR machine. The reaction master mixture for qPCR was prepared by mixing 10 μL of 2X SsoFast EvaGreen Supermix, 1 μL of forward and reverse primer (10 μmol L⁻¹), 1 μL of template solution and 8 μL of water (Fisher Scientific, BP 2470-1). For plate wash, ~1 ng/ μL of genomic DNA was used for qPCR as we are interested in the relative ratio of *C. scindens* and *E. faecalis*. qPCR was performed on the Eco real-time PCR machine (Illumina, Inc, San Diego, CA) with ScinF4 (5'-CGTAACGCGCTCTTCTTCG-3') and ScinR4 (5'-CCTTCTCCAGGTTCTCCCT-3') for *C. scindens* and E.faecalis_F (5'-CGC TTC TTT CCT CCC GAG T-3') and E.faecalis_R (5'-GCC ATG CGG CAT AAA CTG-3'). The two pairs of primers are specific to the targeting species, which was confirmed by qPCR.

We cultivated the two strains separately on SlipChip or on agar plates. To monitor bacterial growth on agar plate, cells were plated on Schaedler Anaerobe Agar separately, incubated at 37 °C and imaged every 24 hours with a Leica MZ 16 stereoscope. The plating experiment was set up with more than three plates for each species. For each time point, one plate was taken out of the anaerobic chamber for imaging and discarded. To image bacterial growth on the SlipChip, bacterial cells from each species were loaded onto a “replica-SlipChip” described in the accompanying paper(3) at a final density of ~10⁵ CFU mL⁻¹ in Schaedler Anaerobe broth. The device was incubated for 24 hours to allow growth of bacteria. The microcolonies were imaged under Leica DMI6000 microscope (Leica Microsystems) with a 20 x/0.7NA Leica objective and a Hamamatsu ORCA-ER camera with 1× coupler under bright field.

On-chip Cultivation of *E. coli* and Splitting of the Microcolonies

E. coli cells were enriched with 50 μg mL⁻¹ of Ampicillin in LB at 34 °C overnight (12 hours) in a rotary shaking incubator at 200 rpm to reach stationary phase. To synchronize cells, overnight culture of each species was then diluted 100-fold and cultured with 10 μg mL⁻¹ of Ampicillin and 40 μmol L⁻¹ IPTG in LB media for 3 hrs. 1 mL culture of cells were then pelleted at 3000 ×g for 5 min and washed 5 times with 1 mL of 1× PBS buffer. Cells were finally suspended in 10 μg mL⁻¹ of Ampicillin and 40 μmol L⁻¹ IPTG in LB media and cell suspension was serially diluted with 10 μg mL⁻¹ of Ampicillin and 40 μmol L⁻¹ IPTG with 0.5% of ultra-low gelling temperature Type IX-A agarose (Sigma-Aldrich) in LB media and mixed to a final density of 2 × 10⁴ and 2 × 10³ CFU mL⁻¹ for *E. coli* strains with GFP and DsRed genes, respectively, and loaded onto replica-SlipChip as described in the accompanying paper(3). SlipChip was incubated at 34 °C for 3 hours and then split into two halves as described in the accompanying paper(3). The bottom half was kept on the holder for colony PCR and the top was preserved at 10 °C on Echo therm chilling plate (Torrey Pines Scientific, Carlsbad, CA) under oil in a Petri dish.

Depositing PCR Reagents on SlipChip

The reaction master mixture was prepared by mixing 100 μL of 2X SsoFast EvaGreen Supermix, 1 μL of forward (DSR_F, 5'-GGACGGCTCCTTCATCTACA-3', 100 μmol L⁻¹) and reverse primer (DSR_R, 5'-GGTGATGTCCAGCTTGGAGT-3', 100 μmol L⁻¹), 10 μL of 10 μg mL⁻¹ BSA solution, and 68 μL of 2.5% (w/v) ultra-low gelling temperature agarose in water. This mixture was then loaded onto the SlipChip for depositing PCR reagents described in the SI of the accompanying paper (3) by replacing tetradecane in loading channels and this SlipChip for depositing PCR reagent was split to obtain 1,000 droplets deposited on one half of the SlipChip.

Combining the Replica-SlipChip with the PCR Chip

The PCR chip preloaded with PCR reagents was taken off the holder and combined with the bottom piece of the replica chip by aligning through-holes with the pins. A binder clip (5/32" inch capacity, 1/2" inch size, officemax, Itasca, IL) was used to clamp the two plates together, allowing the combined SlipChip to be removed from the holder and the oil without misalignment.

Fluorescence Imaging of PCR Results and *E. coli* with GFP and DsRed Fluorescent Proteins

Fluorescence images were acquired with a Leica DMI6000 microscope (Leica Microsystems) with a 10 x/0.4NA Leica objective and a Hamamatsu ORCA-ER camera with 1× coupler. An L5 filter with an exposure time of 500 ms was used to collect images. For quantitative analysis, fluorescent intensity of a fluorescence reference slide for L5 filter was recorded and used for background

correction. Images were acquired and analyzed by using Metamorph imaging system version 6.3r1 (Universal Imaging) and ImageJ by the National Institutes of Health (<http://rsb.info.nih.gov/ij/download.html>). Processing was applied equally to the entire image.

Preparation of M2GSC Medium

This protocol is adapted from reference (7).

1L M2GSC medium contains the following ingredients:

10 g of casitone, 2.5 g of yeast extract, 4 g of NaHCO₃, 2 g of cellobiose, 2 g of soluble starch, 300 mL of rumen fluid, 2 g of glucose, 1 g of cysteine, 0.45 g of K₂HPO₄, 0.45g of KH₂PO₄, 0.9 g of (NH₄)₂SO₄, 0.9 g of NaCl, 0.09 g of MgSO₄ 7H₂O, 0.09 g of CaCl₂, 15 g of Agar Noble and 1 mg of resazurin.

Preparation of M2LC medium

We prepare the basal medium containing: 10 g of casitone, 2.5 g of yeast extract, 4 g of NaHCO₃, 2 g of cellobiose, 2 g of soluble starch, 2 g of glucose, 1 g of cysteine, 0.45 g of K₂HPO₄, 0.45g of KH₂PO₄, 0.9 g of (NH₄)₂SO₄, 0.9 g of NaCl, 0.09 g of MgSO₄ 7H₂O, 0.09 g of CaCl₂, 15 g of Agar Noble and 1 mg of resazurin in 700 mL of water.

We mixed 70 µL of the basal medium with 30 µL supernatant of autoclaved luminal sample.

Handling Frozen Stock Solutions of Bacterial Samples in an Anaerobic Chamber

10 µL aliquots of homogenized brush samples and ~50 µL aliquots of homogenized luminal samples were stored in -80 °C freezer. For cultivation, the brush sample was transferred from the freezer to an anaerobic chamber on dry ice with GasPak systems.

Microbial Cultivation from the Biopsy with M2GSC Medium and Performing Plate Wash

An aliquot of cecum brush sample was serially diluted in GBSS buffer. 18 µL of the 10⁴ dilution was plated onto four M2GSC agar plates (4.5 µL for each plate) yielding ~250 colonies per plate after three days of incubation at 37 °C (model# 10-140E, Quincy lab Inc) in an anaerobic chamber (Coylab). Plate wash was performed following a previously described protocol (6) with minor modifications. Cell scrapers were used to collect cultivar into 1 mL of GBSS buffer. The plate wash solutions from four plates were combined into a single tube and mixed by vortexing. 50 µL of the combined solution was centrifuged at 6000× g for 10 minutes to pellet the cells. Genomic DNA was extracted using QiaAmp kit (Qiagen) and quantified by Quanti-it DNA high sensitivity quantification kit (Invitrogen). The experiment was carried out in triplicates. The volume of autoclaved luminal fluid was not enough to prepare plate medium; therefore we did not perform the bulk culture the sample with M2LC medium on agar plates.

Microbial Cultivation from the Biopsy with M2LC and M2GSC Medium and Performing Chip Wash

An aliquot of cecum brush sample was serially diluted in GBSS buffer and then in M2LC. 10⁴ dilution of the brush sample was loaded onto a 3,200 well SlipChip (loading volume of 18 µL and is consistent with sample used the plate wash) and incubated (model# 10-140E, Quincy lab Inc) for three days at 37 °C in an anaerobic chamber (Coylab). Chip wash was performed and the chip wash solution was centrifuged at 6000× g for 10 minutes to pellet the cells. Genomic DNA was extracted using QiaAmp minikit (Qiagen) and quantified by Quanti-it DNA high sensitivity quantification kit (Invitrogen). The experiment was carried out with triplicate devices.

Designing Primers for 16S V1V3 rRNA Gene for Miseq High Throughput Sequencing

We chose high-throughput sequencing for three reasons: First, high-throughput sequencing can be used to profile the community at great depth, and is cost-effective and less labor-intensive than cloning of universally amplified PCR product and Sanger sequencing; Second, compared with testing with primers targeting different groups of microbes, high-throughput sequencing is intrinsically multiplexed and can be used to detect multiple targets simultaneously. This feature is well suited for the “Most Wanted” list, as 45 high priority targets are defined for human gut microbiome. Third, designing and validating primers or probes for specific targets at the resolution of individual OTUs for a complex community from short reads can be challenging for non-experts, and high-throughput sequencing can be used to retrieve the target of interest before the effort for designing target-specific primers.

The primers for variable region V1V3 of 16S rRNA gene was designed similar to that of V4 region of 16s rRNA gene (8, 9). Primer Prospector (10) was used to design the linker region with reference sequences from Greengenes (11) February 2013 release. Possible interactions between barcodes and new pad and linker regions that may yield secondary structures were also screened with Primer Prospector.

16S rRNA Gene Library Construction for Miseq High Throughput Sequencing

The library was prepared according to published protocol. 20 ng of genomic DNA extracted from chip wash solution with M2LC medium or plate wash solutions with M2GSC medium were used in each 50 µL reaction mix. The mixture contained X µL of template DNA (adjusted to 20 ng), (13.5-X) µL of H₂O (Fisher Scientific, BP 2470), 20 µL of 5 Primer Hot MasterMix (5 prime: cat # 2200410), and 1 µL of Primer mix (10µM of Forward primer and barcoded Reverse primer). The PCR reaction was set up in triplicates and PCR product was purified by Agencourt AmPure XP beads (Beckman Coulter Inc, A63881) followed by Qiaquick PCR

purification kit (Qiagen). The purified PCR product was pooled in equal molar quantified by Kapa library quantification kit (Kapa Biosystems, KK4824) and sent for sequencing at GenoSeq Core of UCLA (Los Angeles, CA).

Data Analysis for High Throughput Sequencing of 16S V4 rRNA Gene

OTUs were chosen *de novo* with mothur (12) to identify candidate targets. The results were summarized as an OTU (Operational taxonomic unit) table. The OTU table from chip wash M2LC medium and plate wash with M2GSC medium was sub-sampled to 12599 reads per sample and summarized at genus level using QIIME (13). The relative abundance of each OTU from the two methods is presented in Fig. S4.

Data Analysis for High Throughput Sequencing of 16S V1V3 rRNA Gene

2×250 bp paired end reads were assembled using PANDASeq (14) and de-replicated with usearch (15). The de-replicated reads were sorted by abundance and clustered at 97% identity. Chimeric reads were detected using UCHIME (16) with both *de novo* and reference-based methods. The filtered reads were then searched against the HMP's "Most Wanted" list for targets within the identity of 97% using usearch v6.0.293. Alignment of the sequence from chip wash with the sequence of OTU158 from the most wanted list is shown in Fig. S5. Detailed scripts are provided in the SI below.

Using qPCR to Quantify Bacterial Genomic DNA from the Total Bacteria and OTU158

Primers for PCR were ordered from Integrated DNA Technologies (Coralville, IA). SsoFast EvaGreen Supermix (2X) was purchased from Bio-Rad Laboratories (Hercules, CA). 1.5 ng purified gDNA was used to prepare the reaction mixture of a total volume of 30 µL. Water (Fisher Scientific, BP 2470) was used as negative control. Universal primers for the V4 region of 16S rRNA gene (515F, 5'-GTGCCAGCMGCCGCGGTAA-3', 806R, 5'-GGACTACHVGGGTWTCTAAT-3') were used to quantify total bacterial load, and OTU158 specific primers (158F, 5'-AGA ATC TAC TGA AAG AGT TTT CGG A-3', 158R, 5'-TTC TAG AGG TAC CGT CTT CTG CT-3') were used to quantify the concentration of OTU158. The mixture was split into 3 aliquots and loaded onto the Eco real-time PCR machine (Illumina, Inc, San Diego, CA). Reactions were incubated for 2 min at 98 °C, followed by 40 cycles of 5 s at 98 °C, 3 s at 60 °C. Data analysis was performed using Eco software.

Using Splitting Technology and the On-chip PCR Method to isolate the bacterium: isolate microfluidicus 1

An aliquot of cecum brush sample was serially diluted in GBSS buffer and then in M2LC medium. 10⁴ dilution of the brush sample was loaded onto a 1,000 well replica-SlipChip (3) and incubated (model# 10-140E, Quincy lab Inc) for two days at 37 °C in an anaerobic chamber (Coylab). The replica-SlipChip was split as described in the accompanying paper (3), and on-chip PCR was performed and analyzed as described above with the following modification: The PCR reaction master mixture was prepared by mixing 150 µL of KAPA 2G Robust Hot Start Readymix (KAPA BIOSYSTEMS), 1.5 µL of forward and 1.5 µL of reverse primer (100 µmol L⁻¹), 15 µL of 10 µg mL⁻¹ BSA solution, and 94.5 µL of 2.5% (w/v) ultra-low gelling temperature agarose in water, and 7.5 µL of 40X SYBR green (Sigma-Aldrich). The staining of cell material with SYBR green was observed and could be used to estimate the number of microcolonies grown on device could be estimated. Microbes from the PCR-positive wells on the plate for sample preservation was retrieved as described in the accompanying paper (3), and plated on M2GSC plate. After two days of incubation, the cluster of colonies was used for both colony PCR and streaking additional plates.

16S rRNA Gene Analysis for isolate microfluidicus 1

Genomic DNA for PCR amplification was isolated using QiaAmp kit (Qiagen) following the manufacturer's protocol with the following modification. We added a bead-beating step using lysing matrix B (MP Biomedicals 6911-500) that was shaken using a Mini-Beadbeater-16 (BioSpec Products, Inc.) for 1 min. The 16S rRNA gene was amplified by PCR using AccuPrimer Pfx DNA polymerase (Invitrogen). Primers 8F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3') (17) were used for PCR amplification. PCR amplification was performed by Biorad thermocycler with 2 min incubation at 95 °C, followed by 34 cycles at 95 °C for 15s, 55 °C for 30s and 68 °C for 90s. Amplified PCR product was cloned into TOPO vector (Invitrogen) and transformed into TOPO10 *E. coli* cells (Invitrogen) on LB/Amp+ medium. The plates were incubated at 37 °C overnight and single colonies were picked for liquid culture. Plasmids were purified from cells using Qia miniprep kit (Qiagen). Plasmid DNA was then amplified by PCR with the same protocol as described above using M13F/M13R primers (Invitrogen). PCR products were purified using Qia quick PCR purification kit (Qiagen).

Sequencing PCR Products and Data Analysis

PCR products were sequenced by Laragen, Inc. (Culver City, CA) using T3 and T7 as sequencing primers (Invitrogen). The paired-end reads were assembled in Seqman Pro (DNASTAR) and manually trimmed to remove the adapters and PCR primers in Microsoft Word. 15 assembled sequences were aligned using muscle (18) and usearch (15).

TEM

TEM was performed in the Jensen laboratory electron microscopy facility at the California Institute of Technology with 200 mesh formvar/ carbon grids on TECNAI 120 keV TEM (FEI, Hillsboro, OR) equipped with a Gatan 2k by 2k CCD camera for image acquisition.

Optical Microscopy

Optical microscopy of the isolate was obtained by suspending the cells in PBS buffer and imaged using a 63×/1.2 NA Leica objective with a Leica DMI6000 microscope (Leica Microsystems) and a Hamamatsu ORCAER camera.

Ribosomal Database Project (RDP) classification of 16S rRNA gene of OTU158

Taxonomic assignment of the sequencing results for OTU158 (isolate microfluidicus 1) was generated using the online RDP classifier with 16S rRNA training set 9. The results are summarized below:

Classification on sequence of OTU158 retrieved from high throughput sequencing of V4 region of 16S rRNA gene:
Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Ruminococcaceae(100); Oscillibacter(100);

Classification on sequence of OTU158 retrieved from high throughput sequencing of V1V3 region of 16S rRNA gene:
Root(100);Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Ruminococcaceae(100);Oscillibacter(99);

Classification on sequence of two types of full length 16S rRNA gene of isolate microfluidicus 1 from Sanger sequencing:
Root(100%) Bacteria(100%) Firmicutes(100%) Clostridia(100%) Clostridiales(100%) Ruminococcaceae(100%) Oscillibacter(75%);
Root(100%) Bacteria(100%) Firmicutes(100%) Clostridia(100%) Clostridiales(100%) Ruminococcaceae(100%) Oscillibacter(84%);

Numbers in parentheses give the classification confidence level; threshold is 80%.

Phylogeny

Phylogenetic analyses of 16S rRNA gene sequences were performed using the software package ARB(19) as well as MrBayes (20). Automatic alignments of sequences obtained from our culture as well as from reference strains were manually refined within ARB. A consensus tree was constructed based on maximum-likelihood (ML) calculation (using the Hasegawa, Kishino and Yano substitution model), and by collapsing all nodes with parsimony bootstrap (5,000 iterations) support $\leq 50\%$ or Bayesian support below $\leq 70\%$. Conditions for Bayesian inference were as follows: 2 parallel runs; 1,000,000 tree generations; sample frequency 100; final split frequency 0.007; potential scale reduction factor 1.006; burnin of 25% of sample. For phylogenetic analyses only sequences of cultured members of the *Clostridia* for which the 16S rRNA sequence was available were considered. Using a manually designed sequence filter we excluded highly variable in-del positions from the analysis, resulting in 1,371 alignment positions for tree calculations.

