

RDP: Release 11

SeqMatch :: Result

**Seqmatch:** version 3**RDP Data:** release11_6**Data Set:** both type and non-type strains, both environmental (uncultured) sequences and isolates, both near-full-length or short sequences, good quality sequences**Comments:** 3351829 sequences were included in the search
The screening was based on 7-base oligomers**Query Submit Date:** Thu Mar 23 10:48:25 EDT 2023Match hit format: short ID, orientation, similarity score, S_ab score, unique common oligomers and sequence full name. More [help](#) is available.**Lineage:****Results for Query Sequence: LL5, 694 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Caulobacteriales (20)

family Caulobacteraceae (20)

genus Brevundimonas (20)

S000016026	not_calculated 0.991 1321	Brevundimonas vesicularis; ATCC 11426 (T); AJ007801
S000017941	not_calculated 0.991 1219	alpha proteobacterium VUN10077; AF137356
S000112396	not_calculated 0.991 1344	Brevundimonas vesicularis; LMG 2350 (T); AJ227780
S000112771	not_calculated 0.991 1344	Brevundimonas vesicularis; LMG 11141; AJ227781
S000112773	not_calculated 0.991 1344	Brevundimonas sp. V4.BO.07; AJ227800
S000113250	not_calculated 0.991 1344	Brevundimonas intermedia; ATCC 15262(T); AJ227786
S000371153	not_calculated 1.000 0544	uncultured bacterium; Kazan-MN12BT3-285; AY593393
S001420253	not_calculated 1.000 0505	uncultured bacterium; C2_65H09f; AB483509
S001420254	not_calculated 1.000 0505	uncultured bacterium; C2_65J21f; AB483510
S001420341	not_calculated 1.000 0505	uncultured bacterium; C2_S4A01f; AB483597
S001420342	not_calculated 1.000 0505	uncultured bacterium; C2_S4D12f; AB483598
S001420343	not_calculated 1.000 0505	uncultured bacterium; C2_S4H10f; AB483599
S001420344	not_calculated 1.000 0505	uncultured bacterium; C2_S4I05f; AB483600
S001421083	not_calculated 1.000 0505	uncultured bacterium; N2_12B20f; AB484339
S001421084	not_calculated 1.000 0505	uncultured bacterium; N2_12F08f; AB484340
S001421085	not_calculated 1.000 0505	uncultured bacterium; N2_12P07f; AB484341
S001422066	not_calculated 1.000 0505	uncultured bacterium; N2_S4F03f; AB485322
S002411029	not_calculated 1.000 0536	Brevundimonas sp. CB1-I; HQ876726
S003614866	not_calculated 1.000 0511	Brevundimonas sp. TW_LB_DL4; JX402644
S004483400	not_calculated 1.000 0533	Brevundimonas sp. sed039; KR067623

Lineage:**Results for Query Sequence: LL4, 602 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Sphingomonadales (20)

family Sphingomonadaceae (20)

genus Sphingobium (20)

S000127496	not_calculated 1.000 1333	Sphingobium yanoikuyae; KF706; AB109749
S000130603	not_calculated 1.000 1341	Sphingomonas sp.; B1; X94099
S000130607	not_calculated 1.000 1345	Sphingobium yanoikuyae; PAH-degrading; X85023
S000379067	not_calculated 1.000 1227	Sphingobium yanoikuyae; DD109; AY574367
S000391716	not_calculated 1.000 1316	Sphingobium yanoikuyae; AF331661
S000437529	not_calculated 1.000 1336	Sphingobium yanoikuyae; B1; U37524
S000538425	not_calculated 1.000 1258	estrogen-degrading bacterium KC14; DQ066444
S000568813	not_calculated 1.000 1001	Sphingomonas sp. 14DN-61; AB200352
S000605852	not_calculated 1.000 1331	Sphingomonas sp. PF-D; DQ202285
S000751080	not_calculated 1.000 1356	Sphingomonas sp. H-1; EF012277
S000752101	not_calculated 1.000 1356	Sphingomonas sp. ZnH-1; EF061133
S000905547	not_calculated 1.000 1249	uncultured delta proteobacterium; COREB41; EF562226
S000907483	not_calculated 1.000 0656	uncultured alpha proteobacterium; MS071A1_A02; EF697268
S000907536	not_calculated 1.000 0640	uncultured alpha proteobacterium; MS071A1_F01; EF697321
S000907639	not_calculated 1.000 0672	uncultured alpha proteobacterium; MS072A1_G12; EF697424
S000907643	not_calculated 1.000 0568	uncultured alpha proteobacterium; MS072A1_H04; EF697428
S000915046	not_calculated 1.000 0672	uncultured alpha proteobacterium; MS136A1_C11; EF704831
S001034313	not_calculated 1.000 1174	uncultured Sphingomonas sp.; 1P-1-C04; EU704732
S001034601	not_calculated 1.000 1170	uncultured Sphingomonas sp.; 1P-2-E24; EU705020
S001177388	not_calculated 1.000 1281	uncultured Sphingobium sp.; G13-S-1-B02; FJ191702

Lineage:**Results for Query Sequence: LLX12A, 634 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Mycobacteriales (20)

family Dietziaceae (20)

genus Dietzia (20)