Fluorescence *in situ* Hybridization

16S rRNA targeted FISH was carried out following established protocols (21). In brief, formaldehyde- and ethanol-fixed samples were hybridized at 46°C with FAM- and Cy3-labeled oligonucleotide probes for 16 hours in a formamide-containing humid chamber. To test whether cell wall digestion leads to an increase in fluorescence detection and/or labeling intensity, before hybridization samples were pre-treated with either (i) 10 mg mL⁻¹ lysozyme in TE buffer (1 h at 37°C in a humid chamber); (ii) 15 µg mL⁻¹ proteinase K in TE buffer (10 min at room temperature, *i.e.* 23°C) followed by 0.01 M HCl (10 min at 23°C); or (iii) a 1:1 mix of acetone:methanol (15 min at 23°C). Formamide concentrations in the hybridization buffer were as recommended: 20-35% for probe mix EUB338 I-III (22, 23) and control probe NonEUB338 (24); 35% for probe Arch915 (25); 20% for probe EUK516 (22). The two newly designed probes Clostr183-I (AAA GAT CAT GCG ACC TCT) and Clostr183-II (AAG AAT CAT GCG ACC CCT) were hybridized at 15% (at concentrations >20% we did not observe any fluorescence signal). Via competition for the same binding site, these probes are able to distinguish between the two 16S rRNA gene sequence types obtained from our culture. After hybridization, slides were washed for 10 min in pre-warmed washing buffer at 48°C. Then, they were dipped into pre-cooled deionized water (4°C) and dried using pressurized air. Slides were mounted with DAPI/Citifluor and analyzed using an Olympus BX51 epifluorescence microscope. Fluorescence images were analyzed using the software provided by the microscope manufacturer and ImageJ by the National Institutes of Health (<http://rsb.info.nih.gov/ij/download.html>). No unspecific labeling was observed when control probe NonEUB338 (9) was applied to our samples.

Whole Genome Sequencing

The genome of isolate microfluidicus 1 was sequenced on Illumina Hiseq 2000 and assembled using a combination of velvet (26) and GapCloser (27). We obtained 83 contigs with N50 length of 131 kbp.

Scripts for Identifying Targets from “Most Wanted” list from paired-end Miseq reads

```
File name: get_target_all
#!/bin/bash
#file created on Dec 2, 2012
#Author= “Liang Ma”
#Email= liangma.chem@gmail.com
# usage example: get_target_all ~/Downloads/reads/
#set environmental variables
#usearch program
export u=/Users/Liang/scripts/usearch/usearch6.0.293_i86osx32_lm
#reference database for UCHIME
export UCHIME_REFUDB=/Users/Liang/scripts/Database/gold.fa
# fasta file of consensus sequence from most wanted list, high priority group
export MostWanted=/Users/Liang/scripts/Database/MostWanted.fa
export scriptsHome=/Users/Liang/scripts
# $1 is the folder containing fastq files with paired end reads
cd $1
for file in $(ls| grep .*R1.*\.fastq)
do
FN=$(echo $file|grep -o .*R)
FileR="$FN"2_001.fastq
#assemble reads with pandaseq
pandaseq -f $file -r $FileR -o 10 > "$FN.fa"
$u -derep_fulllength $FN.fa -output "derep_$FN.fa".fa -sizeout
readname='results'
mkdir -p $FN$readname
cd $FN$readname
$scriptsHome/get_target1 ../derep_$FN.fa.fa"
cd $1
done
```

```
File name: get_target1
#!/bin/bash
#file created on Dec 2, 2012
#Author= “Liang Ma”
#Email= liangma.chem@gmail.com
# usage example: get_target1 reads.fa
if [ x$1 == x ] ; then
    echo Missing FASTA filename >> /dev/stderr
    exit 1
fi
if [ x$UCHIME_REFUDB == x ] ; then
    echo Must set \${UCHIME_REFUDB} >> /dev/stderr
    exit 1
fi
if [ x$MostWanted == x ] ; then
    echo Must set \${MostWanted} >> /dev/stderr
    exit 1
fi
# Sort by decreasing size
$u -sortbysize $1 -output bysize.fa
#cluster at 97% identity
$u -cluster_smallmem bysize.fa -id 0.97 -sizein -sizeout -centroids 97.fa
# Chimera filter with UCHIME de novo
$u -uchime_denovo 97.fa -chimeras ch.fa -nonchimeras nonch.fa -uchimeout denovo.uchime
# Chimera filter with UCHIME ref
$u -uchime_ref nonch.fa -db $UCHIME_REFUDB -nonchimeras filtered.fa -strand plus -uchimeout ref.uchime
# find hits with MostWanted list
$u -usearch_global filtered.fa -db $MostWanted -id 0.97 -strand plus -fastapairs mostwanted.fastapairs
```

> Sequence of *rrnA* of 16S rRNA gene of isolate microfluidicus 1

GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAGAATCTACTGAAAGAGGATTCGTCCACGGAAGTAGAGGAAAGTGCCGGACGGGT
 GAGTAACGCGTGAGGAACCTGCCTTGAAGAGGGGGACAACAGTTGGAAACGACTGCTAATACCGCATGACGCATAGAGGGTCGCATGATTCTTATGCCA
 AAGATTTATCGCTTCAAGATGGCCCTCGCGTCTGATTAGTAGTTGGCGGGGTAACGGCCCAACAGGCGACGATCAGTAGCCGGACTGAGAGGTTGAA
 CGGCCACATTGGGACTGAGATACGGCCAGACTCTACGGGAGGCAGCAGTGGGGAATATTGGCAATGGGCGCAAGCCTGACCCAGCAACGCCGCG
 TGAAGGAAGAAGGCTTTCGGGTTGTAAACTTCTTTTAAGAGGGAAGAGCAGAAGACGGTACCTCTAGAATAAGCCACGGCTAACTACGTGCCAGCAGC
 CGCGGTAATACGTAGGTGCAAGCGTTGTCCGATTTACTGGGTGTAAAGGCGTGCAGCCGGGTCTGCAAGTCAGATGTGAAATCCATGGGCTCAAC
 CCATGAACTGCATTTGAAACTGTAGATCTTGAGTGTGCGAGGGGCAATCGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCA
 GTGGCGAAGGCGGATTGCTGGACGATAACTGACGGTGAGGCGCGAAAGTGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCACACTGTAAACG
 ATGAATACTAGGTGTGCGGGGACTGACCCCTGCGTGCCGAGTAAACACAATAAGTATTCCACCTGGGGAGTACGATCGCAAGGTTGAAACTCAAAG
 GAATTGACGGGGGCCCCGACAAAGCGGTGGATTATGTGGTTAATTCCAAGCAACGCGAAGAACCTTACCAGGGTTTGACATCTGTAAACGAAGTAGA
 GATACATTAGGTGCCCTTCGGGGAAAGCAGAGACAGGTGGTGCATGGTTGTCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGC
 AACCCCTATTGTTAGTTGCTACGCAAGAGCACTACTAGCAGACTGCCGTTGACAAAACGGAGGAAGGTGGGGACGACGTCAAATATCATGCCCTTA
 TATCTGGGCTACACAGTAATAACAATGCGGCTAACAGAGGGAAGCAAAGCCGCGAGGCAGAGCAAAACCCCAAAAGCCGTCACGTTCCGATTGT
 AGGCTGCAACTCGCCTGCATGAAGTCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGCGCTTGTACACACCCCGCTCA
 CACCATGAGAGTCGGGAACACCCGAAGTCCGTAGCCTAACCTGAAAAAGGAGGGCGCGGCCGAAGGTGGGTTGATAATTGGGGTG

> Sequence of *rrnB* of 16S rRNA gene of isolate microfluidicus 1

GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAGAATCTACTGAAAGAGTTCGACAAATGGAAGTAGAGGAAAGTGCCGGACGGGT
 GAGTAACGCGTGAGGAACCTGCCTTGAAGAGGGGGACAACAGTTGGAAACGACTGCTAATACCGCATGACGCATAGAGGGTCGCATGATTCTTATGCCA
 AAGATTTATCGCTTCAAGATGGCCCTCGCGTCTGATTAGTAGTTGGCGGGGTAACGGCCCAACAGGCGACGATCAGTAGCCGGACTGAGAGGTTGAA
 CGGCCACATTGGGACTGAGATACGGCCAGACTCTACGGGAGGCAGCAGTGGGGAATATTGGCAATGGGCGCAAGCCTGACCCAGCAACGCCGCG
 TGAAGGAAGAAGGCTTTCGGGTTGTAAACTTCTTTTAAGAGGGAAGAGCAGAAGACGGTACCTCTAGAATAAGCCACGGCTAACTACGTGCCAGCAGC
 CGCGGTAATACGTAGGTGCAAGCGTTGTCCGATTTACTGGGTGTAAAGGCGTGCAGCCGGGTCTGCAAGTCAGATGTGAAATCCATGGGCTCAAC
 CCATGAACTGCATTTGAAACTGTAGATCTTGAGTGTGCGAGGGGCAATCGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCA
 GTGGCGAAGGCGGATTGCTGGACGATAACTGACGGTGAGGCGCGAAAGTGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCACACTGTAAACG
 ATGAATACTAGGTGTGCGGGGACTGACCCCTGCGTGCCGAGTAAACACAATAAGTATTCCACCTGGGGAGTACGATCGCAAGGTTGAAACTCAAAG
 GAATTGACGGGGGCCCCGACAAAGCGGTGGATTATGTGGTTAATTCCAAGCAACGCGAAGAACCTTACCAGGGTTTGACATCTGTAAACGAAGTAGA
 GATACATTAGGTGCCCTTCGGGGAAAGCAGAGACAGGTGGTGCATGGTTGTCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGC
 AACCCCTATTGTTAGTTGCTACGCAAGAGCACTACTAGCAGACTGCCGTTGACAAAACGGAGGAAGGTGGGGACGACGTCAAATATCATGCCCTTA
 TATCTGGGCTACACAGTAATAACAATGCGGCTAACAGAGGGAAGCAAAGCCGCGAGGCAGAGCAAAACCCCAAAAGCCGTCACGTTCCGATTGT
 AGGCTGCAACTCGCCTGCATGAAGTCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGCGCTTGTACACACCCCGCTCA
 CACCATGAGAGTCGGGAACACCCGAAGTCCGTAGCCTAACCTGAAAAAGGAGGGCGCGGCCGAAGGTGGGTTGATAATTGGGGTG

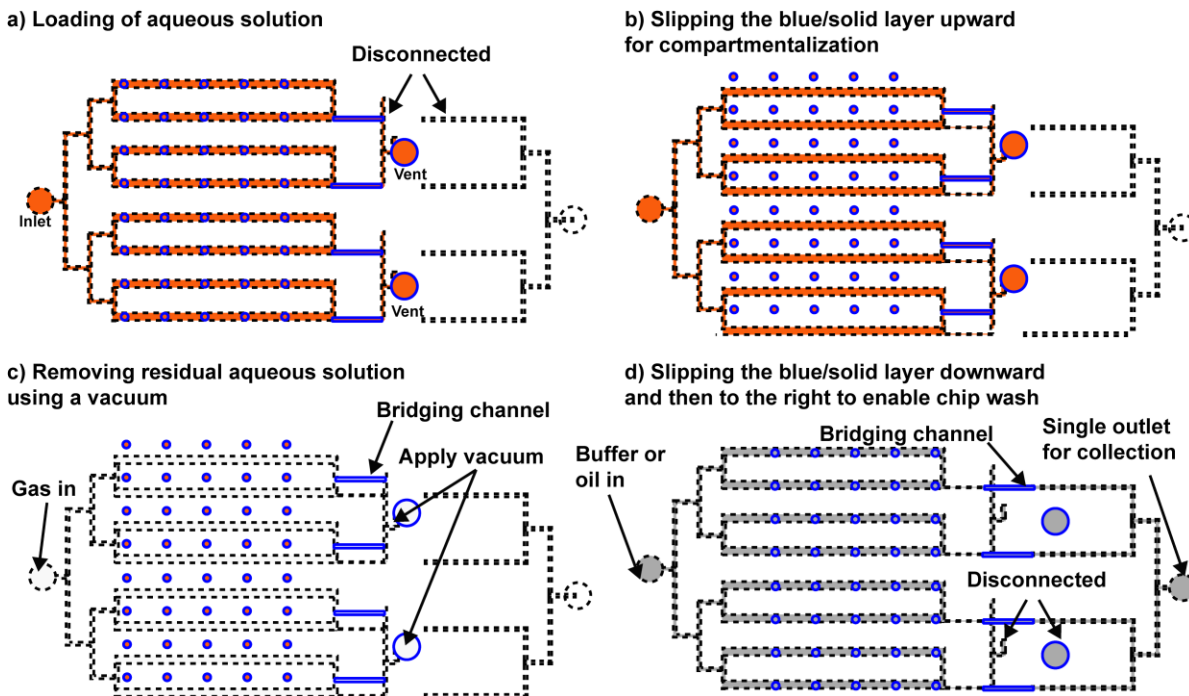


Fig. S1 Illustration of operation of the device showing how the bridging channels, vents and outlet for collection were used during chip wash. This schematic drawing uses a simplified design with fewer wells to illustrate the principle.

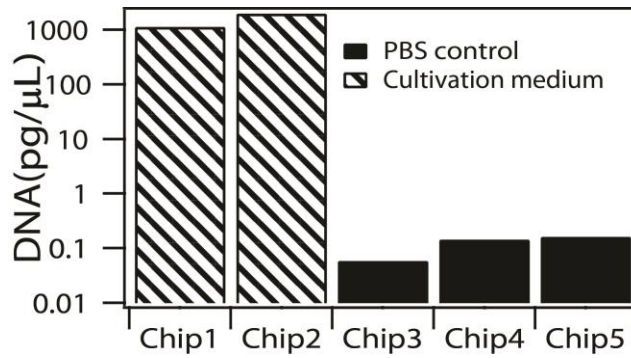


Fig. S2 Validation of the chip wash method with a model microorganism, *E. coli*. *E. coli* cells were loaded onto SlipChip with either medium for cultivation or a PBS buffer that does not support growth of cells. The cultivar was collected by chip wash method and DNA was extracted and quantified using qPCR. A 10,000-fold increase in the amount of DNA was observed between the condition that supports growth of *E. coli* vs. the non-growth control.

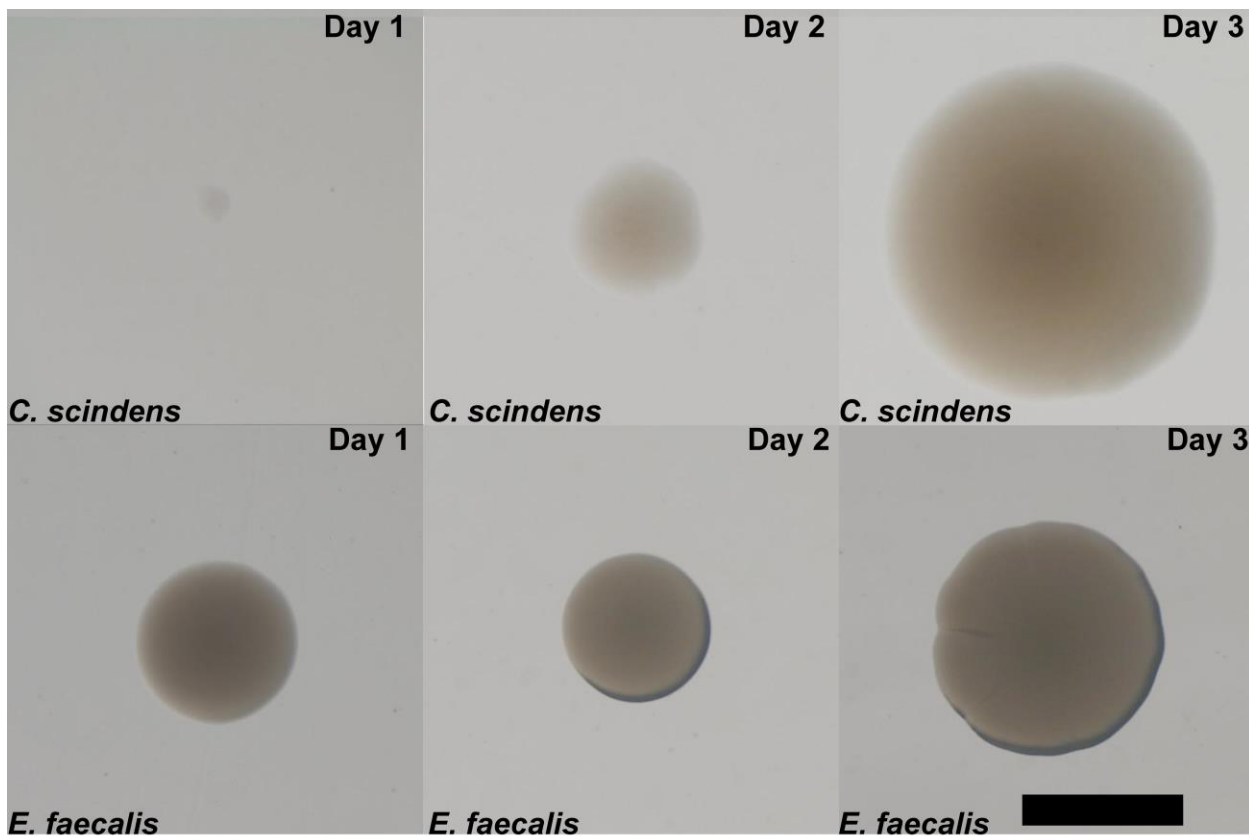
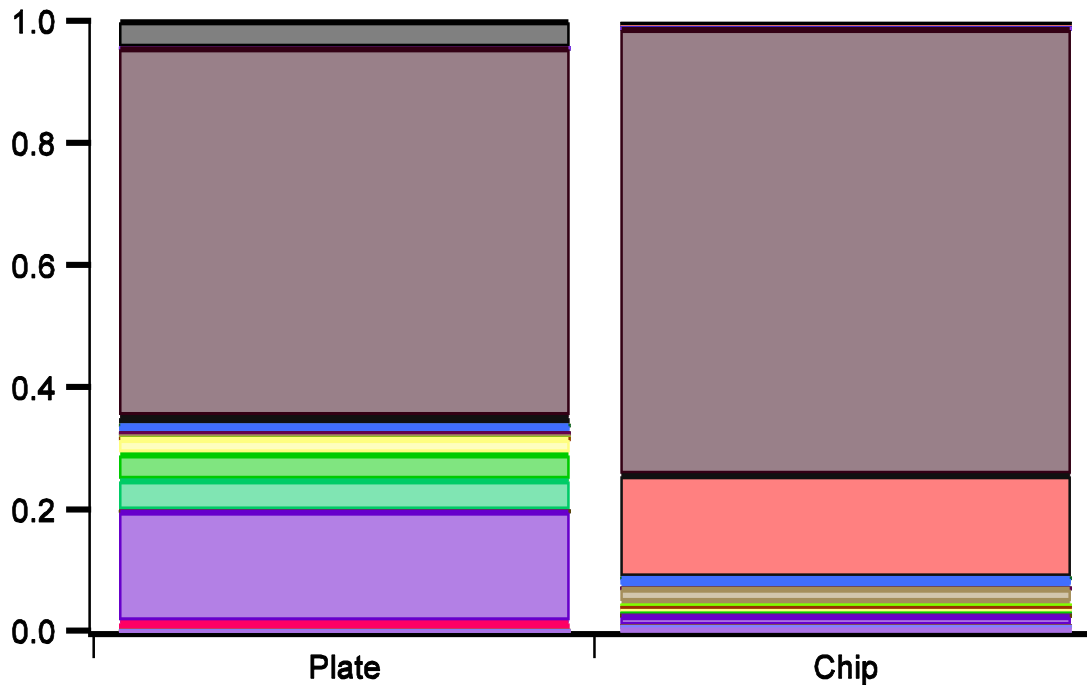


Fig. S3 Photograph showing time series of growth of *Clostridium scindens* and *Enterococcus faecalis* on agar plate. Scale bar is 1 mm.



- Bacteria;Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium
- Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;Collinsella
- Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;Eggerthella
- Bacteria;Actinobacteria;Actinobacteria;Coriobacteriales;Coriobacteriaceae;Gordonibacter
- Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Anaerorhabdus
- Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides
- Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Parabacteroides
- Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;unclassified;unclassified
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Anaerostipes
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Blautia
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Clostridium_XIVa
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Clostridium_XIVb
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Coproccoccus
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Dorea
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiracea_incertae_sedis
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia
- Bacteria;Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;unclassified
- Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Faecalibacterium
- Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Flavonifractor
- Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Oscillibacter
- Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;Subdoligranulum
- Bacteria;Firmicutes;Clostridia;Clostridiales;Ruminococcaceae;unclassified
- Bacteria;Firmicutes;Clostridia;Clostridiales;unclassified;unclassified
- Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Clostridium_XVIII
- Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Coproccoccus
- Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;unclassified
- Bacteria;Firmicutes;Negativicutes;Selenomonadales;Veillonellaceae;Dialister
- Bacteria;Firmicutes;unclassified;unclassified;unclassified;unclassified
- Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas
- Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Silanimonas
- Bacteria;unclassified;unclassified;unclassified;unclassified;unclassified

Fig. S4 Bar chart of relative abundance of OTUs grouped at genus level from 16S rDNA V4 high throughput sequencing of chip wash cultivar with M2LC and plate wash cultivar with M2GSC. We observed that more *Clostridium XIII* and *Bifidobacterium* can be observed from the plate wash solution, while some members such as *Gordonibacter*, *Anaerostipes*, *Oscillibacter* and *Silanimonas* can only be observed from chip wash method.

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ACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAGAATCTACTGAAAGAGTTTTCGG
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|
ACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAGAATCTACTGAAAGAGTTTTCGG
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|
ACAATGGAAGTAGAGGAAAGTGGCGGACGGGTGAGTAACGCGTGAGGAACCTGCCTTGAA
|
|
|
ACAATGGAAGTAGAGGAAAGTGGCGGACGGGTGAGTAACGCGTGAGGAACCTGCCTTGAA
|
|
|
GAGGGGGACAACAGTTGAAACGACTGCTAATACCGCATGACGCATAGGGGTCGCATGAT
|
|
|
GAGGGGGACAACAGTTGAAACGACTGCTAATACCGCATGACGCATAGAGGTCGCATGAT
|
|
|
TTTTATGCCAAAGATTTATCGCTGAAAGATGGCCTCGCGTCTGATTAGCTAGTTGGTGGG
|
|
|
CTTTATGCCAAAGATTTATCGCTTCAAGATGGCCTCGCGTCTGATTAGCTAGTTGGCGGG
|
|
|
GTAACGGCCACCAAGGCGACGATCAGTAGCCGGACTGAGAGGTTGAACGGCCACATTGG
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GTAACGGCCACCAAGGCGACGATCAGTAGCCGGACTGAGAGGTTGAACGGCCACATTGG
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GACTGAGATACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGGCAATGGGC
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|
GACTGAGATACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGGCAATGGGC
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|
GCAAGCCTGACCCAGCAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAACCTCTTT
|
|
|
GCAAGCCTGACCCAGCAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAACCTCTTT
|
|
|
TAAGAGGGAAGAGCAGAAGACGGTACCTCTAGAATAAGCCACGGCTAACTACGTG
|
|
|
TAAGAGGGAAGAGCAGAAGACGGTACCTCTAGAATAAGCCACGGCTAACTACGTG

```

TOP: Consensus sequence from member OTU_158_V1V3 of Most Wanted list

BOTTOM: Consensus sequence from chip wash 16s rDNA V1V3 survey

Fig. S5 Identifying OTU158 from high throughput sequencing of V1V3 region of 16S rRNA gene of the chip wash solution. The sequence retrieved from high throughput sequencing aligned well with the consensus sequence of OTU158 from HMP's "Most Wanted" list.

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GGGTGAGTAACGCGTGAGGAACCTGCCTTGAAGAGGGGGACAACAGTTGAAACGACTGC
|
|
|
GGGTGAGT-ACGCGTGAGGAACCTGCCTTGAAGAGGGGGACAACAGTTGAAACGACTGC
|
|
|
TAATACCGCATGACGCATAGGGGTCGCATGATTTTTATGCCAAAGATTTATCGCTGAAAG
|
|
|
TAATACCGCATGACGCATAGAGGTGCGATGATCTTTATGCCAAAGATTTATCGCTTCAAG
|
|
|
ATGGCCTCGCGTCTGATTAGCTAGTTGGTGGGGTAACGGCCACCAAGGCGACGATCAGT
|
|
|
ATGGCCTCGCGTCTGATTAGCTAGTTGGCAGGGTAACGGCCACCAAGGCGACGATCAGT
|
|
|
AGCCGGACTGAGAGGTTGAACGGCCACATTGGGACTGAGATACGGCCAGACTCCTACGG
|
|
|
AGCCGGACTGAGAGGTTGAACGGCCACATTGGGACTGAGATACGGCCAGACTCCTACGG
|
|
|
GAGGCAGCAGTGGGGAATATTGGGCAATGGGCGAAGCCTGACCCAGCAACGCCGCGTGA
|
|
|
GAGGCAGCAGTGGGGAATATTGGGCAATGGGCGAAGCCTGACCCAGCAACGCCGCGTGA
|
|
|
AGGAAGAAGGCTTTCGGGTTGTAACCTCTTTAAGA
|
|
|
AGGAAGAAGGCTTTCGGGTTGTAACCTCTTTAAGA

```

TOP: Consensus sequence from member OTU_158_V1V3 of Most Wanted list

BOTTOM: Partial sequence from chip wash PCR with primers targeting OTU_158_V1V3

Fig. S6 Validating species specific primers for OTU158 by Sanger sequencing. The sequence retrieved from Sanger sequencing aligned well with the consensus sequence of OTU158 from HMP's "Most Wanted" list.

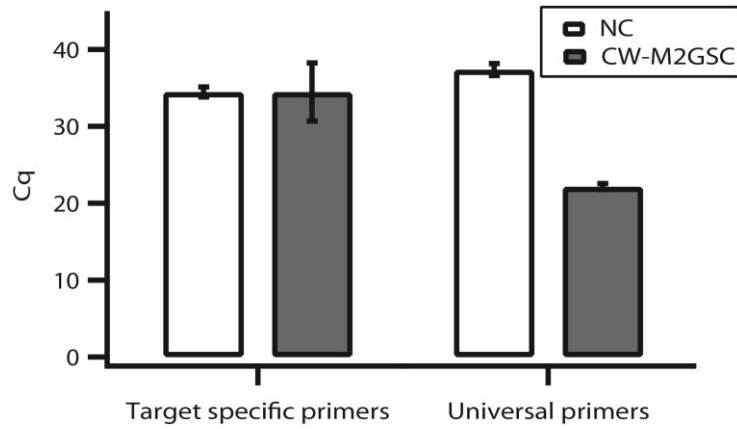


Fig. S7 qPCR with target specific primers (left) showing that the target was not present in chip wash solution of M2GSC nor in the blank negative control; Universal primers of 16s rDNA (right) showed that both chip wash contained bacterial genomic DNA and had a lower Cq value than the blank negative control. NC is negative control, and CW-M2GSC is chip wash with M2GSC medium.

**Partial sequence
from PCR product
of OTU-158 specific primers
with scale-up culture**

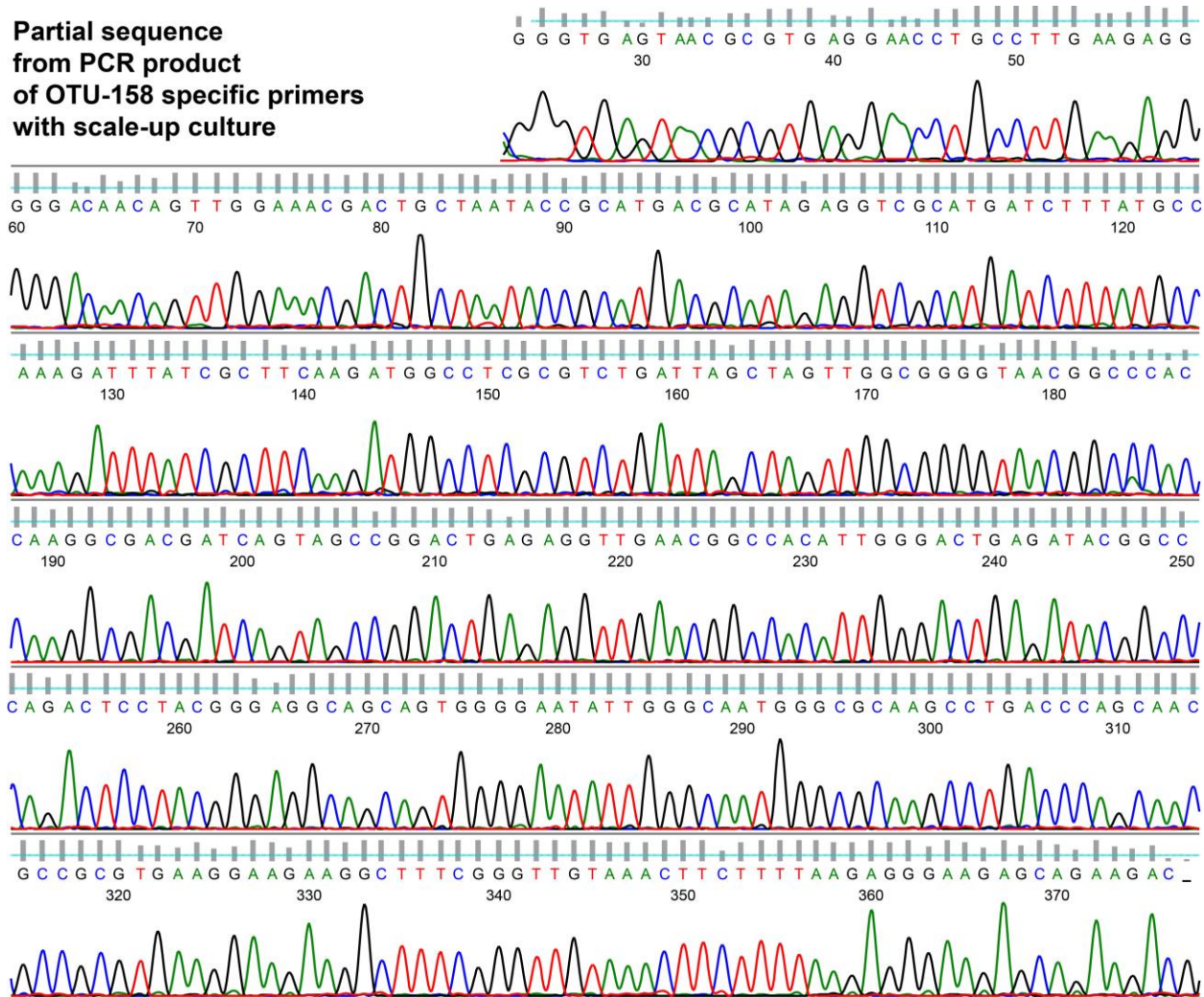


Fig. S8 Chromatogram from Sanger sequencing of positive PCR product of the first scale-up culture with target-specific primers.

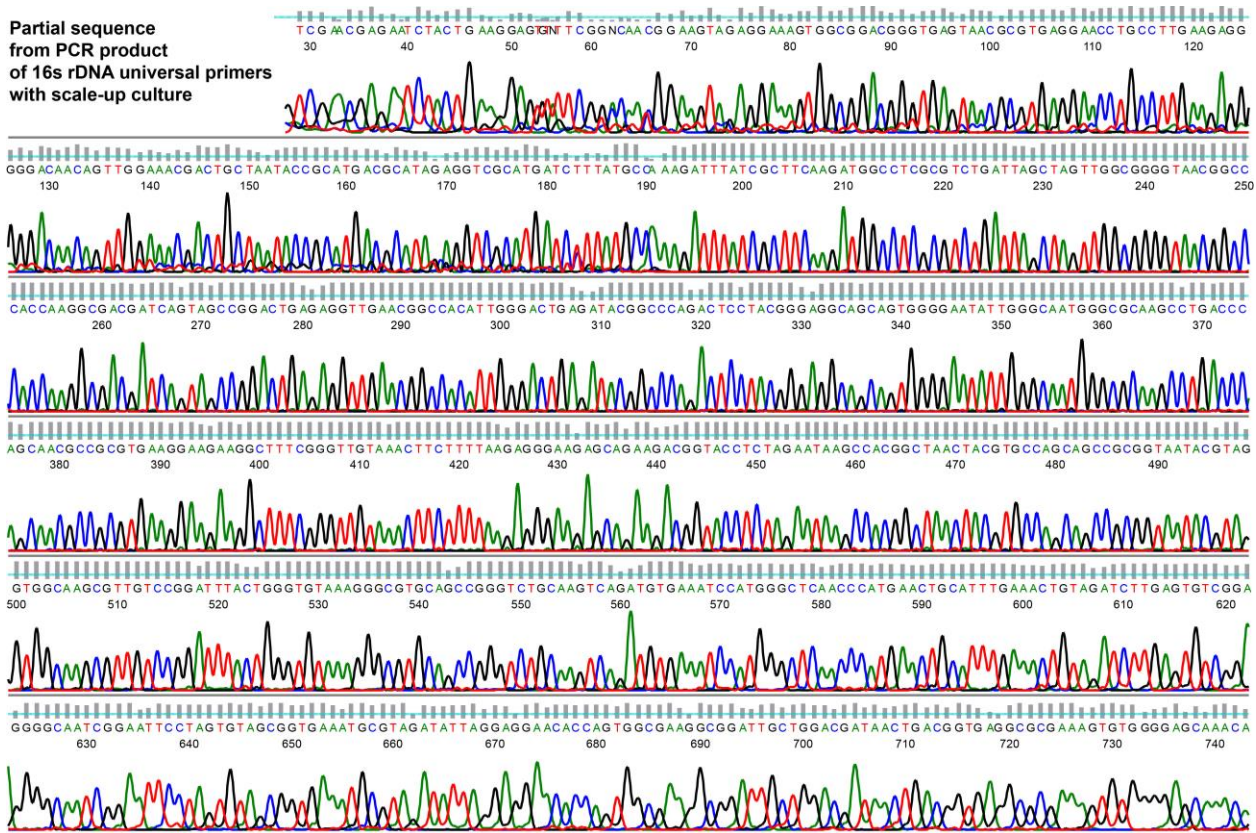


Fig. S9 Validating the scale-up colonies from the splitting SlipChip approach by Sanger sequencing of the positive PCR product of the first scale-up culture using universal primers. No contamination was observed, with minor heterogeneity at the beginning of the chromatogram.

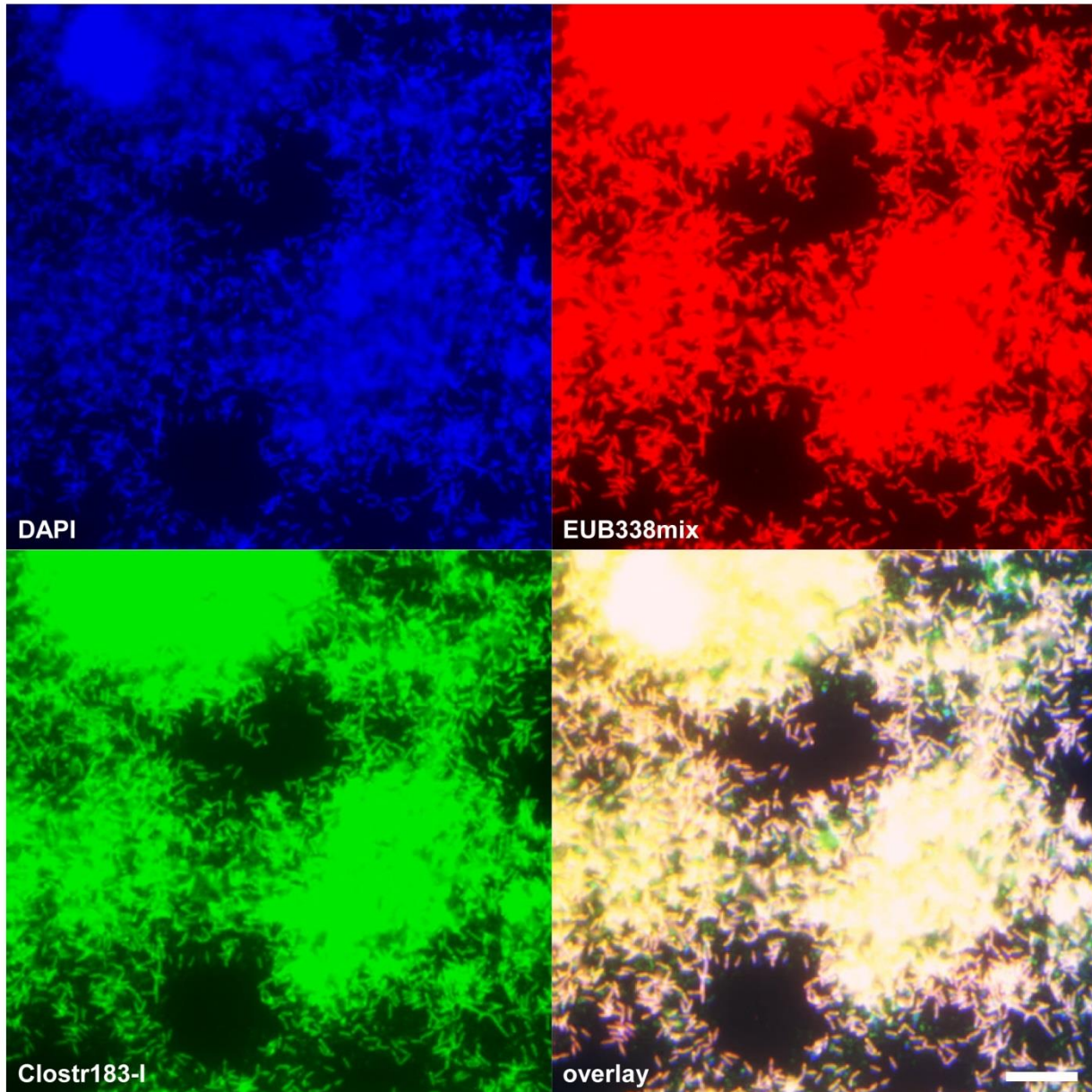


Fig. S10 FISH visualization of bacterial cells within pure culture of isolate microfluidicus 1. All cells detected by the general bacterial probe mix EUB338 I-III are also detected via the newly designed Clostr183-I probe, targeting isolate microfluidicus 1. While some cells (as identified by DAPI) did not bind any of these two probes, no archaea or eukaryotes were detected. Thus, FISH-negative cells are likely sporulating cells with substantially decreased ribosome content as compared to log-phase cells. Scale bar is 10 μm .