S000001586	not_calculated 1.000 1234	Dietzia sp. R19; Y08315
S000002346	not_calculated 1.000 1234	Dietzia sp. R23; Y08316
S000007762	not_calculated 1.000 1234	Dietzia sp. R30; Y08317
S000021256	not_calculated 1.000 1234	Dietzia sp. R18; Y08314
S000022367	not_calculated 1.000 1234	Dietzia sp. R32; Y08318
S000331657	not_calculated 1.000 1346	Dietzia daqingensis; 263; AY603001

S000331658	not_calculated	1.000	1322	Dietzia daqingensis; 263; AY603002
S000537378	not_calculated	1.000	1390	Dietzia sp. P27-19; DQ060380
S000544157	not_calculated	1.000	1410	Dietzia natronolimnaea; AC21r; AJ717372
S000544158	not_calculated	1.000	1405	Dietzia natronolimnaea; CV46; AJ717373
S000640972	not_calculated	1.000	0806	Dietzia sp. 291_(IO)_102mbsf; DQ344839
S000730707	not_calculated	1.000	0808	Dietzia sp. LOT4; DQ839173
S000775767	not_calculated	1.000	1404	Dietzia natronolimnaea; LLA; DQ333285
S000860079	not_calculated	1.000	1359	Dietzia sp. 1/4_C7/16_33; EF540468
S000925437	not_calculated	1.000	1372	Dietzia sp. F09TDL; AB266602
S000925438	not_calculated	1.000	1382	Dietzia sp. W02TDL; AB266603
S000995867	not_calculated	1.000	1367	Dietzia cercidiphylli (T); YIM 65002; EU375846
S001093299	not_calculated	1.000	1311	Dietzia dagingensis; JAM-AC0601; AB362252
S001095826	not_calculated	1.000	1398	Dietzia natronolimnaea; TPL19; EU373398
S001264033	not_calculated	1.000	1359	Dietzia natronolimnaea; DSM 44860; FJ468329

Lineage:**Results for Query Sequence: WG23A, 687 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Caulobacterales (20)

family Caulobacteraceae (20)

genus Brevundimonas (20)

S000113250	not_calculated	0.983	1344	Brevundimonas intermedia; ATCC 15262(T); AJ227786
S000371153	not_calculated	0.989	0544	uncultured bacterium; Kazan-MN12BT3-285; AY593393
S000382694	not_calculated	0.983	1336	Brevundimonas intermedia; MBIC2712, ATCC15262; AB023784
S000639898	not_calculated	0.983	1347	Brevundimonas sp. CHNTR43; DQ337577
S000764930	not_calculated	0.983	1141	uncultured Brevundimonas sp.; RBE2Cl-150; EF111191
S000841764	not_calculated	0.992	0589	Brevundimonas sp. SSRS6-4; AB299746
S001292092	not_calculated	0.983	0801	Brevundimonas sp. AKB-2008-JO6; AM988993
S001352776	not_calculated	0.986	0485	Brevundimonas sp. WH011; FJ866676
S001420253	not_calculated	0.988	0505	uncultured bacterium; C2_65H09f; AB483509
S001420254	not_calculated	0.988	0505	uncultured bacterium; C2_65J21f; AB483510
S001420341	not_calculated	0.988	0505	uncultured bacterium; C2_S4A01f; AB483597
S001420342	not_calculated	0.988	0505	uncultured bacterium; C2_S4D12f; AB483598
S001420343	not_calculated	0.988	0505	uncultured bacterium; C2_S4H10f; AB483599
S001420344	not_calculated	0.988	0505	uncultured bacterium; C2_S4I05f; AB483600
S001421083	not_calculated	0.988	0505	uncultured bacterium; N2_12B20f; AB484339
S001421084	not_calculated	0.988	0505	uncultured bacterium; N2_12F08f; AB484340
S001421085	not_calculated	0.988	0505	uncultured bacterium; N2_12P07f; AB484341
S001422066	not_calculated	0.988	0505	uncultured bacterium; N2_S4F03f; AB485322
S002415342	not_calculated	0.983	0826	uncultured bacterium; d21112b26; FR687151
S003614866	not_calculated	0.988	0511	Brevundimonas sp. TW_LB_DL4; JX402644

Lineage:**Results for Query Sequence: WG21, 831 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Bacteroidetes (20)

class Flavobacteriia (20)

order Flavobacteriales (20)

family Flavobacteriaceae (20)

genus Flavobacterium (20)