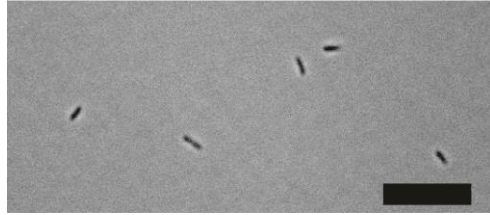


Fig. S11 Optical microscopy of isolate microfluidicus 1. Scale bar is 20 μm .

Detailed Contribution Description

LM and RFI designed the experiment as described in Figure 1. LM designed, performed experiments, and analyzed the data in Figures 2, 4, and 5. LM and JK designed, performed experiments, and analyzed the data in Figure 3. RH designed and performed FISH experiments and phylogenetic analyses for Figure 6, wrote the corresponding Results and Discussion and Supporting Information sections, and helped to edit the paper. NH was involved in clinical specimen acquisition and preparation in Figure 5A. IH performed all procedures for clinical specimen acquisition in Figure 5A. EC designed the study and clinical operations in Figure 5A. MK helped with device infrastructure and performed the experiment in SI Figure 11.

Table S1

#metadata of OTU_158_V1V3 and OTU_896_V1V3, retrieved from http://www.hmpdacc.org/most_wanted/ on Apr 27, 2012

| otuID | otu_158_V1V3 | otu_896_V1V3 |
|----------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| priorityGroup | HIGH PRIORITY/MOST WANTED | HIGH PRIORITY/MOST WANTED |
| variableRegion | V1V3 | V1V3 |
| count454 | 14888 | 788 |
| consensusLength | 475 | 463 |
| consensusSequence | ACGCTGGCGGCGTGCTTAACACATGCAAGTCGA ACGAGAATCTACTGAAAGAGTTTTTCGGACAATG GAAGTAGAGGAAAGTGGCGGACGGTGAGTA ACGCGTGGGAAACCTGCCTTGAAGAGGGGGAC AACAGTTGGAAACGACTGCTAATACCCGATGAC GCATAGGGGTGCGCATGATTTTTATGCCAAAGAT TTATCGCTGAAAGATGGCCTCGCTGCTGATTAG CTATGTTGGGGTAAACGCGCCCAAGGGCGA CGATCAGTAGCCGACTGAGAGGTTGAACGGC CACATTGGGACTGAGATACGGCCAGACTCCTA CGGGAGGCAGCAGTGGGAATATTGGCAATG GGCGCAAGCCTGACCAGCAACGCCGCGTGAAG GGAAGAAAGGCTTTGGGGTTGTAACCTCTTTA AGAGGGAAGAGCAGAAGACGGTACCTCTAGAA TAAGCCACGGCTAACTACGTG | TGCTTAACACATGCAAGTCGAACGAGAATCTGCTG AAGGAGGATTCGTCCAACGGAAGTAGAGGAAAGT GGCGGACGGTGAGTAACCGCTGAGGAACCTGCC TTGAAGAGGGGGACAACAGTTGAAACGACTGCT AATACCGCATGACGCATAGGGGTGCGCATGATCTTT ATGCCAAAGATTTATCGCTCAAGATGGCCTCGCG TCTGATTAGCTGTTGGCGGGTAACGGCCCA AGGCGACGATCAGTAGCCGACTGAGAGGTTGAA CGGCCACATTGGGACTGAGATACGGCCAGACTCC TACGGGAGGCAGCAGTGGGAATATTGGCAATG GGCGCAAGCCTGACCAGCAACGCCGCGTGAAG AAGAAGGCTTTGGGGTTGTAACCTCTTTAAGAG GGAAGAGCAGAAGACGGTACCTCTAGAA ACGGCTAACTACGTG |
| rdpSummary | Root(100);Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Ruminococcales(100);Oscillibacter(99) | Root(100);Bacteria(100);Firmicutes(100);Clostridia(100);Clostridiales(100);Ruminococcales(100);Oscillibacter(94) |
| UCHIMERefScore | 0.038 | 0.0612 |
| UCHIMEDenovoScore | 0 | 0.1856 |
| maxUCHIMEScore | 0.038 | 0.1856 |
| UCHIMEVerdict | neither | neither |
| toGoldGlobalPercentIdentity | 90.59 | 88.44 |
| toGoldGlobalBestHit | 249174 | 32020 |
| toGoldHumanGlobalPercentIdentity | 87.29 | 88.44 |

| | | |
|------------------------------------------|-----------|-----------|
| toGoldHumanGlobalBestHit | 804634 | 32020 |
| toHMPStrainsGlobalPercentIdentity | 87.29 | 88.44 |
| toHmpStrainsGlobalBestHit | 804634 | 32020 |
| toSilvaGlobalPercentIdentity | 98.95 | 99.78 |
| toSilvaGlobalBestHit | Uni08zxx | Uni022fr |
| toGreengenesNamedGlobalPercentIdentity | 92.45 | 91.61 |
| toGreengenesNamedGlobalBestHit | 607206 | 607206 |
| toGreengenesUnnamedGlobalPercentIdentity | 91.08 | 91.16 |
| toGreengenesUnnamedGlobalBestHit | 244027 | 812374 |
| maxFraction | 0.6979866 | 0.3489933 |
| maxFractionBodyHabitat | Stool | Stool |
| 454_seqCounts_Stool | 13561 | 709 |
| 454_seqCounts_Buccal mucosa | 8 | 3 |
| 454_seqCounts_Hard palate | 37 | 1 |
| 454_seqCounts_Keratinized gingiva | 3 | 0 |
| 454_seqCounts_Palatine Tonsils | 6 | 0 |
| 454_seqCounts_Saliva | 11 | 0 |
| 454_seqCounts_Subgingival plaque | 0 | 0 |
| 454_seqCounts_Supragingival plaque | 0 | 0 |
| 454_seqCounts_Throat | 19 | 1 |
| 454_seqCounts_Tongue dorsum | 0 | 2 |
| 454_seqCounts_Anterior nares | 161 | 6 |
| 454_seqCounts_L_Antecubital fossa | 364 | 15 |
| 454_seqCounts_L_Retroauricular crease | 112 | 8 |
| 454_seqCounts_R_Antecubital fossa | 341 | 37 |
| 454_seqCounts_R_Retroauricular crease | 204 | 6 |
| 454_seqCounts_Mid vagina | 7 | 0 |
| 454_seqCounts_Posterior fornix | 10 | 0 |
| 454_seqCounts_Vaginal introitus | 44 | 0 |
| 454_seqCounts_positive | 0 | 0 |
| 454_seqCounts_water | 0 | 0 |
| 454_subjectCounts_Stool | 104 | 52 |
| 454_subjectCounts_Buccal mucosa | 5 | 2 |
| 454_subjectCounts_Hard palate | 9 | 1 |

| | | |
|----------------------------------------------|-------------|-------------|
| 454_subjectCounts_Keratinized gingiva | 3 | 0 |
| 454_subjectCounts_Palatine Tonsils | 4 | 0 |
| 454_subjectCounts_Saliva | 6 | 0 |
| 454_subjectCounts_Subgingival plaque | 0 | 0 |
| 454_subjectCounts_Supragingival plaque | 0 | 0 |
| 454_subjectCounts_Throat | 3 | 1 |
| 454_subjectCounts_Tongue dorsum | 0 | 1 |
| 454_subjectCounts_Anterior nares | 18 | 3 |
| 454_subjectCounts_L_Antecubital fossa | 22 | 6 |
| 454_subjectCounts_L_Retroauricular crease | 13 | 3 |
| 454_subjectCounts_R_Antecubital fossa | 21 | 5 |
| 454_subjectCounts_R_Retroauricular crease | 11 | 1 |
| 454_subjectCounts_Mid vagina | 2 | 0 |
| 454_subjectCounts_Posterior fornix | 2 | 0 |
| 454_subjectCounts_Vaginal introitus | 9 | 0 |
| 454_subjectCounts_positive | 0 | 0 |
| 454_subjectCounts_water | 0 | 0 |
| 454_subjectfractions_Stool | 0.6979866 | 0.3489933 |
| 454_subjectfractions_Buccal mucosa | 0.035714287 | 0.014285714 |
| 454_subjectfractions_Hard palate | 0.06666667 | 0.007407407 |
| 454_subjectfractions_Keratinized gingiva | 0.021276595 | 0 |
| 454_subjectfractions_Palatine Tonsils | 0.028368793 | 0 |
| 454_subjectfractions_Saliva | 0.045801528 | 0 |
| 454_subjectfractions_Subgingival plaque | 0 | 0 |
| 454_subjectfractions_Supragingival plaque | 0 | 0 |
| 454_subjectfractions_Throat | 0.022222223 | 0.007407407 |
| 454_subjectfractions_Tongue dorsum | 0 | 0.006896552 |
| 454_subjectfractions_Anterior nares | 0.1294964 | 0.021582734 |
| 454_subjectfractions_L_Antecubital fossa | 0.16058394 | 0.04379562 |
| 454_subjectfractions_L_Retroauricular crease | 0.084415585 | 0.019480519 |
| 454_subjectfractions_R_Antecubital fossa | 0.15 | 0.035714287 |
| 454_subjectfractions_R_Retroauricular crease | 0.07096774 | 0.006451613 |
| 454_subjectfractions_Mid vagina | 0.02739726 | 0 |
| 454_subjectfractions_Posterior fornix | 0.028169014 | 0 |

| | | |
|----------------------------------------------|-------------|----------|
| 454_subjectfractions_Vaginal introitus | 0.13235295 | 0 |
| 454_subjectfractions_positive | 0 | 0 |
| 454_subjectfractions_water | 0 | 0 |
| 454_RelativeAbundanceStool | 0.007333881 | 3.07E-04 |
| 454_RelativeAbundanceBuccal mucosa | 0.00000398 | 9.16E-07 |
| 454_RelativeAbundanceHard palate | 0.0000995 | 9.62E-07 |
| 454_RelativeAbundanceKeratinized gingiva | 0.00000379 | 0 |
| 454_RelativeAbundancePalatine Tonsils | 0.00000542 | 0 |
| 454_RelativeAbundanceSaliva | 0.0000109 | 0 |
| 454_RelativeAbundanceSubgingival plaque | 0 | 0 |
| 454_RelativeAbundanceSupragingival plaque | 0 | 0 |
| 454_RelativeAbundanceThroat | 0.0000492 | 7.04E-07 |
| 454_RelativeAbundanceTongue dorsum | 0 | 8.48E-07 |
| 454_RelativeAbundanceAnterior nares | 0.00013 | 5.07E-06 |
| 454_RelativeAbundanceL_Antecubital fossa | 0.000338 | 8.00E-06 |
| 454_RelativeAbundanceL_Retroauricular crease | 0.000153 | 4.02E-06 |
| 454_RelativeAbundanceR_Antecubital fossa | 0.000878 | 3.11E-05 |
| 454_RelativeAbundanceR_Retroauricular crease | 0.0001 | 9.22E-07 |
| 454_RelativeAbundanceMid vagina | 0.00000316 | 0 |
| 454_RelativeAbundancePosterior fornix | 0.00000454 | 0 |
| 454_RelativeAbundanceVaginal introitus | 0.0000574 | 0 |
| 454_RelativeAbundancepositive | 0 | 0 |
| 454_RelativeAbundancewater | 0 | 0 |

Table S2

searching for 16S rRNA gene of
 Caecococcus microfluidicus isolated in
 this paper in nr database by BLAST
 # Database: nr
 # Fields: subject ids, % identity,
 alignment length, mismatches, gap
 opens, q. start, q. end, s. start, s. end,
 evalue, bit score

#apply filter: percent identity greater or equal to 97%, and alignment length greater or equal to 250

| | | | | | | | | | | |
|----------------------------|-------|------|---|---|---|------|----|------|---|------|
| gi 319500066 gb HQ792927.1 | 99.86 | 1453 | 2 | 0 | 1 | 1453 | 1 | 1453 | 0 | 2673 |
| gi 261261403 gb GQ897250.1 | 99.72 | 1453 | 4 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2662 |
| gi 261261244 gb GQ897091.1 | 99.72 | 1453 | 4 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2662 |
| gi 126112143 gb EF401832.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111973 gb EF401662.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111971 gb EF401660.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111482 gb EF401171.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111445 gb EF401134.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111306 gb EF400995.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111276 gb EF400965.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 126111154 gb EF400843.1 | 99.66 | 1453 | 5 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2656 |
| gi 261261148 gb GQ896995.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2651 |
| gi 126112165 gb EF401854.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2651 |
| gi 126111704 gb EF401393.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2651 |
| gi 126111580 gb EF401269.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2651 |
| gi 126111559 gb EF401248.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2651 |
| gi 126111536 gb EF401225.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2651 |
| gi 126111075 gb EF400764.1 | 99.59 | 1453 | 6 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2651 |
| gi 319493440 gb HQ786301.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 1 | 1453 | 0 | 2645 |
| gi 261261697 gb GQ897544.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2645 |
| gi 261261684 gb GQ897531.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2645 |
| gi 261261500 gb GQ897347.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2645 |
| gi 261261113 gb GQ896960.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2645 |

| | | | | | | | | | | |
|----------------------------|-------|------|----|---|----|------|----|------|---|------|
| gi 126115125 gb EF404805.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2645 |
| gi 126111760 gb EF401449.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2645 |
| gi 126111328 gb EF401017.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2645 |
| gi 126111235 gb EF400924.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2645 |
| gi 126111138 gb EF400827.1 | 99.52 | 1453 | 7 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2645 |
| gi 319495953 gb HQ788814.1 | 99.93 | 1434 | 1 | 0 | 20 | 1453 | 1 | 1434 | 0 | 2643 |
| gi 126111646 gb EF401335.1 | 99.52 | 1453 | 6 | 1 | 1 | 1453 | 21 | 1472 | 0 | 2643 |
| gi 126111403 gb EF401092.1 | 99.52 | 1453 | 6 | 1 | 1 | 1453 | 21 | 1472 | 0 | 2643 |
| gi 126111287 gb EF400976.1 | 99.52 | 1453 | 6 | 1 | 1 | 1453 | 21 | 1472 | 0 | 2643 |
| gi 261262538 gb GQ898389.1 | 99.45 | 1453 | 8 | 0 | 1 | 1453 | 20 | 1472 | 0 | 2639 |
| gi 261262369 gb GQ898220.1 | 99.45 | 1453 | 8 | 0 | 1 | 1453 | 20 | 1472 | 0 | 2639 |
| gi 126115648 gb EF405325.1 | 99.45 | 1453 | 8 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2639 |
| gi 126115366 gb EF405043.1 | 99.45 | 1453 | 8 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2639 |
| gi 126115362 gb EF405039.1 | 99.45 | 1453 | 8 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2639 |
| gi 126111838 gb EF401527.1 | 99.45 | 1453 | 8 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2639 |
| gi 6456061 gb AF132255.1 | 99.52 | 1452 | 3 | 4 | 4 | 1453 | 24 | 1473 | 0 | 2639 |
| gi 319482775 gb HQ775636.1 | 99.52 | 1449 | 7 | 0 | 5 | 1453 | 1 | 1449 | 0 | 2638 |
| gi 319499423 gb HQ792284.1 | 99.45 | 1450 | 8 | 0 | 2 | 1451 | 1 | 1450 | 0 | 2634 |
| gi 319488021 gb HQ780882.1 | 99.65 | 1441 | 5 | 0 | 4 | 1444 | 3 | 1443 | 0 | 2634 |
| gi 261262337 gb GQ898188.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 20 | 1472 | 0 | 2634 |
| gi 261261861 gb GQ897712.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2634 |
| gi 126115512 gb EF405189.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2634 |
| gi 126115207 gb EF404884.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2634 |
| gi 126112029 gb EF401718.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2634 |
| gi 126111899 gb EF401588.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2634 |
| gi 126111893 gb EF401582.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2634 |
| gi 126111713 gb EF401402.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2634 |
| gi 126111061 gb EF400750.1 | 99.38 | 1453 | 9 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2634 |
| gi 319487719 gb HQ780580.1 | 99.38 | 1450 | 9 | 0 | 4 | 1453 | 1 | 1450 | 0 | 2628 |
| gi 261262554 gb GQ898405.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 20 | 1472 | 0 | 2628 |
| gi 126112132 gb EF401821.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| gi 126112111 gb EF401800.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| gi 126112073 gb EF401762.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| gi 126112033 gb EF401722.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |

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|---------------------------|-------|------|----|---|---|------|----|------|---|------|
| g 126112002 gb EF401691.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111979 gb EF401668.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111925 gb EF401614.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111813 gb EF401502.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111660 gb EF401349.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111649 gb EF401338.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111596 gb EF401285.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111542 gb EF401231.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111535 gb EF401224.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111465 gb EF401154.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111399 gb EF401088.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111378 gb EF401067.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111376 gb EF401065.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111363 gb EF401052.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111353 gb EF401042.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111323 gb EF401012.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111201 gb EF400890.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111135 gb EF400824.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 126111085 gb EF400774.1 | 99.31 | 1453 | 10 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2628 |
| g 319490773 gb HQ783634.1 | 99.31 | 1450 | 10 | 0 | 4 | 1453 | 1 | 1450 | 0 | 2623 |
| g 261261792 gb GQ897639.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2623 |
| g 126115092 gb EF404772.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2623 |
| g 126114933 gb EF404613.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2623 |
| g 126112161 gb EF401850.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126112160 gb EF401849.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126112061 gb EF401750.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111968 gb EF401657.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111930 gb EF401619.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111902 gb EF401591.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111879 gb EF401568.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111753 gb EF401442.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111737 gb EF401426.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111613 gb EF401302.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 126111405 gb EF401094.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |

| | | | | | | | | | | |
|---------------------------|-------|------|----|---|----|------|----|------|---|------|
| g 126111362 gb EF401051.1 | 99.24 | 1453 | 11 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2623 |
| g 319488801 gb HQ781662.1 | 99.24 | 1452 | 10 | 1 | 2 | 1452 | 1 | 1452 | 0 | 2619 |
| g 319499925 gb HQ792786.1 | 99.44 | 1441 | 8 | 0 | 13 | 1453 | 1 | 1441 | 0 | 2617 |
| g 319492434 gb HQ785295.1 | 99.17 | 1454 | 11 | 1 | 1 | 1453 | 2 | 1455 | 0 | 2617 |
| g 319488912 gb HQ781773.1 | 99.24 | 1450 | 11 | 0 | 4 | 1453 | 1 | 1450 | 0 | 2617 |
| g 261262501 gb GQ898352.1 | 99.17 | 1451 | 12 | 0 | 3 | 1453 | 20 | 1470 | 0 | 2617 |
| g 261260989 gb GQ896836.1 | 99.17 | 1453 | 12 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2617 |
| g 126111846 gb EF401535.1 | 99.17 | 1453 | 12 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2617 |
| g 126111498 gb EF401187.1 | 99.17 | 1453 | 12 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2617 |
| g 126111494 gb EF401183.1 | 99.17 | 1453 | 12 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2617 |
| g 126111063 gb EF400752.1 | 99.17 | 1453 | 12 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2617 |
| g 126115692 gb EF405369.1 | 99.17 | 1453 | 11 | 1 | 1 | 1453 | 22 | 1473 | 0 | 2615 |
| g 319484767 gb HQ777628.1 | 99.38 | 1442 | 9 | 0 | 12 | 1453 | 1 | 1442 | 0 | 2614 |
| g 319494580 gb HQ787441.1 | 99.17 | 1450 | 12 | 0 | 4 | 1453 | 1 | 1450 | 0 | 2612 |
| g 261261902 gb GQ897753.1 | 99.11 | 1453 | 13 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2612 |
| g 261261832 gb GQ897683.1 | 99.11 | 1453 | 13 | 0 | 1 | 1453 | 18 | 1470 | 0 | 2612 |
| g 126111936 gb EF401625.1 | 99.11 | 1453 | 13 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2612 |
| g 126111726 gb EF401415.1 | 99.11 | 1453 | 13 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2612 |
| g 126111600 gb EF401289.1 | 99.11 | 1453 | 13 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2612 |
| g 126111231 gb EF400920.1 | 99.11 | 1453 | 13 | 0 | 1 | 1453 | 21 | 1473 | 0 | 2612 |
| g 18644507 gb AF371798.1 | 99.58 | 1431 | 4 | 2 | 1 | 1430 | 21 | 1450 | 0 | 2612 |
| g 319494186 gb HQ787047.1 | 99.17 | 1448 | 12 | 0 | 4 | 1451 | 1 | 1448 | 0 | 2608 |
| g 319493693 gb HQ786554.1 | 99.1 | 1451 | 13 | 0 | 3 | 1453 | 1 | 1451 | 0 | 2608 |
| g 240005432 gb GQ158590.1 | 99.17 | 1448 | 12 | 0 | 6 | 1453 | 1 | 1448 | 0 | 2608 |
| g 319499385 gb HQ792246.1 | 99.37 | 1439 | 8 | 1 | 9 | 1446 | 1 | 1439 | 0 | 2606 |
| g 319494484 gb HQ787345.1 | 99.24 | 1444 | 11 | 0 | 1 | 1444 | 5 | 1448 | 0 | 2606 |
| g 319499757 gb HQ792618.1 | 99.24 | 1443 | 11 | 0 | 5 | 1447 | 1 | 1443 | 0 | 2604 |
| g 319466460 gb HQ759321.1 | 99.24 | 1440 | 11 | 0 | 14 | 1453 | 1 | 1440 | 0 | 2601 |
| g 319500228 gb HQ793089.1 | 99.17 | 1444 | 12 | 0 | 7 | 1450 | 1 | 1444 | 0 | 2601 |
| g 319500039 gb HQ792900.1 | 99.37 | 1435 | 9 | 0 | 1 | 1435 | 3 | 1437 | 0 | 2601 |
| g 319494363 gb HQ787224.1 | 99.03 | 1450 | 14 | 0 | 4 | 1453 | 1 | 1450 | 0 | 2601 |
| g 126115689 gb EF405366.1 | 98.97 | 1453 | 15 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2601 |
| g 126115469 gb EF405146.1 | 98.97 | 1453 | 15 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2601 |
| g 126115408 gb EF405085.1 | 98.97 | 1453 | 15 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2601 |

| | | | | | | | | | | |
|----------------------------|-------|------|----|---|----|------|----|------|---|------|
| gi 319517965 gb HQ810826.1 | 99.03 | 1449 | 14 | 0 | 3 | 1451 | 1 | 1449 | 0 | 2599 |
| gi 319494413 gb HQ787274.1 | 99.17 | 1442 | 12 | 0 | 12 | 1453 | 1 | 1442 | 0 | 2597 |
| gi 319489028 gb HQ781889.1 | 99.1 | 1444 | 13 | 0 | 10 | 1453 | 1 | 1444 | 0 | 2595 |
| gi 240006081 gb GQ159239.1 | 98.9 | 1453 | 16 | 0 | 1 | 1453 | 1 | 1453 | 0 | 2595 |
| gi 126115476 gb EF405153.1 | 98.9 | 1453 | 16 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2595 |
| gi 126115363 gb EF405040.1 | 98.9 | 1453 | 16 | 0 | 1 | 1453 | 22 | 1474 | 0 | 2595 |
| gi 319495888 gb HQ788749.1 | 99.24 | 1438 | 10 | 1 | 17 | 1453 | 1 | 1438 | 0 | 2593 |
| gi 319494567 gb HQ787428.1 | 99.1 | 1443 | 13 | 0 | 11 | 1453 | 1 | 1443 | 0 | 2593 |
| gi 319494832 gb HQ787693.1 | 99.17 | 1439 | 12 | 0 | 1 | 1439 | 8 | 1446 | 0 | 2591 |
| gi 319466750 gb HQ759611.1 | 99.37 | 1430 | 9 | 0 | 19 | 1448 | 1 | 1430 | 0 | 2591 |
| gi 319487696 gb HQ780557.1 | 99.03 | 1444 | 14 | 0 | 1 | 1444 | 7 | 1450 | 0 | 2590 |
| gi 240006082 gb GQ159240.1 | 98.83 | 1453 | 17 | 0 | 1 | 1453 | 1 | 1453 | 0 | 2590 |
| gi 240006079 gb GQ159237.1 | 98.83 | 1454 | 15 | 2 | 1 | 1453 | 1 | 1453 | 0 | 2590 |
| gi 319493543 gb HQ786404.1 | 99.1 | 1440 | 13 | 0 | 14 | 1453 | 1 | 1440 | 0 | 2588 |
| gi 319488000 gb HQ780861.1 | 99.03 | 1443 | 14 | 0 | 1 | 1443 | 10 | 1452 | 0 | 2588 |
| gi 240006083 gb GQ159241.1 | 98.83 | 1453 | 16 | 1 | 1 | 1453 | 1 | 1452 | 0 | 2588 |
| gi 170522519 gb EU531967.1 | 99.17 | 1438 | 10 | 2 | 1 | 1438 | 1 | 1436 | 0 | 2588 |
| gi 319496000 gb HQ788861.1 | 99.16 | 1436 | 12 | 0 | 18 | 1453 | 1 | 1436 | 0 | 2586 |
| gi 319494044 gb HQ786905.1 | 99.03 | 1441 | 14 | 0 | 1 | 1441 | 4 | 1444 | 0 | 2584 |
| gi 319487727 gb HQ780588.1 | 98.89 | 1447 | 16 | 0 | 2 | 1448 | 1 | 1447 | 0 | 2584 |
| gi 319485110 gb HQ777971.1 | 98.96 | 1444 | 15 | 0 | 10 | 1453 | 1 | 1444 | 0 | 2584 |
| gi 319449343 gb HQ742204.1 | 99.1 | 1438 | 13 | 0 | 1 | 1438 | 1 | 1438 | 0 | 2584 |
| gi 324959751 gb HQ716104.1 | 98.76 | 1453 | 18 | 0 | 1 | 1453 | 19 | 1471 | 0 | 2584 |
| gi 240006080 gb GQ159238.1 | 98.76 | 1454 | 15 | 3 | 1 | 1453 | 1 | 1452 | 0 | 2582 |
| gi 319517807 gb HQ810668.1 | 98.96 | 1437 | 15 | 0 | 17 | 1453 | 1 | 1437 | 0 | 2571 |
| gi 319494034 gb HQ786895.1 | 98.96 | 1436 | 15 | 0 | 18 | 1453 | 1 | 1436 | 0 | 2569 |
| gi 319499806 gb HQ792667.1 | 98.75 | 1443 | 18 | 0 | 11 | 1453 | 1 | 1443 | 0 | 2566 |
| gi 319495841 gb HQ788702.1 | 98.88 | 1434 | 16 | 0 | 18 | 1451 | 1 | 1434 | 0 | 2560 |
| gi 319466752 gb HQ759613.1 | 98.54 | 1441 | 20 | 1 | 4 | 1443 | 1 | 1441 | 0 | 2543 |
| gi 319466850 gb HQ759711.1 | 98.33 | 1440 | 24 | 0 | 12 | 1451 | 1 | 1440 | 0 | 2527 |
| gi 319487726 gb HQ780587.1 | 98.33 | 1436 | 22 | 2 | 1 | 1436 | 3 | 1436 | 0 | 2518 |
| gi 319466599 gb HQ759460.1 | 98.52 | 1423 | 19 | 2 | 12 | 1434 | 2 | 1422 | 0 | 2510 |
| gi 319500123 gb HQ792984.1 | 97.99 | 1445 | 28 | 1 | 1 | 1445 | 6 | 1449 | 0 | 2507 |
| gi 110446538 gb DQ806753.1 | 99.56 | 1368 | 6 | 0 | 1 | 1368 | 32 | 1399 | 0 | 2494 |

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|----------------------------|-------|------|----|---|----|------|----|------|---|------|
| gi 219533792 gb FJ510597.1 | 99.63 | 1364 | 5 | 0 | 2 | 1365 | 13 | 1376 | 0 | 2492 |
| gi 319499960 gb HQ792821.1 | 97.65 | 1448 | 34 | 0 | 4 | 1451 | 1 | 1448 | 0 | 2486 |
| gi 110446177 gb DQ806392.1 | 99.42 | 1370 | 6 | 2 | 1 | 1368 | 33 | 1402 | 0 | 2484 |
| gi 388933029 gb JQ188146.1 | 99.85 | 1350 | 2 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2483 |
| gi 388933200 gb JQ188317.1 | 99.85 | 1350 | 2 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2483 |
| gi 388932914 gb JQ188031.1 | 99.85 | 1350 | 2 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2483 |
| gi 110441168 gb DQ800768.1 | 99.42 | 1368 | 8 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2483 |
| gi 319466572 gb HQ759433.1 | 98.71 | 1397 | 18 | 0 | 5 | 1401 | 1 | 1397 | 0 | 2481 |
| gi 219534086 gb FJ510891.1 | 99.49 | 1363 | 7 | 0 | 1 | 1363 | 10 | 1372 | 0 | 2479 |
| gi 388928035 gb JQ183152.1 | 99.78 | 1350 | 3 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2477 |
| gi 388935405 gb JQ190522.1 | 99.78 | 1350 | 3 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2477 |
| gi 388933350 gb JQ188467.1 | 99.78 | 1350 | 3 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2477 |
| gi 388933228 gb JQ188345.1 | 99.78 | 1350 | 3 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2477 |
| gi 110449771 gb DQ809986.1 | 99.34 | 1368 | 9 | 0 | 1 | 1368 | 32 | 1399 | 0 | 2477 |
| gi 110449667 gb DQ809882.1 | 99.34 | 1368 | 9 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2477 |
| gi 110448825 gb DQ809040.1 | 99.34 | 1368 | 9 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2477 |
| gi 110436401 gb DQ796001.1 | 99.34 | 1368 | 9 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2477 |
| gi 388933272 gb JQ188389.1 | 99.7 | 1352 | 2 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2473 |
| gi 219531115 gb FJ507920.1 | 99.63 | 1354 | 5 | 0 | 12 | 1365 | 1 | 1354 | 0 | 2473 |
| gi 388931523 gb JQ186640.1 | 99.7 | 1350 | 4 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2471 |
| gi 388935595 gb JQ190712.1 | 99.7 | 1350 | 4 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2471 |
| gi 388935367 gb JQ190484.1 | 99.7 | 1350 | 4 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2471 |
| gi 388935044 gb JQ190161.1 | 99.7 | 1350 | 4 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2471 |
| gi 219536114 gb FJ512919.1 | 99.34 | 1365 | 9 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2471 |
| gi 219531116 gb FJ507921.1 | 99.34 | 1365 | 9 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2471 |
| gi 192988166 gb EU778163.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2471 |
| gi 192981066 gb EU775089.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2471 |
| gi 192976430 gb EU772453.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2471 |
| gi 169278176 gb EU462701.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2471 |
| gi 169278092 gb EU462617.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2471 |
| gi 110441305 gb DQ800905.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2471 |
| gi 110436243 gb DQ795843.1 | 99.27 | 1368 | 10 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2471 |
| gi 388933965 gb JQ189082.1 | 99.7 | 1350 | 3 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2470 |
| gi 219531114 gb FJ507919.1 | 99.34 | 1365 | 8 | 1 | 1 | 1365 | 11 | 1374 | 0 | 2470 |

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|----------------------------|-------|------|----|---|---|------|----|------|---|------|
| gi 388928800 gb JQ183917.1 | 99.63 | 1350 | 5 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2466 |
| gi 388935165 gb JQ190282.1 | 99.63 | 1350 | 5 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2466 |
| gi 388934187 gb JQ189304.1 | 99.63 | 1350 | 5 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2466 |
| gi 219536113 gb FJ512918.1 | 99.27 | 1365 | 10 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2466 |
| gi 192981058 gb EU775081.1 | 99.2 | 1368 | 11 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2466 |
| gi 110446130 gb DQ806345.1 | 99.2 | 1368 | 11 | 0 | 1 | 1368 | 4 | 1371 | 0 | 2466 |
| gi 62764679 gb AY985189.1 | 99.63 | 1350 | 5 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2466 |
| gi 219533341 gb FJ510146.1 | 99.27 | 1364 | 10 | 0 | 1 | 1364 | 11 | 1374 | 0 | 2464 |
| gi 110449111 gb DQ809326.1 | 99.2 | 1368 | 10 | 1 | 1 | 1368 | 33 | 1399 | 0 | 2464 |
| gi 388931569 gb JQ186686.1 | 99.56 | 1352 | 4 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2462 |
| gi 388931221 gb JQ186338.1 | 99.56 | 1350 | 6 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2460 |
| gi 388930259 gb JQ185376.1 | 99.56 | 1350 | 6 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2460 |
| gi 388928405 gb JQ183522.1 | 99.56 | 1350 | 6 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2460 |
| gi 388934145 gb JQ189262.1 | 99.56 | 1350 | 6 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2460 |
| gi 388933765 gb JQ188882.1 | 99.56 | 1350 | 6 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2460 |
| gi 219536112 gb FJ512917.1 | 99.19 | 1365 | 11 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2460 |
| gi 219536107 gb FJ512912.1 | 99.19 | 1365 | 11 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2460 |
| gi 219536108 gb FJ512913.1 | 99.19 | 1365 | 11 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2460 |
| gi 219533791 gb FJ510596.1 | 99.19 | 1365 | 11 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2460 |
| gi 192976454 gb EU772477.1 | 99.12 | 1368 | 12 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2460 |
| gi 169278049 gb EU462574.1 | 99.12 | 1368 | 12 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2460 |
| gi 110449321 gb DQ809536.1 | 99.12 | 1368 | 12 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2460 |
| gi 219533340 gb FJ510145.1 | 99.19 | 1364 | 11 | 0 | 1 | 1364 | 11 | 1374 | 0 | 2459 |
| gi 214017356 gb FJ362969.1 | 99.41 | 1355 | 8 | 0 | 1 | 1355 | 1 | 1355 | 0 | 2459 |
| gi 219533343 gb FJ510148.1 | 99.26 | 1360 | 10 | 0 | 5 | 1364 | 15 | 1374 | 0 | 2457 |
| gi 169276654 gb EU461179.1 | 99.05 | 1370 | 11 | 2 | 1 | 1368 | 21 | 1390 | 0 | 2457 |
| gi 388929811 gb JQ184928.1 | 99.48 | 1351 | 6 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2455 |
| gi 388928407 gb JQ183524.1 | 99.48 | 1350 | 7 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2455 |
| gi 388935013 gb JQ190130.1 | 99.48 | 1350 | 7 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2455 |
| gi 388935324 gb JQ190441.1 | 99.48 | 1350 | 7 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2455 |
| gi 388932549 gb JQ187666.1 | 99.48 | 1351 | 6 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2455 |
| gi 219536106 gb FJ512911.1 | 99.12 | 1365 | 12 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2455 |
| gi 192981007 gb EU775030.1 | 99.05 | 1368 | 13 | 0 | 1 | 1368 | 25 | 1392 | 0 | 2455 |
| gi 110448398 gb DQ808613.1 | 99.05 | 1368 | 13 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2455 |