S000722062	not_calculated	0.992	1363	Flavobacterium sp. YO10; DQ778309
S000722063	not_calculated	0.994	1369	Flavobacterium sp. YO11; DQ778310
S000722064	not_calculated	1.000	1330	Flavobacterium sp. YO15; DQ778311
S000736238	not_calculated	0.991	0766	Flavobacterium sp. EPACd10; DQ922756
S001046232	not_calculated	0.984	1325	Flavobacterium johnsoniae; 188; EU730945
S001168052	not_calculated	0.985	0393	uncultured bacterium; sscpBac_AB2; FM179197
S001168057	not_calculated	0.982	0394	uncultured bacterium; sscpBac_A2; FM179202
S001168059	not_calculated	0.982	0394	uncultured bacterium; sscpBac_A8; FM179204
S001168062	not_calculated	0.982	0394	uncultured bacterium; sscpBac_B5; FM179207
S001168091	not_calculated	1.000	0394	uncultured bacterium; sscpBac_K5; FM179236
S001326244	not_calculated	0.984	0753	uncultured bacterium; MA00094D04; FJ772290
S001326249	not_calculated	0.983	0718	uncultured bacterium; MA00094F03; FJ772295
S001326347	not_calculated	0.983	0719	uncultured bacterium; MA00070G12; FJ772393
S001341637	not_calculated	0.982	0796	uncultured Bacteroidetes bacterium; MeF05cnp11F6; FJ828057
S002223161	not_calculated	0.988	0782	Flavobacterium sp. B257; FR696355
S003277855	not_calculated	0.992	1288	Flavobacterium sp. 698-1-08; HE774302
S003919304	not_calculated	0.983	1296	Flavobacterium sp. T123L.10.PLAT.SE.H.Kidney.N; JX287857
S003919305	not_calculated	0.992	1297	Flavobacterium sp. T124L.10.PLAT.SE.H.Kidney.N; JX287858
S004006057	not_calculated	0.990	0676	Flavobacterium sp. T123.10.PLAT.SE.H.Kidney.N; JX287604
S004006058	not_calculated	0.990	0676	Flavobacterium sp. T124.10.PLAT.SE.H.Kidney.N; JX287605

Lineage:**Results for Query Sequence: LL1, 598 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Micrococcales (20)

family Micrococcaceae (20)

genus Kocuria (20)

S000711449	not_calculated	0.977	0704	Kocuria sp. A05; AM284987
S000903102	not_calculated	0.982	1299	Kocuria sp. TK815; EU045306
S001015898	not_calculated	0.973	0943	Bacterium PE_IPFFC13; EU476033
S003286892	not_calculated	0.977	1008	Kocuria rosea; NCCP-718; AB735689
S003804637	not_calculated	0.988	1290	Kocuria rosea; 72; KC843411
S004043774	not_calculated	0.977	0952	Kocuria rosea; BD12OL1-R58; FR877712
S004043804	not_calculated	0.973	0952	Kocuria rosea; BD12OL1-S48; FR877742
S004053346	not_calculated	0.988	1329	Kocuria sp. FB6; KF444432
S004084681	not_calculated	0.977	1355	Kocuria rosea; 1-Sj-6-1-5-M; KJ009471

S004454024	not_calculated	0.988 0987	Kocuria rosea; PVL14; KP072779
S004457330	not_calculated	0.977 0766	Kocuria sp. ET5s10.21; LN615076
S004457331	not_calculated	0.977 0698	Kocuria sp. ET5sH1.1; LN615077
S004457365	not_calculated	0.977 0645	Kocuria sp. Pia1s11.2; LN615111
S004457376	not_calculated	0.977 0712	Kocuria sp. SC5s6.1; LN615122
S004457377	not_calculated	0.977 0759	Kocuria sp. SC5s4.2; LN615123
S004458991	not_calculated	0.988 1097	Kocuria rosea; 0312MAR28B7; LN774766
S004483411	not_calculated	0.977 0525	Kocuria sp. sed333; KR067634
S004488126	not_calculated	0.975 0512	Kocuria sp. s7r3; KR263100
S004498311	not_calculated	0.978 0816	Kocuria rosea; HQB635; KT758560
S004538049	not_calculated	0.977 1316	Kocuria rosea; KNUSC1032; KP342208

Lineage:**Results for Query Sequence: WG40, 674 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000558121	not_calculated	0.993 1397	Pseudomonas fluorescens; FLM05-1; DQ084459
S001015370	not_calculated	0.993 1370	Pseudomonas lundensis; a301; EU434368
S001059393	not_calculated	0.993 1319	uncultured bacterium; PB1_ aai26b05; EU460294
S001418535	not_calculated	0.993 1351	Pseudomonas sp. HW08; FJ999660
S001495216	not_calculated	0.993 1285	uncultured bacterium; nbw229e06c1; GQ069152
S001495227	not_calculated	0.993 1285	uncultured bacterium; nbw229f10c1; GQ069163
S001495264	not_calculated	0.993 1281	uncultured bacterium; nbw230b08c1; GQ069200
S001495676	not_calculated	0.993 1285	uncultured bacterium; nbw230e08c1; GQ069612
S001495736	not_calculated	0.993 1285	uncultured bacterium; nbw231e08c1; GQ069672
S001495782	not_calculated	0.993 1284	uncultured bacterium; nbw232b09c1; GQ069718
S002056531	not_calculated	0.993 1286	uncultured bacterium; ncd15f11c1; HM251505
S002056981	not_calculated	0.993 1285	uncultured bacterium; ncd22g02c1; HM251955
S002057115	not_calculated	0.993 1286	uncultured bacterium; ncd24h03c1; HM252089
S002119264	not_calculated	0.993 1285	uncultured bacterium; ncd405e02c1; HM314238
S002128060	not_calculated	0.993 1286	uncultured bacterium; ncd406b11c1; HM323034
S002128144	not_calculated	0.993 1287	uncultured bacterium; ncd407g05c1; HM323118
S002128158	not_calculated	0.993 1285	uncultured bacterium; ncd407f04c1; HM323132
S002128351	not_calculated	0.993 1285	uncultured bacterium; ncd410g11c1; HM323325
S002134865	not_calculated	0.993 1283	uncultured bacterium; ncd939c02c1; HM329839
S002137849	not_calculated	0.993 1284	uncultured bacterium; ncd1062b10c1; HM332823

Lineage:**Results for Query Sequence: WG42, 673 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Mycobacteriales (20)

family Mycobacteriaceae (20)

genus Mycobacterium (20)

S000250696	not_calculated	1.000 1380	Mycobacterium sacrum; BN 3151; AY235429
S000428130	not_calculated	1.000 1254	Mycobacterium sp. CH-1; AF054278
S000432488	not_calculated	1.000 1336	Mycobacterium frederiksbergense; VM0531; AF544629
S000980941	not_calculated	1.000 0953	marine sponge bacterium FILTER6B101; EU346419
S000981040	not_calculated	1.000 0820	marine sponge bacterium plateOTU31; EU346518
S001001550	not_calculated	1.000 1144	uncultured Mycobacterium sp.; Sc59; EU375206
S001019877	not_calculated	1.000 1235	Mycobacterium sp. 18-08; EU167961
S001019882	not_calculated	1.000 1284	Mycobacterium sp. 20-01; EU167966
S001019883	not_calculated	1.000 1293	Mycobacterium sp. 20-02; EU167967
S001019885	not_calculated	1.000 1292	Mycobacterium sp. 20-05; EU167969
S001139959	not_calculated	1.000 0758	uncultured bacterium; Mar_CL-090544_OTU-1; EU808564
S001139963	not_calculated	1.000 0838	uncultured bacterium; Mar_CL-09056_OTU-1; EU808568
S001154608	not_calculated	1.000 0828	Mycobacterium sp. FS-YC6689; EU836191
S001490273	not_calculated	1.000 1261	uncultured bacterium; nbw68c02c1; GQ064209
S001493298	not_calculated	1.000 1260	uncultured bacterium; nbw1125b10c1; GQ067234
S001611325	not_calculated	1.000 0794	Mycobacterium sp. BALT-12-S17; FM998723
S002155999	not_calculated	1.000 1336	Mycobacterium sacrum; Qtx-19; GU201853
S002225495	not_calculated	1.000 1281	Mycobacterium sp. CCB AU 25324; HM107174
S002687870	not_calculated	1.000 1260	uncultured bacterium; ncd2031f10c1; JF167937
S003610779	not_calculated	1.000 1039	Mycobacterium sp. BB36; FR693306

Lineage:**Results for Query Sequence: WG43, 673 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Bacteroidetes (20)

class Flavobacteriia (20)

order Flavobacteriales (20)

family Flavobacteriaceae (20)

genus Flavobacterium (20)

S000544095	not_calculated	0.897 1306	Flavobacterium sp. 10B; AJ698832
S000701813	not_calculated	0.909 0806	Flavobacterium sp. RI02; DQ530115
S000701847	not_calculated	0.893 0727	Flavobacterium johnsoniae; RI27; DQ530149
S000808170	not_calculated	0.948 0478	uncultured bacterium; MA61_2003T1c_46; EF377830
S000808195	not_calculated	0.935 0508	uncultured bacterium; MA61_2003T1c_20; EF377855
S000808735	not_calculated	0.896 0749	uncultured bacterium; MA43_2003DFb_C11; EF378395
S000979099	not_calculated	0.906 1392	Flavobacterium sp. R-32568; AM403636
S001253265	not_calculated	0.899 0515	uncultured Bacteroidetes bacterium; MA161H04; FJ532826
S001253298	not_calculated	0.934 0408	uncultured Bacteroidetes bacterium; MA161H01; FJ532859
S001253568	not_calculated	0.914 0521	uncultured Bacteroidetes bacterium; MA00164C04; FJ533129
S001341703	not_calculated	0.947 0748	uncultured Bacteroidetes bacterium; MEf05b11D11; FJ828123
S001576873	not_calculated	0.911 1398	Flavobacterium banpakuense (T); 15F3; GQ281770

S002056081	not_calculated	0.902	1285	uncultured bacterium; ncd09c06c1; HM251055
S002223142	not_calculated	0.899	0807	Flavobacterium sp. B167; FR696336
S002232284	not_calculated	0.963	1405	Flavobacterium chungbukense (T); CS100; HM627539
S002240951	not_calculated	0.892	1289	uncultured bacterium; nby263c01c1; HM808322
S002245916	not_calculated	0.892	1289	uncultured bacterium; nby262b11c1; HM813287
S004078079	not_calculated	0.963	1366	Flavobacterium sp. 200Cs-4; AB897657
S004089498	not_calculated	0.908	1317	Flavobacterium sp. TV3aMay; KJ482884
S004595568	not_calculated	0.891	0569	uncultured bacterium; I-R_A12; LC023463

Lineage:**Results for Query Sequence: LLX17, 673 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Propionibacteriales (20)

family Nocardioidaceae (20)

genus Aeromicrobium (20)