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|----------------------------|-------|------|----|---|----|------|----|------|---|------|
| gi 62760514 gb AY981024.1 | 99.48 | 1350 | 7 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2455 |
| gi 388935424 gb JQ190541.1 | 99.41 | 1354 | 4 | 4 | 1 | 1350 | 1 | 1354 | 0 | 2453 |
| gi 219536110 gb FJ512915.1 | 99.12 | 1364 | 12 | 0 | 2 | 1365 | 13 | 1376 | 0 | 2453 |
| gi 219535544 gb FJ512349.1 | 99.12 | 1364 | 12 | 0 | 2 | 1365 | 11 | 1374 | 0 | 2453 |
| gi 219533017 gb FJ509822.1 | 99.12 | 1364 | 12 | 0 | 1 | 1364 | 11 | 1374 | 0 | 2453 |
| gi 219533015 gb FJ509820.1 | 99.19 | 1361 | 11 | 0 | 4 | 1364 | 14 | 1374 | 0 | 2453 |
| gi 388930479 gb JQ185596.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388930251 gb JQ185368.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388928126 gb JQ183243.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388934631 gb JQ189748.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388934877 gb JQ189994.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388934922 gb JQ190039.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388934445 gb JQ189562.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388933151 gb JQ188268.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 322160786 gb JF175380.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 219535545 gb FJ512350.1 | 99.12 | 1363 | 11 | 1 | 3 | 1365 | 12 | 1373 | 0 | 2449 |
| gi 219533789 gb FJ510594.1 | 99.05 | 1366 | 11 | 2 | 1 | 1365 | 11 | 1375 | 0 | 2449 |
| gi 219533342 gb FJ510147.1 | 99.12 | 1362 | 12 | 0 | 3 | 1364 | 13 | 1374 | 0 | 2449 |
| gi 214018748 gb FJ364361.1 | 99.26 | 1356 | 10 | 0 | 1 | 1356 | 21 | 1376 | 0 | 2449 |
| gi 169291316 gb EU475841.1 | 98.98 | 1368 | 14 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2449 |
| gi 110436585 gb DQ796185.1 | 98.98 | 1368 | 14 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2449 |
| gi 62764715 gb AY985225.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 62763312 gb AY983822.1 | 99.41 | 1350 | 8 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2449 |
| gi 388933707 gb JQ188824.1 | 99.41 | 1350 | 6 | 2 | 1 | 1348 | 1 | 1350 | 0 | 2447 |
| gi 219533339 gb FJ510144.1 | 99.19 | 1358 | 11 | 0 | 7 | 1364 | 6 | 1363 | 0 | 2447 |
| gi 219533338 gb FJ510143.1 | 99.05 | 1364 | 13 | 0 | 1 | 1364 | 11 | 1374 | 0 | 2447 |
| gi 110436110 gb DQ795710.1 | 99.05 | 1364 | 13 | 0 | 1 | 1364 | 33 | 1396 | 0 | 2447 |
| gi 388934590 gb JQ189707.1 | 99.33 | 1352 | 7 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2446 |
| gi 219531117 gb FJ507922.1 | 99.26 | 1354 | 10 | 0 | 12 | 1365 | 1 | 1354 | 0 | 2446 |
| gi 388934888 gb JQ190005.1 | 99.26 | 1356 | 4 | 6 | 1 | 1350 | 1 | 1356 | 0 | 2444 |
| gi 388934140 gb JQ189257.1 | 99.33 | 1351 | 8 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2444 |
| gi 388933499 gb JQ188616.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2444 |
| gi 322160776 gb JF175370.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2444 |
| gi 219535543 gb FJ512348.1 | 98.97 | 1365 | 14 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2444 |

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|------------------------------------|-------|------|----|---|----|------|----|------|---|------|
| gi 219531288 gb FJ508093.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2444 |
| gi 219531287 gb FJ508092.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2444 |
| gi 219531286 gb FJ508091.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2444 |
| gi 219531284 gb FJ508089.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2444 |
| gi 219531285 gb FJ508090.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2444 |
| gi 214022757 gb FJ368373.1 | 99.19 | 1356 | 11 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2444 |
| gi 214018691 gb FJ364304.1 | 99.19 | 1356 | 11 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2444 |
| gi 192968905 gb EU764690.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2444 |
| gi 62765741 gb AY986251.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2444 |
| gi 62764956 gb AY985466.1 | 99.33 | 1350 | 9 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2444 |
| gi 219536109 gb FJ512914.1 | 98.97 | 1364 | 14 | 0 | 2 | 1365 | 13 | 1376 | 0 | 2442 |
| gi 219536105 gb FJ512910.1 | 98.97 | 1365 | 13 | 1 | 1 | 1365 | 11 | 1374 | 0 | 2442 |
| gi 219531289 gb FJ508094.1 | 99.41 | 1346 | 8 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2442 |
| gi 219531118 gb FJ507923.1 | 99.19 | 1355 | 11 | 0 | 11 | 1365 | 1 | 1355 | 0 | 2442 |
| gi 388928236 gb JQ183353.1 | 99.26 | 1352 | 8 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2440 |
| gi 388934843 gb JQ189960.1 | 99.26 | 1352 | 8 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2440 |
| gi 388933452 gb JQ188569.1 | 99.26 | 1353 | 7 | 3 | 1 | 1350 | 1 | 1353 | 0 | 2440 |
| gi 62765667 gb AY986177.1 | 99.26 | 1352 | 8 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2440 |
| gi 388931911 gb JQ187028.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388931775 gb JQ186892.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388931727 gb JQ186844.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388930236 gb JQ185353.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388928164 gb JQ183281.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388928479 gb JQ183596.1 | 99.26 | 1351 | 9 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2438 |
| gi 388928666 gb JQ183783.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388935278 gb JQ190395.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388934715 gb JQ189832.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388934682 gb JQ189799.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388933162 gb JQ188279.1 | 99.33 | 1347 | 9 | 0 | 4 | 1350 | 4 | 1350 | 0 | 2438 |
| gi 388933068 gb JQ188185.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 388930723 gb JQ185840.1 ;gi 388 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 219535542 gb FJ512347.1 | 98.9 | 1365 | 15 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2438 |
| gi 219533788 gb FJ510593.1 | 98.9 | 1365 | 15 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2438 |
| gi 219531276 gb FJ508081.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2438 |

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|------------------------------------|-------|------|----|---|---|------|----|------|---|------|
| gi 219531277 gb FJ508082.1 ;gi 219 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2438 |
| gi 214017889 gb FJ363502.1 | 99.12 | 1356 | 12 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2438 |
| gi 214017490 gb FJ363103.1 | 99.12 | 1356 | 12 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2438 |
| gi 192970039 gb EU765824.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 192968817 gb EU764602.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 192968594 gb EU764379.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 192981510 gb EU775533.1 | 98.83 | 1368 | 16 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2438 |
| gi 169285159 gb EU469684.1 | 98.83 | 1368 | 16 | 0 | 1 | 1368 | 32 | 1399 | 0 | 2438 |
| gi 62759235 gb AY979745.1 ;gi 3889 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62765196 gb AY985706.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62765128 gb AY985638.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62765091 gb AY985601.1 | 99.26 | 1351 | 8 | 2 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62764908 gb AY985418.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62764829 gb AY985339.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62763469 gb AY983979.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62763277 gb AY983787.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62757651 gb AY978161.1 | 99.26 | 1350 | 10 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 62757223 gb AY977733.1 | 99.26 | 1351 | 8 | 2 | 1 | 1350 | 1 | 1350 | 0 | 2438 |
| gi 322160944 gb JF175538.1 | 99.26 | 1350 | 9 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2436 |
| gi 322153252 gb JF167846.1 | 99.26 | 1350 | 9 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2436 |
| gi 219533790 gb FJ510595.1 | 98.9 | 1365 | 14 | 1 | 1 | 1365 | 11 | 1374 | 0 | 2436 |
| gi 219531275 gb FJ508080.1 | 99.26 | 1349 | 10 | 0 | 2 | 1350 | 17 | 1365 | 0 | 2436 |
| gi 214018920 gb FJ364534.1 | 98.83 | 1367 | 16 | 0 | 1 | 1367 | 1 | 1367 | 0 | 2436 |
| gi 388931650 gb JQ186767.1 | 99.19 | 1352 | 9 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2435 |
| gi 219533344 gb FJ510149.1 | 98.97 | 1360 | 14 | 0 | 5 | 1364 | 15 | 1374 | 0 | 2435 |
| gi 219533016 gb FJ509821.1 | 99.04 | 1357 | 13 | 0 | 8 | 1364 | 17 | 1373 | 0 | 2435 |
| gi 219532157 gb FJ508962.1 | 98.9 | 1363 | 14 | 1 | 1 | 1363 | 11 | 1372 | 0 | 2435 |
| gi 62765608 gb AY986118.1 | 99.19 | 1353 | 8 | 3 | 1 | 1350 | 1 | 1353 | 0 | 2435 |
| gi 62765449 gb AY985959.1 | 99.19 | 1352 | 9 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2435 |
| gi 388931501 gb JQ186618.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| gi 388928698 gb JQ183815.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| gi 388928240 gb JQ183357.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| gi 388935772 gb JQ190889.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| gi 388934425 gb JQ189542.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |

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|---------------------------|-------|------|----|---|----|------|----|------|---|------|
| g 322146999 gb JF161593.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 219531283 gb FJ508088.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2433 |
| g 219531282 gb FJ508087.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 16 | 1365 | 0 | 2433 |
| g 214021126 gb FJ366742.1 | 99.26 | 1348 | 9 | 1 | 10 | 1356 | 35 | 1382 | 0 | 2433 |
| g 214020057 gb FJ365672.1 | 99.26 | 1347 | 10 | 0 | 10 | 1356 | 2 | 1348 | 0 | 2433 |
| g 192980034 gb EU774057.1 | 98.76 | 1368 | 17 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2433 |
| g 62765226 gb AY985736.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62765100 gb AY985610.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62765074 gb AY985584.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62764776 gb AY985286.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62763468 gb AY983978.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62763355 gb AY983865.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62759806 gb AY980316.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 62757414 gb AY977924.1 | 99.19 | 1350 | 11 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2433 |
| g 219531272 gb FJ508077.1 | 99.26 | 1346 | 10 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2431 |
| g 219531273 gb FJ508078.1 | 99.26 | 1346 | 10 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2431 |
| g 219531270 gb FJ508075.1 | 99.26 | 1346 | 10 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2431 |
| g 214026068 gb FJ371687.1 | 99.04 | 1355 | 13 | 0 | 1 | 1355 | 1 | 1355 | 0 | 2431 |
| g 214018797 gb FJ364410.1 | 98.83 | 1364 | 16 | 0 | 1 | 1364 | 1 | 1364 | 0 | 2431 |
| g 62763276 gb AY983786.1 | 99.19 | 1350 | 10 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2431 |
| g 388928008 gb JQ183125.1 | 99.11 | 1353 | 9 | 3 | 1 | 1350 | 1 | 1353 | 0 | 2429 |
| g 219531290 gb FJ508095.1 | 99.26 | 1345 | 10 | 0 | 1 | 1345 | 16 | 1360 | 0 | 2429 |
| g 219531280 gb FJ508085.1 | 99.26 | 1345 | 10 | 0 | 1 | 1345 | 16 | 1360 | 0 | 2429 |
| g 219531268 gb FJ508073.1 | 99.26 | 1345 | 10 | 0 | 1 | 1345 | 16 | 1360 | 0 | 2429 |
| g 388931810 gb JQ186927.1 | 99.11 | 1351 | 11 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2427 |
| g 388931288 gb JQ186405.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388928632 gb JQ183749.1 | 99.11 | 1351 | 10 | 2 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388928637 gb JQ183754.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388930665 gb JQ185782.1 | 99.11 | 1351 | 10 | 2 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388928400 gb JQ183517.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388935714 gb JQ190831.1 | 99.11 | 1354 | 5 | 6 | 2 | 1350 | 3 | 1354 | 0 | 2427 |
| g 388934827 gb JQ189944.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388933351 gb JQ188468.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 319484570 gb HQ777431.1 | 97.6 | 1417 | 32 | 2 | 19 | 1435 | 1 | 1415 | 0 | 2427 |

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|---------------------------|-------|------|----|---|---|------|----|------|---|------|
| g 322160977 gb JF175571.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 219535541 gb FJ512346.1 | 98.75 | 1365 | 17 | 0 | 1 | 1365 | 11 | 1375 | 0 | 2427 |
| g 214026245 gb FJ371864.1 | 98.97 | 1357 | 13 | 1 | 1 | 1356 | 1 | 1357 | 0 | 2427 |
| g 192970466 gb EU766251.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 192970348 gb EU766133.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 192968537 gb EU764322.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 192966307 gb EU762092.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 192966162 gb EU761947.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 169278050 gb EU462575.1 | 98.68 | 1368 | 18 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2427 |
| g 110433710 gb DQ793310.1 | 98.68 | 1368 | 18 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2427 |
| g 62759181 gb AY979691.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 62765793 gb AY986303.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 62764702 gb AY985212.1 | 99.11 | 1350 | 12 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2427 |
| g 388934664 gb JQ189781.1 | 99.04 | 1354 | 9 | 4 | 1 | 1350 | 1 | 1354 | 0 | 2425 |
| g 322147187 gb JF161781.1 | 99.11 | 1350 | 11 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2425 |
| g 219531281 gb FJ508086.1 | 99.11 | 1350 | 11 | 1 | 1 | 1350 | 16 | 1364 | 0 | 2425 |
| g 219531274 gb FJ508079.1 | 99.18 | 1346 | 11 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2425 |
| g 219531271 gb FJ508076.1 | 99.18 | 1346 | 11 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2425 |
| g 219531269 gb FJ508074.1 | 99.18 | 1346 | 11 | 0 | 1 | 1346 | 16 | 1361 | 0 | 2425 |
| g 219531279 gb FJ508084.1 | 99.11 | 1349 | 10 | 2 | 1 | 1348 | 16 | 1363 | 0 | 2423 |
| g 62764920 gb AY985430.1 | 99.04 | 1353 | 10 | 3 | 1 | 1350 | 1 | 1353 | 0 | 2423 |
| g 388930615 gb JQ185732.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| g 388930442 gb JQ185559.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| g 388929030 gb JQ184147.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| g 388928543 gb JQ183660.1 | 99.04 | 1351 | 11 | 2 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| g 219533787 gb FJ510592.1 | 98.68 | 1366 | 16 | 2 | 1 | 1365 | 11 | 1375 | 0 | 2422 |
| g 214026073 gb FJ371692.1 | 98.89 | 1356 | 15 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2422 |
| g 192970627 gb EU766412.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| g 192970356 gb EU766141.1 | 99.04 | 1351 | 12 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2422 |
| g 192969098 gb EU764883.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| g 192981375 gb EU775398.1 | 98.61 | 1368 | 19 | 0 | 1 | 1368 | 32 | 1399 | 0 | 2422 |
| g 169287503 gb EU472028.1 | 98.61 | 1368 | 19 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2422 |
| g 110437813 gb DQ797413.1 | 98.61 | 1368 | 19 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2422 |
| g 110437539 gb DQ797139.1 | 98.61 | 1368 | 19 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2422 |

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|----------------------------|-------|------|----|---|----|------|----|------|---|------|
| gi 62759154 gb AY979664.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| gi 62759099 gb AY979609.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| gi 62765862 gb AY986372.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| gi 62765215 gb AY985725.1 | 99.04 | 1350 | 13 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2422 |
| gi 322147075 gb JF161669.1 | 99.04 | 1350 | 12 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2420 |
| gi 192967875 gb EU763660.1 | 98.97 | 1354 | 10 | 4 | 1 | 1350 | 1 | 1354 | 0 | 2420 |
| gi 62764708 gb AY985218.1 | 98.97 | 1354 | 10 | 4 | 1 | 1350 | 1 | 1354 | 0 | 2420 |
| gi 388934798 gb JQ189915.1 | 98.96 | 1352 | 12 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2418 |
| gi 192970605 gb EU766390.1 | 98.97 | 1353 | 11 | 3 | 1 | 1350 | 1 | 1353 | 0 | 2418 |
| gi 192988214 gb EU778185.1 | 98.54 | 1371 | 17 | 3 | 1 | 1368 | 9 | 1379 | 0 | 2418 |
| gi 110441542 gb DQ801142.1 | 98.54 | 1371 | 17 | 3 | 1 | 1368 | 9 | 1379 | 0 | 2418 |
| gi 388930601 gb JQ185718.1 | 98.96 | 1351 | 12 | 2 | 1 | 1350 | 1 | 1350 | 0 | 2416 |
| gi 388928546 gb JQ183663.1 | 98.96 | 1352 | 11 | 3 | 1 | 1350 | 1 | 1351 | 0 | 2416 |
| gi 388928362 gb JQ183479.1 | 98.96 | 1350 | 14 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2416 |
| gi 388934972 gb JQ190089.1 | 98.96 | 1351 | 13 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2416 |
| gi 319498064 gb HQ790925.1 | 98.4 | 1375 | 20 | 2 | 23 | 1396 | 1 | 1374 | 0 | 2416 |
| gi 219531266 gb FJ508071.1 | 99.11 | 1344 | 12 | 0 | 1 | 1344 | 16 | 1359 | 0 | 2416 |
| gi 214022030 gb FJ367646.1 | 98.82 | 1356 | 16 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2416 |
| gi 192970585 gb EU766370.1 | 99.04 | 1349 | 10 | 3 | 1 | 1346 | 1 | 1349 | 0 | 2416 |
| gi 192970493 gb EU766278.1 | 98.96 | 1351 | 13 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2416 |
| gi 192966008 gb EU761793.1 | 98.96 | 1352 | 11 | 3 | 1 | 1350 | 1 | 1351 | 0 | 2416 |
| gi 169285267 gb EU469792.1 | 98.54 | 1368 | 20 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2416 |
| gi 169278106 gb EU462631.1 | 98.54 | 1369 | 18 | 2 | 1 | 1368 | 21 | 1388 | 0 | 2416 |
| gi 169278096 gb EU462621.1 | 98.54 | 1368 | 20 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2416 |
| gi 169276721 gb EU461246.1 | 98.54 | 1368 | 20 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2416 |
| gi 110445418 gb DQ805633.1 | 98.54 | 1369 | 19 | 1 | 1 | 1368 | 21 | 1389 | 0 | 2416 |
| gi 214018755 gb FJ364368.1 | 98.82 | 1355 | 16 | 0 | 1 | 1355 | 1 | 1355 | 0 | 2414 |
| gi 388932925 gb JQ188042.1 | 98.89 | 1352 | 13 | 2 | 1 | 1350 | 1 | 1352 | 0 | 2412 |
| gi 169291281 gb EU475806.1 | 98.47 | 1370 | 19 | 2 | 1 | 1368 | 21 | 1390 | 0 | 2412 |
| gi 388935011 gb JQ190128.1 | 98.89 | 1350 | 15 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2410 |
| gi 388933914 gb JQ189031.1 | 98.82 | 1355 | 11 | 5 | 1 | 1350 | 1 | 1355 | 0 | 2409 |
| gi 388933284 gb JQ188401.1 | 98.82 | 1355 | 11 | 5 | 1 | 1350 | 1 | 1355 | 0 | 2409 |
| gi 219536111 gb FJ512916.1 | 98.61 | 1364 | 14 | 5 | 3 | 1365 | 12 | 1371 | 0 | 2409 |
| gi 192965883 gb EU761668.1 | 98.82 | 1355 | 11 | 5 | 1 | 1350 | 1 | 1355 | 0 | 2409 |