S000027750	not_calculated	0.897	0632	Nocardioides sp. 2.20; AJ299233
S000028280	not_calculated	0.914	0603	Nocardioides sp. 2.14; AJ299232
S000433700	not_calculated	0.912	0442	uncultured actinomycete; ACT-A2; AJ427636
S000860070	not_calculated	0.972	1342	Aeromicrobium sp. 1_C7_65; EF540459
S000860077	not_calculated	0.896	1336	Aeromicrobium sp. 1/4_C7/16_31; EF540466
S000893634	not_calculated	0.874	1315	Aeromicrobium kwangyangensis; CW35; EF693740
S000968355	not_calculated	0.984	0492	bacterium EP1.29; EU279889
S001154138	not_calculated	0.872	1337	Aeromicrobium kwangyangensis; DS23; EU834249
S001199074	not_calculated	0.869	1286	Aeromicrobium sp. I_Gauze_W_12_4; FJ267536
S001255820	not_calculated	0.889	0751	uncultured bacterium; C042; FJ561558
S002973444	not_calculated	0.877	0740	uncultured bacterium; A083_BATS; HM032273
S002973478	not_calculated	0.897	0741	uncultured bacterium; A171_BATS; HM032307
S003537983	not_calculated	0.869	1368	uncultured bacterium; AC1C2BD02; JQ428031
S003747861	not_calculated	0.868	1297	Aeromicrobium sp. Sr29; JX949248
S003789365	not_calculated	0.869	1332	Aeromicrobium sp. Es15; JQ977434
S004231673	not_calculated	0.886	1306	Aeromicrobium sp. W-NaCl-1; KM083518
S004492038	not_calculated	0.871	0680	Aeromicrobium sp. VO41-3; KT152267
S004531243	not_calculated	0.900	1319	Aeromicrobium sp. VO40-3; KM406763
S004594968	not_calculated	0.869	0564	uncultured bacterium; RB-A-1_G09; LC022863
S004596305	not_calculated	0.888	0561	uncultured bacterium; TB-A-1_H04; LC024200

Lineage:**Results for Query Sequence: LL9, 601 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Propionibacteriales (20)

family Nocardioidaceae (20)

genus Aeromicrobium (20)

S000027750	not_calculated	0.884	0632	Nocardioides sp. 2.20; AJ299233
S000433700	not_calculated	0.912	0442	uncultured actinomycete; ACT-A2; AJ427636
S000533383	not_calculated	0.882	1277	Nocardioides sp. 43/14; AY571805
S000605629	not_calculated	0.908	1244	Nocardioidaceae bacterium SM2; DQ195813
S000860070	not_calculated	0.983	1342	Aeromicrobium sp. 1_C7_65; EF540459
S000860077	not_calculated	0.908	1336	Aeromicrobium sp. 1/4_C7/16_31; EF540466
S000893634	not_calculated	0.884	1315	Aeromicrobium kwangyangensis; CW35; EF693740
S000968355	not_calculated	0.939	0492	bacterium EP1.29; EU279889
S001154138	not_calculated	0.882	1337	Aeromicrobium kwangyangensis; DS23; EU834249
S001255820	not_calculated	0.902	0751	uncultured bacterium; C042; FJ561558
S001874242	not_calculated	0.890	0846	Aeromicrobium sp. CNRA13; GU300713
S002973430	not_calculated	0.884	0732	uncultured bacterium; A062_BATS; HM032259
S002973444	not_calculated	0.910	0740	uncultured bacterium; A083_BATS; HM032273
S002973478	not_calculated	0.912	0741	uncultured bacterium; A171_BATS; HM032307
S003054374	not_calculated	0.887	0934	uncultured bacterium; gs186; JF420792
S003789365	not_calculated	0.892	1332	Aeromicrobium sp. Es15; JQ977434
S004231673	not_calculated	0.897	1306	Aeromicrobium sp. W-NaCl-1; KM083518
S004492037	not_calculated	0.903	0690	Aeromicrobium sp. VO38-3; KT152266
S004492038	not_calculated	0.912	0680	Aeromicrobium sp. VO41-3; KT152267
S004531243	not_calculated	0.913	1319	Aeromicrobium sp. VO40-3; KM406763

Lineage:**Results for Query Sequence: LL8, 642 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000966025	not_calculated	0.991	1333	Pseudomonas sp. G3DM-12; EU037274
S000966026	not_calculated	0.991	1363	Pseudomonas sp. G3DM-13; EU037275
S000966040	not_calculated	0.991	1404	Pseudomonas sp. G3DM-86; EU037289
S001167883	not_calculated	0.991	0719	uncultured bacterium; P3bac_4; FM179028
S001167903	not_calculated	0.991	0732	uncultured bacterium; P3bac_29; FM179048
S001167912	not_calculated	0.991	0777	uncultured bacterium; P3bac_38; FM179057
S001167913	not_calculated	0.991	0701	uncultured bacterium; P3bac_71; FM179058
S001167915	not_calculated	0.991	0675	uncultured bacterium; P3bac_73; FM179060
S001167921	not_calculated	0.991	0716	uncultured bacterium; P3bac_83; FM179066
S001167923	not_calculated	0.991	0767	uncultured bacterium; P3bac_85; FM179068
S001167925	not_calculated	0.991	0765	uncultured bacterium; P3bac_87; FM179070
S001167928	not_calculated	0.991	0732	uncultured bacterium; P3bac_90; FM179073
S001167933	not_calculated	0.991	0757	uncultured bacterium; P3bac_96; FM179078
S001167937	not_calculated	0.991	0740	uncultured bacterium; P3bac_102; FM179082
S001167941	not_calculated	0.991	0732	uncultured bacterium; P3bac_106; FM179086