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|----------------------------|-------|------|----|----|----|------|----|------|---|------|
| gi 110445082 gb DQ805297.1 | 98.39 | 1370 | 20 | 2 | 1 | 1368 | 4 | 1373 | 0 | 2407 |
| gi 388935520 gb JQ190637.1 | 98.82 | 1351 | 15 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2405 |
| gi 388935228 gb JQ190345.1 | 98.81 | 1350 | 16 | 0 | 1 | 1350 | 1 | 1350 | 0 | 2405 |
| gi 214026130 gb FJ371749.1 | 99.18 | 1335 | 11 | 0 | 1 | 1335 | 1 | 1335 | 0 | 2405 |
| gi 214017608 gb FJ363221.1 | 98.67 | 1356 | 18 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2405 |
| gi 214017504 gb FJ363117.1 | 98.67 | 1356 | 18 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2405 |
| gi 192972226 gb EU768011.1 | 98.89 | 1348 | 13 | 2 | 1 | 1346 | 1 | 1348 | 0 | 2405 |
| gi 169282771 gb EU467296.1 | 99.1 | 1338 | 12 | 0 | 14 | 1351 | 1 | 1338 | 0 | 2405 |
| gi 219532455 gb FJ509260.1 | 98.6 | 1359 | 17 | 2 | 1 | 1359 | 11 | 1367 | 0 | 2403 |
| gi 214026456 gb FJ372075.1 | 99.03 | 1340 | 13 | 0 | 17 | 1356 | 3 | 1342 | 0 | 2403 |
| gi 192970718 gb EU766503.1 | 98.74 | 1354 | 13 | 4 | 1 | 1350 | 1 | 1354 | 0 | 2403 |
| gi 192980909 gb EU774932.1 | 98.32 | 1368 | 23 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2399 |
| gi 192980191 gb EU774214.1 | 99.1 | 1335 | 12 | 0 | 1 | 1335 | 21 | 1355 | 0 | 2399 |
| gi 388930741 gb JQ185858.1 | 98.67 | 1354 | 14 | 4 | 1 | 1350 | 1 | 1354 | 0 | 2398 |
| gi 388930096 gb JQ185213.1 | 98.67 | 1355 | 13 | 4 | 1 | 1350 | 1 | 1355 | 0 | 2398 |
| gi 388928799 gb JQ183916.1 | 98.67 | 1355 | 13 | 5 | 1 | 1350 | 1 | 1355 | 0 | 2398 |
| gi 192970812 gb EU766597.1 | 98.67 | 1355 | 13 | 5 | 1 | 1350 | 1 | 1355 | 0 | 2398 |
| gi 214023970 gb FJ369588.1 | 99.03 | 1336 | 13 | 0 | 1 | 1336 | 9 | 1344 | 0 | 2396 |
| gi 192980961 gb EU774984.1 | 98.25 | 1368 | 24 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2394 |
| gi 219531267 gb FJ508072.1 | 98.88 | 1340 | 14 | 1 | 1 | 1340 | 16 | 1354 | 0 | 2390 |
| gi 322145055 gb JF159649.1 | 98.59 | 1351 | 18 | 1 | 1 | 1350 | 1 | 1351 | 0 | 2388 |
| gi 214018819 gb FJ364432.1 | 98.45 | 1356 | 21 | 0 | 1 | 1356 | 1 | 1356 | 0 | 2388 |
| gi 192968638 gb EU764423.1 | 98.53 | 1356 | 14 | 6 | 1 | 1350 | 1 | 1356 | 0 | 2388 |
| gi 388930393 gb JQ185510.1 | 98.38 | 1362 | 10 | 12 | 1 | 1350 | 1 | 1362 | 0 | 2383 |
| gi 192981465 gb EU775488.1 | 98.1 | 1368 | 26 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2383 |
| gi 110437046 gb DQ796646.1 | 98.1 | 1370 | 23 | 3 | 1 | 1368 | 33 | 1401 | 0 | 2383 |
| gi 169278195 gb EU462720.1 | 98.03 | 1368 | 27 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2377 |
| gi 169278110 gb EU462635.1 | 98.03 | 1368 | 27 | 0 | 1 | 1368 | 21 | 1388 | 0 | 2377 |
| gi 62765348 gb AY985858.1 | 98.31 | 1363 | 10 | 13 | 1 | 1350 | 1 | 1363 | 0 | 2377 |
| gi 214026121 gb FJ371740.1 | 98.23 | 1356 | 24 | 0 | 1 | 1356 | 21 | 1376 | 0 | 2372 |
| gi 169285018 gb EU469543.1 | 98.66 | 1339 | 17 | 1 | 1 | 1339 | 1 | 1338 | 0 | 2372 |
| gi 214026227 gb FJ371846.1 | 98.51 | 1345 | 15 | 5 | 17 | 1356 | 1 | 1345 | 0 | 2368 |
| gi 192970133 gb EU765918.1 | 98.3 | 1353 | 19 | 4 | 1 | 1350 | 1 | 1352 | 0 | 2368 |
| gi 322145018 gb JF159612.1 | 98.3 | 1350 | 22 | 1 | 1 | 1350 | 1 | 1349 | 0 | 2364 |

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|----------------------------|-------|------|----|----|-----|------|-----|------|---|------|
| gi 192970441 gb EU766226.1 | 98.16 | 1357 | 18 | 7 | 1 | 1350 | 1 | 1357 | 0 | 2361 |
| gi 169278124 gb EU462649.1 | 99.54 | 1293 | 6 | 0 | 76 | 1368 | 1 | 1293 | 0 | 2355 |
| gi 214018742 gb FJ364355.1 | 98.5 | 1332 | 20 | 0 | 1 | 1332 | 1 | 1332 | 0 | 2350 |
| gi 388928549 gb JQ183666.1 | 97.87 | 1361 | 17 | 12 | 1 | 1350 | 1 | 1360 | 0 | 2342 |
| gi 388934849 gb JQ189966.1 | 97.67 | 1375 | 7 | 25 | 1 | 1350 | 1 | 1375 | 0 | 2338 |
| gi 319487794 gb HQ780655.1 | 97.45 | 1374 | 29 | 6 | 84 | 1453 | 65 | 1436 | 0 | 2338 |
| gi 192981006 gb EU775029.1 | 97.51 | 1368 | 34 | 0 | 1 | 1368 | 33 | 1400 | 0 | 2338 |
| gi 110446384 gb DQ806599.1 | 99.46 | 1285 | 7 | 0 | 84 | 1368 | 90 | 1374 | 0 | 2335 |
| gi 110438803 gb DQ798403.1 | 99.38 | 1288 | 6 | 2 | 67 | 1352 | 15 | 1302 | 0 | 2333 |
| gi 192969094 gb EU764879.1 | 97.78 | 1354 | 22 | 8 | 5 | 1350 | 6 | 1359 | 0 | 2327 |
| gi 110440827 gb DQ800427.1 | 99.69 | 1272 | 4 | 0 | 97 | 1368 | 1 | 1272 | 0 | 2327 |
| gi 110449954 gb DQ810169.1 | 97.37 | 1368 | 33 | 3 | 1 | 1368 | 25 | 1389 | 0 | 2324 |
| gi 388928120 gb JQ183237.1 | 97.3 | 1368 | 17 | 20 | 1 | 1350 | 1 | 1366 | 0 | 2303 |
| gi 110441294 gb DQ800894.1 | 97.01 | 1370 | 37 | 3 | 1 | 1368 | 33 | 1400 | 0 | 2300 |
| gi 192970021 gb EU765806.1 | 99.45 | 1266 | 5 | 2 | 87 | 1350 | 93 | 1358 | 0 | 2298 |
| gi 110436797 gb DQ796397.1 | 99.29 | 1261 | 8 | 1 | 109 | 1368 | 1 | 1261 | 0 | 2278 |
| gi 169282930 gb EU467455.1 | 97.3 | 1335 | 35 | 1 | 1 | 1335 | 34 | 1367 | 0 | 2265 |
| gi 61620028 gb AY850435.1 | 99.52 | 1243 | 6 | 0 | 67 | 1309 | 9 | 1251 | 0 | 2263 |
| gi 169287428 gb EU471953.1 | 99.05 | 1261 | 9 | 3 | 111 | 1368 | 1 | 1261 | 0 | 2259 |
| gi 169282916 gb EU467441.1 | 97.22 | 1331 | 36 | 1 | 1 | 1331 | 35 | 1364 | 0 | 2252 |
| gi 169287473 gb EU471998.1 | 97.13 | 1288 | 32 | 3 | 84 | 1368 | 88 | 1373 | 0 | 2169 |
| gi 169285037 gb EU469562.1 | 98.94 | 1130 | 12 | 0 | 222 | 1351 | 136 | 1265 | 0 | 2021 |
| gi 110436563 gb DQ796163.1 | 97.39 | 1148 | 29 | 1 | 222 | 1368 | 235 | 1382 | 0 | 1953 |
| gi 214017950 gb FJ363563.1 | 100 | 1049 | 0 | 0 | 307 | 1355 | 1 | 1049 | 0 | 1938 |
| gi 84626925 gb DQ339838.1 | 100 | 1038 | 0 | 0 | 325 | 1362 | 1 | 1038 | 0 | 1917 |
| gi 22324751 gb AF530344.1 | 99.81 | 1038 | 0 | 1 | 325 | 1362 | 1 | 1036 | 0 | 1905 |
| gi 62753295 gb AY920178.1 | 99.42 | 1039 | 4 | 2 | 325 | 1362 | 1 | 1038 | 0 | 1884 |
| gi 298391468 gb HM478330.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298391173 gb HM478035.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298390963 gb HM477825.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298390562 gb HM477424.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 298390543 gb HM477405.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298389976 gb HM476838.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298389938 gb HM476800.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |

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|-----------------------------|------|------|---|---|-----|------|---|------|---|------|
| gi 298389589 gb HM476451.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 298389422 gb HM476284.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298389379 gb HM476241.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 298389231 gb HM476093.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 298388837 gb HM475699.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258688844 emb FP083306.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 258688642 emb FP083302.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258688592 emb FP083252.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258687382 emb FP082637.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 258687350 emb FP082605.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 258687324 emb FP082579.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 258685368 emb FP081817.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258685243 emb FP075647.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258684705 emb FP075308.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258684256 emb FP075075.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258684063 emb FP081284.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258683838 emb FP081059.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
| gi 258681398 emb FP084863.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258681389 emb FP084854.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258680819 emb FP084484.1 | 100 | 1001 | 0 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1849 |
| gi 258680338 emb FP078738.1 | 100 | 1001 | 0 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1849 |
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| gi 298392754 gb HM479616.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 298391479 gb HM478341.1 | 99.9 | 1001 | 1 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1844 |
| gi 298391366 gb HM478228.1 | 99.9 | 1001 | 1 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1844 |
| gi 298390465 gb HM477327.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 298390259 gb HM477121.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 298389656 gb HM476518.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 298389217 gb HM476079.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 258684984 emb FP081632.1 | 99.9 | 1001 | 1 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1844 |
| gi 258684844 emb FP075447.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 258680857 emb FP084518.1 | 99.9 | 1001 | 1 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1844 |
| gi 258679890 emb FP078489.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 258679841 emb FP078441.1 | 99.9 | 1001 | 1 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1844 |

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|-----------------------------|-------|------|----|---|-----|------|---|------|---|------|
| gi 258679682 emb FP078282.1 | 99.9 | 1001 | 1 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1844 |
| gi 258685337 emb FP081786.1 | 99.8 | 1001 | 2 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1838 |
| gi 258680032 emb FP078631.1 | 99.8 | 1001 | 2 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1838 |
| gi 258679945 emb FP078544.1 | 99.8 | 1001 | 2 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1838 |
| gi 258682949 emb FP080298.1 | 99.7 | 1001 | 3 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1832 |
| gi 258681405 emb FP084870.1 | 99.7 | 1001 | 3 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1832 |
| gi 258681365 emb FP084830.1 | 99.7 | 1001 | 3 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1832 |
| gi 258680303 emb FP078703.1 | 99.7 | 1001 | 3 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1832 |
| gi 258688156 emb FP083014.1 | 99.5 | 1001 | 5 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1821 |
| gi 258687287 emb FP082542.1 | 99.1 | 1001 | 9 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1799 |
| gi 258689133 emb FP077748.1 | 98.8 | 1001 | 12 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1783 |
| gi 258679670 emb FP078270.1 | 98.8 | 1003 | 8 | 2 | 345 | 1345 | 1 | 1001 | 0 | 1783 |
| gi 62753249 gb AY920132.1 | 97.69 | 1039 | 21 | 2 | 325 | 1362 | 1 | 1037 | 0 | 1783 |
| gi 258689128 emb FP077743.1 | 98.6 | 1001 | 14 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1772 |
| gi 258690090 emb FP078109.1 | 98.5 | 1001 | 15 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1766 |
| gi 258679990 emb FP078589.1 | 98.5 | 1001 | 15 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1766 |
| gi 258679817 emb FP078417.1 | 98.3 | 1001 | 17 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1755 |
| gi 62753277 gb AY920160.1 | 97.02 | 1039 | 27 | 3 | 325 | 1362 | 1 | 1036 | 0 | 1744 |
| gi 310840978 gb GU105506.1 | 99.07 | 968 | 9 | 0 | 27 | 994 | 1 | 968 | 0 | 1738 |
| gi 258680809 emb FP084474.1 | 97.9 | 1002 | 20 | 1 | 344 | 1344 | 1 | 1002 | 0 | 1733 |
| gi 298392763 gb HM479625.1 | 97.8 | 1001 | 22 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1727 |
| gi 258684129 emb FP074949.1 | 97.8 | 1001 | 22 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1727 |
| gi 258688530 emb FP083190.1 | 97.7 | 1001 | 23 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1722 |
| gi 258688471 emb FP083131.1 | 97.7 | 1001 | 23 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1722 |
| gi 258687267 emb FP082522.1 | 97.7 | 1001 | 23 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1722 |
| gi 258680259 emb FP078659.1 | 97.7 | 1002 | 21 | 2 | 345 | 1345 | 1 | 1001 | 0 | 1722 |
| gi 258679892 emb FP078491.1 | 97.7 | 1001 | 23 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1722 |
| gi 258679706 emb FP078306.1 | 97.6 | 1002 | 22 | 2 | 344 | 1344 | 1 | 1001 | 0 | 1716 |
| gi 258687656 emb FP082713.1 | 97.5 | 1001 | 25 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1711 |
| gi 310841110 gb GU105638.1 | 98.75 | 961 | 12 | 0 | 27 | 987 | 1 | 961 | 0 | 1709 |
| gi 298392813 gb HM479675.1 | 97.4 | 1001 | 24 | 2 | 344 | 1344 | 1 | 999 | 0 | 1703 |
| gi 258684733 emb FP075336.1 | 97.4 | 1001 | 24 | 2 | 344 | 1344 | 1 | 999 | 0 | 1703 |
| gi 258680334 emb FP078734.1 | 97.3 | 1001 | 27 | 0 | 344 | 1344 | 1 | 1001 | 0 | 1700 |
| gi 258680314 emb FP078714.1 | 97.3 | 1001 | 27 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1700 |

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|-----------------------------|-------|------|----|---|-----|------|----|------|---|------|
| gi 310840826 gb GU105354.1 | 98.95 | 949 | 10 | 0 | 27 | 975 | 1 | 949 | 0 | 1698 |
| gi 258680175 emb FP084224.1 | 97.3 | 1001 | 25 | 2 | 344 | 1344 | 1 | 999 | 0 | 1698 |
| gi 310840972 gb GU105500.1 | 99.36 | 935 | 6 | 0 | 27 | 961 | 1 | 935 | 0 | 1694 |
| gi 310841115 gb GU105643.1 | 98.94 | 944 | 10 | 0 | 32 | 975 | 2 | 945 | 0 | 1688 |
| gi 73427009 gb DQ144095.1 | 99.57 | 925 | 4 | 0 | 511 | 1435 | 1 | 925 | 0 | 1687 |
| gi 258681714 emb FP079519.1 | 97 | 1001 | 30 | 0 | 345 | 1345 | 1 | 1001 | 0 | 1683 |
| gi 258689064 emb FP077679.1 | 97.01 | 1004 | 23 | 7 | 345 | 1345 | 1 | 1000 | 0 | 1681 |
| gi 310840973 gb GU105501.1 | 99.04 | 936 | 9 | 0 | 27 | 962 | 1 | 936 | 0 | 1679 |
| gi 310840928 gb GU105456.1 | 98.83 | 942 | 11 | 0 | 27 | 968 | 1 | 942 | 0 | 1679 |
| gi 310840975 gb GU105503.1 | 98.93 | 936 | 10 | 0 | 27 | 962 | 1 | 936 | 0 | 1674 |
| gi 310840927 gb GU105455.1 | 99.03 | 932 | 9 | 0 | 27 | 958 | 1 | 932 | 0 | 1672 |
| gi 310840976 gb GU105504.1 | 98.82 | 936 | 11 | 0 | 27 | 962 | 1 | 936 | 0 | 1668 |
| gi 310841112 gb GU105640.1 | 99.03 | 928 | 9 | 0 | 27 | 954 | 1 | 928 | 0 | 1664 |
| gi 310841093 gb GU105621.1 | 97.72 | 967 | 20 | 2 | 27 | 992 | 1 | 966 | 0 | 1663 |
| gi 310841111 gb GU105639.1 | 99.24 | 918 | 7 | 0 | 24 | 941 | 1 | 918 | 0 | 1657 |
| gi 310841173 gb GU105701.1 | 99.34 | 912 | 4 | 2 | 28 | 938 | 1 | 911 | 0 | 1650 |
| gi 310841037 gb GU105565.1 | 99.12 | 913 | 8 | 0 | 29 | 941 | 1 | 913 | 0 | 1642 |
| gi 383385719 gb JQ799156.1 | 97.89 | 948 | 18 | 2 | 507 | 1453 | 1 | 947 | 0 | 1639 |
| gi 310840926 gb GU105454.1 | 99.12 | 910 | 8 | 0 | 27 | 936 | 1 | 910 | 0 | 1637 |
| gi 310841163 gb GU105691.1 | 98.91 | 915 | 10 | 0 | 27 | 941 | 1 | 915 | 0 | 1635 |
| gi 310840866 gb GU105394.1 | 99.01 | 912 | 9 | 0 | 27 | 938 | 1 | 912 | 0 | 1635 |
| gi 310836892 gb GU101420.1 | 99.55 | 897 | 4 | 0 | 29 | 925 | 1 | 897 | 0 | 1635 |
| gi 310840980 gb GU105508.1 | 99.33 | 901 | 6 | 0 | 27 | 927 | 1 | 901 | 0 | 1631 |
| gi 310842043 gb GU106571.1 | 98.8 | 915 | 11 | 0 | 24 | 938 | 1 | 915 | 0 | 1629 |
| gi 310841348 gb GU105876.1 | 99.12 | 905 | 8 | 0 | 24 | 928 | 1 | 905 | 0 | 1628 |
| gi 310840979 gb GU105507.1 | 99.44 | 894 | 5 | 0 | 27 | 920 | 1 | 894 | 0 | 1624 |
| gi 310842898 gb GU107426.1 | 98.9 | 908 | 10 | 0 | 31 | 938 | 1 | 908 | 0 | 1622 |
| gi 310840856 gb GU105384.1 | 99.77 | 881 | 2 | 0 | 28 | 908 | 1 | 881 | 0 | 1616 |
| gi 310840807 gb GU105335.1 | 99.77 | 880 | 2 | 0 | 26 | 905 | 1 | 880 | 0 | 1615 |
| gi 239620487 gb FJ651880.1 | 99.44 | 889 | 5 | 0 | 1 | 889 | 27 | 915 | 0 | 1615 |
| gi 310841256 gb GU105784.1 | 98.89 | 898 | 10 | 0 | 28 | 925 | 1 | 898 | 0 | 1604 |
| gi 239620493 gb FJ651886.1 | 99.21 | 889 | 7 | 0 | 1 | 889 | 27 | 915 | 0 | 1604 |
| gi 310842899 gb GU107427.1 | 98.36 | 912 | 15 | 0 | 27 | 938 | 1 | 912 | 0 | 1602 |
| gi 310842632 gb GU107160.1 | 98.78 | 900 | 11 | 0 | 27 | 926 | 1 | 900 | 0 | 1602 |

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|---------------------------|-------|-----|----|---|-----|------|----|-----|---|------|
| g 310838465 gb GU102993.1 | 98.89 | 897 | 10 | 0 | 24 | 920 | 1 | 897 | 0 | 1602 |
| g 310842230 gb GU106758.1 | 98.88 | 896 | 10 | 0 | 24 | 919 | 1 | 896 | 0 | 1600 |
| g 310843290 gb GU107818.1 | 99.77 | 868 | 2 | 0 | 24 | 891 | 1 | 868 | 0 | 1592 |
| g 310842840 gb GU107368.1 | 98.45 | 905 | 13 | 1 | 28 | 931 | 1 | 905 | 0 | 1592 |
| g 310841113 gb GU105641.1 | 98.55 | 898 | 13 | 0 | 29 | 926 | 1 | 898 | 0 | 1587 |
| g 291331103 gb GU957635.1 | 98.88 | 889 | 10 | 0 | 1 | 889 | 27 | 915 | 0 | 1587 |
| g 310842044 gb GU106572.1 | 98.66 | 894 | 12 | 0 | 24 | 917 | 1 | 894 | 0 | 1585 |
| g 310841152 gb GU105680.1 | 98.77 | 892 | 10 | 1 | 27 | 918 | 1 | 891 | 0 | 1585 |
| g 310840857 gb GU105385.1 | 98.55 | 897 | 13 | 0 | 28 | 924 | 1 | 897 | 0 | 1585 |
| g 291328328 gb GU954860.1 | 99.43 | 873 | 5 | 0 | 1 | 873 | 29 | 901 | 0 | 1585 |
| g 310841879 gb GU106407.1 | 99.54 | 868 | 4 | 0 | 33 | 900 | 2 | 869 | 0 | 1581 |
| g 295651187 gb HM013421.1 | 98.76 | 889 | 11 | 0 | 1 | 889 | 28 | 916 | 0 | 1581 |
| g 239620005 gb FJ651398.1 | 98.76 | 889 | 11 | 0 | 1 | 889 | 16 | 904 | 0 | 1581 |
| g 291328488 gb GU955020.1 | 98.76 | 889 | 10 | 1 | 2 | 889 | 3 | 891 | 0 | 1580 |
| g 310841909 gb GU106437.1 | 99.54 | 866 | 4 | 0 | 27 | 892 | 1 | 866 | 0 | 1578 |
| g 239619923 gb FJ651316.1 | 99.42 | 869 | 5 | 0 | 21 | 889 | 1 | 869 | 0 | 1578 |
| g 169279765 gb EU464290.1 | 98.02 | 908 | 18 | 0 | 461 | 1368 | 18 | 925 | 0 | 1578 |
| g 291331104 gb GU957636.1 | 98.65 | 889 | 12 | 0 | 1 | 889 | 27 | 915 | 0 | 1576 |
| g 239620484 gb FJ651877.1 | 98.65 | 889 | 12 | 0 | 1 | 889 | 27 | 915 | 0 | 1576 |
| g 239620008 gb FJ651401.1 | 98.65 | 889 | 12 | 0 | 1 | 889 | 17 | 905 | 0 | 1576 |
| g 310839154 gb GU103682.1 | 98.98 | 879 | 9 | 0 | 27 | 905 | 1 | 879 | 0 | 1574 |
| g 310841445 gb GU105973.1 | 99.77 | 857 | 2 | 0 | 21 | 877 | 1 | 857 | 0 | 1572 |
| g 291328286 gb GU954818.1 | 98.54 | 889 | 13 | 0 | 1 | 889 | 28 | 916 | 0 | 1570 |
| g 239620488 gb FJ651881.1 | 98.54 | 889 | 13 | 0 | 1 | 889 | 27 | 915 | 0 | 1570 |
| g 239619382 gb FJ650775.1 | 98.54 | 889 | 13 | 0 | 1 | 889 | 27 | 915 | 0 | 1570 |
| g 310840977 gb GU105505.1 | 99.42 | 864 | 5 | 0 | 27 | 890 | 1 | 864 | 0 | 1568 |
| g 291328529 gb GU955061.1 | 98.43 | 889 | 14 | 0 | 1 | 889 | 28 | 916 | 0 | 1565 |
| g 310842046 gb GU106574.1 | 98.53 | 885 | 13 | 0 | 24 | 908 | 1 | 885 | 0 | 1563 |
| g 310841342 gb GU105870.1 | 99.77 | 852 | 2 | 0 | 24 | 875 | 1 | 852 | 0 | 1563 |
| g 310838205 gb GU102733.1 | 98.32 | 892 | 13 | 2 | 25 | 916 | 1 | 890 | 0 | 1563 |
| g 310837149 gb GU101677.1 | 99.42 | 860 | 5 | 0 | 33 | 892 | 3 | 862 | 0 | 1561 |
| g 310835970 gb GU100498.1 | 99.3 | 863 | 6 | 0 | 29 | 891 | 1 | 863 | 0 | 1561 |
| g 291331110 gb GU957642.1 | 98.31 | 889 | 15 | 0 | 1 | 889 | 27 | 915 | 0 | 1559 |
| g 239619213 gb FJ650606.1 | 98.31 | 888 | 15 | 0 | 1 | 888 | 27 | 914 | 0 | 1557 |

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|----------------------------|-------|-----|----|---|-----|------|----|-----|---|------|
| g 310842067 gb GU106595.1 | 99.53 | 854 | 4 | 0 | 24 | 877 | 1 | 854 | 0 | 1555 |
| g 310841114 gb GU105642.1 | 99.3 | 860 | 6 | 0 | 29 | 888 | 1 | 860 | 0 | 1555 |
| g 239619393 gb FJ650786.1 | 98.63 | 877 | 12 | 0 | 1 | 877 | 27 | 903 | 0 | 1554 |
| g 529080432 gb KF229853.1 | 98.96 | 866 | 9 | 0 | 24 | 889 | 1 | 866 | 0 | 1550 |
| g 310840808 gb GU105336.1 | 98.74 | 872 | 11 | 0 | 27 | 898 | 1 | 872 | 0 | 1550 |
| g 239619345 gb FJ650738.1 | 98.63 | 874 | 12 | 0 | 1 | 874 | 27 | 900 | 0 | 1548 |
| g 310841380 gb GU105908.1 | 99.53 | 849 | 4 | 0 | 29 | 877 | 1 | 849 | 0 | 1546 |
| g 291331651 gb GU958183.1 | 97.98 | 890 | 16 | 2 | 1 | 889 | 28 | 916 | 0 | 1543 |
| g 310838473 gb GU103001.1 | 99.64 | 843 | 3 | 0 | 24 | 866 | 1 | 843 | 0 | 1541 |
| g 310839536 gb GU104064.1 | 98.62 | 870 | 10 | 2 | 24 | 892 | 1 | 869 | 0 | 1539 |
| g 291331102 gb GU957634.1 | 99.41 | 848 | 5 | 0 | 42 | 889 | 1 | 848 | 0 | 1539 |
| g 239620288 gb FJ651681.1 | 98.73 | 866 | 11 | 0 | 1 | 866 | 11 | 876 | 0 | 1539 |
| g 310838146 gb GU102674.1 | 98.73 | 866 | 10 | 1 | 25 | 890 | 1 | 865 | 0 | 1537 |
| g 529083001 gb KF232422.1 | 98.62 | 867 | 12 | 0 | 1 | 867 | 23 | 889 | 0 | 1535 |
| g 529080529 gb KF229950.1 | 98.84 | 861 | 10 | 0 | 2 | 862 | 1 | 861 | 0 | 1535 |
| g 291329410 gb GU955942.1 | 98.73 | 864 | 11 | 0 | 1 | 864 | 14 | 877 | 0 | 1535 |
| g 529080654 gb KF230075.1 | 99.06 | 854 | 8 | 0 | 1 | 854 | 21 | 874 | 0 | 1533 |
| g 310841035 gb GU105563.1 | 98.5 | 868 | 13 | 0 | 28 | 895 | 1 | 868 | 0 | 1531 |
| g 169287659 gb EU472184.1 | 97.44 | 898 | 23 | 0 | 471 | 1368 | 1 | 898 | 0 | 1531 |
| g 310838633 gb GU103161.1 | 99.64 | 837 | 3 | 0 | 33 | 869 | 3 | 839 | 0 | 1530 |
| g 310842151 gb GU106679.1 | 99.4 | 840 | 5 | 0 | 27 | 866 | 1 | 840 | 0 | 1524 |
| g 310842099 gb GU106627.1 | 99.4 | 840 | 5 | 0 | 27 | 866 | 1 | 840 | 0 | 1524 |
| g 310841955 gb GU106483.1 | 99.4 | 840 | 5 | 0 | 24 | 863 | 1 | 840 | 0 | 1524 |
| g 310841878 gb GU106406.1 | 99.4 | 840 | 5 | 0 | 24 | 863 | 1 | 840 | 0 | 1524 |
| g 310838817 gb GU103345.1 | 99.64 | 834 | 3 | 0 | 29 | 862 | 1 | 834 | 0 | 1524 |
| g 310838576 gb GU103104.1 | 99.52 | 837 | 3 | 1 | 27 | 863 | 1 | 836 | 0 | 1522 |
| g 310841036 gb GU105564.1 | 98.38 | 865 | 14 | 0 | 28 | 892 | 1 | 865 | 0 | 1520 |
| g 164454293 dbj AB265290.1 | 97.53 | 889 | 21 | 1 | 478 | 1366 | 1 | 888 | 0 | 1519 |
| g 310841954 gb GU106482.1 | 99.05 | 845 | 8 | 0 | 33 | 877 | 1 | 845 | 0 | 1517 |
| g 310841907 gb GU106435.1 | 99.4 | 835 | 5 | 0 | 29 | 863 | 1 | 835 | 0 | 1515 |
| g 310838717 gb GU103245.1 | 99.52 | 833 | 3 | 1 | 33 | 865 | 3 | 834 | 0 | 1515 |
| g 310833518 gb GU098046.1 | 99.52 | 832 | 4 | 0 | 33 | 864 | 1 | 832 | 0 | 1515 |
| g 310841908 gb GU106436.1 | 99.28 | 837 | 6 | 0 | 27 | 863 | 1 | 837 | 0 | 1513 |
| g 118136060 gb EF071471.1 | 98.82 | 849 | 10 | 0 | 1 | 849 | 20 | 868 | 0 | 1513 |

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|---------------------------|-------|-----|----|---|----|-----|----|-----|---|------|
| g 310841536 gb GU106064.1 | 99.16 | 838 | 7 | 0 | 29 | 866 | 1 | 838 | 0 | 1509 |
| g 310841078 gb GU105606.1 | 99.17 | 839 | 6 | 1 | 27 | 864 | 1 | 839 | 0 | 1509 |
| g 310838778 gb GU103306.1 | 99.16 | 838 | 7 | 0 | 28 | 865 | 1 | 838 | 0 | 1509 |
| g 310841959 gb GU106487.1 | 99.28 | 835 | 5 | 1 | 29 | 863 | 1 | 834 | 0 | 1507 |
| g 310841378 gb GU105906.1 | 99.05 | 840 | 8 | 0 | 24 | 863 | 1 | 840 | 0 | 1507 |
| g 310842517 gb GU107045.1 | 98.15 | 863 | 16 | 0 | 27 | 889 | 1 | 863 | 0 | 1506 |
| g 310833629 gb GU098157.1 | 98.82 | 845 | 10 | 0 | 22 | 866 | 1 | 845 | 0 | 1506 |
| g 310840786 gb GU105314.1 | 98.93 | 840 | 9 | 0 | 27 | 866 | 1 | 840 | 0 | 1502 |
| g 310839537 gb GU104065.1 | 98.81 | 843 | 10 | 0 | 24 | 866 | 1 | 843 | 0 | 1502 |
| g 310841875 gb GU106403.1 | 98.47 | 851 | 13 | 0 | 27 | 877 | 1 | 851 | 0 | 1500 |
| g 310840855 gb GU105383.1 | 98.7 | 845 | 11 | 0 | 27 | 871 | 1 | 845 | 0 | 1500 |
| g 310837024 gb GU101552.1 | 98.36 | 856 | 11 | 3 | 27 | 879 | 1 | 856 | 0 | 1500 |
| g 310838419 gb GU102947.1 | 99.88 | 814 | 1 | 0 | 50 | 863 | 4 | 817 | 0 | 1498 |
| g 110440903 gb DQ800503.1 | 99.04 | 835 | 8 | 0 | 1 | 835 | 33 | 867 | 0 | 1498 |
| g 310842583 gb GU107111.1 | 98.36 | 852 | 14 | 0 | 25 | 876 | 1 | 852 | 0 | 1496 |
| g 310840877 gb GU105405.1 | 98.81 | 840 | 10 | 0 | 27 | 866 | 1 | 840 | 0 | 1496 |
| g 310837892 gb GU102420.1 | 98.81 | 840 | 10 | 0 | 24 | 863 | 1 | 840 | 0 | 1496 |
| g 310833517 gb GU098045.1 | 99.16 | 831 | 7 | 0 | 33 | 863 | 1 | 831 | 0 | 1496 |
| g 310842068 gb GU106596.1 | 98.24 | 854 | 15 | 0 | 24 | 877 | 1 | 854 | 0 | 1495 |
| g 399141153 gb JQ265125.1 | 98.69 | 842 | 10 | 1 | 38 | 878 | 1 | 842 | 0 | 1493 |
| g 310842262 gb GU106790.1 | 99.39 | 823 | 5 | 0 | 21 | 843 | 1 | 823 | 0 | 1493 |
| g 310833423 gb GU097951.1 | 99.16 | 829 | 7 | 0 | 36 | 864 | 4 | 832 | 0 | 1493 |
| g 310842231 gb GU106759.1 | 98.58 | 843 | 12 | 0 | 24 | 866 | 1 | 843 | 0 | 1491 |
| g 310842154 gb GU106682.1 | 98.69 | 840 | 11 | 0 | 24 | 863 | 1 | 840 | 0 | 1491 |
| g 310842135 gb GU106663.1 | 98.69 | 840 | 11 | 0 | 27 | 866 | 1 | 840 | 0 | 1491 |
| g 310842045 gb GU106573.1 | 98.69 | 840 | 11 | 0 | 24 | 863 | 1 | 840 | 0 | 1491 |
| g 310841956 gb GU106484.1 | 98.69 | 840 | 11 | 0 | 24 | 863 | 1 | 840 | 0 | 1491 |
| g 310842138 gb GU106666.1 | 98.57 | 840 | 12 | 0 | 27 | 866 | 1 | 840 | 0 | 1485 |
| g 310838495 gb GU103023.1 | 99.03 | 828 | 8 | 0 | 24 | 851 | 1 | 828 | 0 | 1485 |
| g 239620227 gb FJ651620.1 | 98.34 | 844 | 14 | 0 | 35 | 878 | 2 | 845 | 0 | 1482 |
| g 399141562 gb JQ265534.1 | 98.68 | 835 | 9 | 2 | 1 | 833 | 65 | 899 | 0 | 1480 |
| g 310842150 gb GU106678.1 | 98.57 | 837 | 12 | 0 | 27 | 863 | 1 | 837 | 0 | 1480 |
| g 310842101 gb GU106629.1 | 98.45 | 840 | 13 | 0 | 24 | 863 | 1 | 840 | 0 | 1480 |
| g 310842097 gb GU106625.1 | 98.45 | 840 | 13 | 0 | 27 | 866 | 1 | 840 | 0 | 1480 |

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|---------------------------|-------|-----|----|---|----|-----|---|-----|---|------|
| g 310841108 gb GU105636.1 | 97.79 | 861 | 14 | 5 | 39 | 895 | 2 | 861 | 0 | 1480 |
| g 310837285 gb GU101813.1 | 98.91 | 828 | 9 | 0 | 24 | 851 | 1 | 828 | 0 | 1480 |

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