S001167943	not_calculated 0.991 0777	uncultured bacterium; P3bac_108; FM179088
S002957124	not_calculated 1.000 0660	Pseudomonas sp. PE-R2A-2; JN571350
S004593561	not_calculated 0.992 0892	uncultured bacterium; SAB14; KT900430
S004593568	not_calculated 0.992 0892	uncultured bacterium; SAB23; KT900437
S004593572	not_calculated 0.992 0887	uncultured bacterium; SAB29; KT900441

Lineage:**Results for Query Sequence: WG58B, 778 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000428774	not_calculated 0.990 1373	Pseudomonas fragi (T); ATCC 4973; AF094733
S000536157	not_calculated 0.990 1421	uncultured bacterium; rRNA080; AY958853
S000536225	not_calculated 0.990 1406	uncultured bacterium; rRNA148; AY958921
S000536289	not_calculated 0.990 1424	uncultured bacterium; rRNA212; AY958985
S000558123	not_calculated 0.990 1397	Pseudomonas sp. FLM05-3; DQ084461
S000689851	not_calculated 0.990 1411	uncultured bacterium; FS140-145B-02; DQ513010
S000769444	not_calculated 0.990 1218	Pseudomonas fragi; RBE1CD-130; EF111136
S001024544	not_calculated 0.990 1323	uncultured bacterium; nbt210d12; EU534753
S001026044	not_calculated 0.990 1324	uncultured bacterium; nbt61f02; EU536253
S001026785	not_calculated 0.990 1322	uncultured bacterium; nbt218d10; EU536994
S001028927	not_calculated 0.990 1323	uncultured bacterium; nbt98g01; EU539136
S001029223	not_calculated 0.990 1324	uncultured bacterium; nbt103a10; EU539432
S001029494	not_calculated 0.990 1328	uncultured bacterium; nbt244d09; EU539703
S001198163	not_calculated 1.000 0594	Pseudomonas sp. R-35717; W12d; AM886082
S001938124	not_calculated 0.995 0584	uncultured bacterium; Cast047; GU450374
S002880240	not_calculated 0.998 0483	uncultured proteobacterium; Upland_8_4649; JF985351
S003747029	not_calculated 1.000 0714	Pseudomonas sp. EECC-101; JX908921
S003747050	not_calculated 1.000 0564	Pseudomonas sp. EECC-140; JX908943
S004196705	not_calculated 0.994 0671	uncultured bacterium; E51; KJ601425
S004459013	not_calculated 0.990 0687	Ralstonia solanacearum; Rs4; LN794228

Lineage:**Results for Query Sequence: WG58A, 699 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Caulobacterales (20)

family Caulobacteraceae (20)

genus Brevundimonas (20)

S000113250	not_calculated 0.996 1344	Brevundimonas intermedia; ATCC 15262(T); AJ227786
S000371153	not_calculated 0.989 0544	uncultured bacterium; Kazan-MN12BT3-285; AY593393
S000382694	not_calculated 0.996 1336	Brevundimonas intermedia; MBIC2712, ATCC15262; AB023784
S000639898	not_calculated 0.996 1347	Brevundimonas sp. CHNTR43; DQ337577
S000703344	not_calculated 1.000 0443	uncultured alpha proteobacterium; PA-B06; DQ295368
S000764930	not_calculated 0.996 1141	uncultured Brevundimonas sp.; RBE2CI-150; EF111191
S001292092	not_calculated 0.996 0801	Brevundimonas sp. AKB-2008-JO6; AM988993
S001352776	not_calculated 0.990 0485	Brevundimonas sp. WH011; FJ866676
S002411029	not_calculated 0.989 0536	Brevundimonas sp. CB1-1; HQ876726
S002415342	not_calculated 0.996 0826	uncultured bacterium; d21112b26; FR687151
S002415354	not_calculated 0.996 0825	uncultured bacterium; d21112b38; FR687163
S002492014	not_calculated 0.989 0563	uncultured Brevundimonas sp.; ABLBc26; JF268938
S002492015	not_calculated 0.989 0563	uncultured Brevundimonas sp.; ABLBc27; JF268939
S003054368	not_calculated 0.996 0958	uncultured bacterium; gs180; JF420786
S003513097	not_calculated 0.990 1381	uncultured Brevundimonas sp.; ASC787; JQ358589
S004131700	not_calculated 0.996 1042	uncultured bacterium; B-2-10STMZ-29; AB948492
S004131724	not_calculated 0.996 1005	uncultured bacterium; B-2-10Surface-27; AB948516
S004224911	not_calculated 0.989 0550	Brevundimonas sp. Na-MWM53; LK985487
S004530724	not_calculated 0.996 1262	Caulobacteraceae bacterium HP40; KM187473
S004597548	not_calculated 0.996 1365	uncultured Brevundimonas sp.; DCP24-1; LC093420

Lineage:**Results for Query Sequence: LL13, 779 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Betaproteobacteria (20)

order Neisseriales (20)

family Chromobacteriaceae (20)

genus Vogesella (20)

S000389572	not_calculated 0.981 1330	bacterium str. 82348; AF227863
S000865003	not_calculated 0.965 1415	uncultured bacterium; S23_1117; EF573018
S000892547	not_calculated 0.978 1338	Vogesella perlucida (T); DS-28; EF626691
S001098505	not_calculated 0.976 1404	freshwater bacterium LH6-8; EU626190
S001292220	not_calculated 0.965 0801	Vogesella sp. AKB-2008-TE22; AM989121
S001351715	not_calculated 0.965 1347	Vogesella sp. TPS6; FJ821602
S002957107	not_calculated 0.967 0643	Vogesella sp. GRC-1; JN571330
S002984458	not_calculated 0.974 0645	uncultured beta proteobacterium; DG-KL-A6; AB635924
S002984462	not_calculated 0.978 0692	uncultured beta proteobacterium; DG-KL-D10; AB635928
S003258422	not_calculated 0.965 1366	Vogesella perlucida; GR-9; HE614874
S004041235	not_calculated 0.967 0520	uncultured bacterium; BF_M25; HF947371
S004041242	not_calculated 0.975 0518	uncultured bacterium; BF_M33; HF947378
S004041258	not_calculated 0.969 0521	uncultured bacterium; BF_M51; HF947395
S004041261	not_calculated 0.970 0504	uncultured bacterium; BF_M55; HF947398
S004041269	not_calculated 0.974 0496	uncultured bacterium; BF_M66; HF947407
S004041287	not_calculated 0.973 0514	uncultured bacterium; BF_M88; HF947425
S004041293	not_calculated 0.974 0509	uncultured bacterium; BF_M94; HF947431
S004081650	not_calculated 0.965 1296	Vogesella perlucida; HME9289; KF911331

S004220001	not_calculated 0.965 1360	Vibrio cholerae; N4; uncultured; KJ725364
S004598837	not_calculated 0.974 0500	uncultured bacterium; A8; LN794362

Lineage:**Results for Query Sequence: WG27, 601 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Alteromonadales (20)

family Shewanellaceae (20)

genus Shewanella (20)

S000014684	not_calculated 0.987 1408	Shewanella putrefaciens; LMG 26268 T; X81623
S000495369	not_calculated 0.988 0693	Shewanella putrefaciens; KIN80; AY136079
S001169977	not_calculated 0.988 1349	Shewanella sp. S03; FJ002584
S001874667	not_calculated 0.988 1350	Shewanella putrefaciens; WST; GU329909
S001930127	not_calculated 0.988 1372	uncultured bacterium; SedNCB56; FJ849517
S001930134	not_calculated 0.988 1372	uncultured bacterium; SedNCB8; FJ849524
S002287632	not_calculated 0.988 1442	Shewanella sp. W3-18-1; CP000503
S002290338	not_calculated 0.988 1440	Shewanella putrefaciens CN-32; CP000681
S002447549	not_calculated 0.988 0752	Shewanella sp. 02; JF444787
S002474582	not_calculated 0.988 1411	uncultured bacterium; 227; FR853476
S002474744	not_calculated 0.988 1406	uncultured bacterium; 749; FR853638
S003262058	not_calculated 0.988 1313	Shewanella putrefaciens; NBRC 3908; AB680167
S003263441	not_calculated 0.988 1376	Shewanella putrefaciens; NBRC 101726; AB681550
S003720041	not_calculated 0.988 1310	Shewanella putrefaciens; K530; KC607513
S003720042	not_calculated 0.988 1316	Shewanella putrefaciens; K313; KC607514
S003720046	not_calculated 0.988 1289	Shewanella putrefaciens; Sh4; KC607518
S003720053	not_calculated 0.988 1296	Shewanella putrefaciens; GIII41; KC607525
S003752424	not_calculated 0.988 1326	Shewanella sp. S5-8; KC202266
S003752432	not_calculated 0.988 1349	Shewanella sp. S5-28; KC202274
S004064561	not_calculated 0.988 1442	Shewanella putrefaciens CN-32; CP000681

Lineage:**Results for Query Sequence: WG26, 645 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Mycobacteriales (20)

family Nocardiaceae (20)

genus Rhodococcus (20)

S000394065	not_calculated 0.938 1400	Rhodococcus corynebacterioides (T); DSM 20151; AF430066
S000499980	not_calculated 0.935 1351	glacial ice bacterium SB12K-2-5; AF479363
S000560272	not_calculated 0.938 1387	Rhodococcus corynebacterioides; type strain: DSM 20151; X80615
S000892351	not_calculated 0.938 1379	Rhodococcus sp. OS-11; EF612310
S001199107	not_calculated 0.936 1305	Rhodococcus sp. I_GA_W_11_12; FJ267569
S001610073	not_calculated 0.938 1313	Rhodococcus kroppenstedtii; 2P04AA; EU977670
S002077601	not_calculated 0.935 1273	uncultured bacterium; ncd297g05c1; HM272575
S002079324	not_calculated 0.935 1274	uncultured bacterium; ncd550b01c1; HM274298
S002081998	not_calculated 0.935 1274	uncultured bacterium; ncd532b02c1; HM276972
S002083945	not_calculated 0.935 1275	uncultured bacterium; ncd561b09c1; HM278919
S002304573	not_calculated 0.940 1302	Rhodococcus trifolii (T); type strain: T8; FR714843
S002616892	not_calculated 0.958 1277	uncultured bacterium; ncd1313b02c1; JF096959
S002705025	not_calculated 0.958 1278	uncultured bacterium; ncd2152a07c1; JF185092
S003280428	not_calculated 0.961 1429	Rhodococcus sp. MN4-1; JQ396538
S003283700	not_calculated 0.947 0652	bacterium nfme09x71p1; JQ657663
S004082718	not_calculated 0.983 0940	bacterium H02; KF939249
S004155869	not_calculated 0.946 1276	uncultured bacterium; ncd1074a04c1; KF083087
S004215196	not_calculated 0.938 1416	Rhodococcus sp. A2-67; KF441597
S004491239	not_calculated 0.936 1343	Rhodococcus corynebacterioides; HN-41; KT003280
S004507026	not_calculated 0.938 1354	Rhodococcus sp. NA23; LN832018

Lineage:**Results for Query Sequence: WG44, 644 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (19)

S000401983	not_calculated 0.994 1402	uncultured bacterium; 172ds20; AY212623
S000402033	not_calculated 1.000 1437	uncultured bacterium; 226ds5; AY212673
S000402080	not_calculated 1.000 1073	uncultured bacterium; 26ds5; AY212720
S001157789	not_calculated 1.000 1380	uncultured bacterium; M0509_40; EU104125
S001262399	not_calculated 1.000 0789	uncultured bacterium; MBR-30_HF_AS43; FM201040
S001276148	not_calculated 1.000 0942	uncultured Pseudomonadaceae bacterium; GC12m-1-52; EU640649
S001588598	not_calculated 1.000 0729	Pseudomonas sp. T11(2009); FJ765363
S002409004	not_calculated 1.000 1365	bacterium GC26(2011); HQ179034
S002515960	not_calculated 1.000 1414	uncultured bacterium; Dianchi-6; HQ324855
S003218143	not_calculated 1.000 1416	uncultured Pseudomonas sp.; 4.6m32; JN679142
S003752725	not_calculated 1.000 1347	Pseudomonas sp. Z2_S_TSA13; KC213924
S003752726	not_calculated 1.000 1359	Pseudomonas sp. Z2_S_TSA10; KC213925
S004476839	not_calculated 0.997 1212	Pseudomonas sp. 4S_B3_9CS2014; KP762233
S004484221	not_calculated 1.000 0668	Pseudomonas sp. F_31; KR088558
S004530699	not_calculated 1.000 1321	Pseudomonas sp. HP3H; KM187448
S004593518	not_calculated 1.000 0897	uncultured bacterium; CB-12; KT900387
S004593519	not_calculated 1.000 0900	uncultured bacterium; CB-14; KT900388
S004593533	not_calculated 1.000 0891	uncultured bacterium; CB-31; KT900402
S004593641	not_calculated 1.000 0900	uncultured bacterium; WB32; KT900510
unclassified_Pseudomonadaceae (1)		
S004511136	not_calculated 1.000 1406	uncultured bacterium; C102; KJ808096

Lineage:**Results for Query Sequence: LL14, 710 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Chromatiales (20)

family Chromatiaceae (20)

genus Rheinheimera (20)

S000728332	not_calculated	0.972	1410	Rheinheimera chironomi (T); K19414; DQ298025
S001139762	not_calculated	0.930	0615	uncultured bacterium; Fin_CL-050619_OTU-37; EU808367
S0011400359	not_calculated	0.924	1272	uncultured bacterium; nbw776d01c1; GQ009419
S002030456	not_calculated	0.948	0950	uncultured bacterium; HLKB33; GU357731
S002230662	not_calculated	0.962	1288	Rheinheimera sp. 09BSZB-9; HM566014
S002973046	not_calculated	0.930	0797	uncultured bacterium; TFAge93; HE659041
S003255692	not_calculated	0.982	0622	uncultured bacterium; MayA12067; JQ327676
S003619283	not_calculated	0.969	1311	Rheinheimera sp. 208; JQ012966
S003695264	not_calculated	0.937	1096	uncultured bacterium; SEAC1AC041; KC432474
S003695278	not_calculated	0.956	1270	uncultured bacterium; SEAD1BE121; KC432488
S003695297	not_calculated	0.963	0988	uncultured bacterium; SEAD1AA081; KC432507
S003695343	not_calculated	0.935	1275	uncultured bacterium; SEAD1AH021; KC432553
S003765723	not_calculated	0.938	0497	uncultured bacterium; MR7; KC515578
S003944008	not_calculated	0.925	1322	uncultured gamma proteobacterium; vj2_a3; JQ867280
S004055490	not_calculated	0.966	1328	Rheinheimera sp. IW-212; KF556693
S004056011	not_calculated	0.975	1246	Rheinheimera chironomi; Movanagher 3; KF578016
S004084215	not_calculated	0.934	1333	Rheinheimera sp. THG-LS118; KF999725
S004114091	not_calculated	0.963	1419	uncultured bacterium; FMWB33; KF975537
S004534248	not_calculated	0.955	1327	Rheinheimera sp. 61DPR4; KP182151
S004534641	not_calculated	0.932	1318	Rheinheimera sp. MIH20; KP196826

Lineage:**Results for Query Sequence: LL37, 593 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Betaproteobacteria (20)

order Burkholderiales (20)

family Comamonadaceae (2)

unclassified_Comamonadaceae (2)

S003229912	not_calculated	0.922	1431	uncultured bacterium; s63; JN868744
S003551764	not_calculated	0.922	1407	uncultured bacterium; A8; JQ814729

family Burkholderiales_incertae_sedis (15)

genus Paucibacter (15)

S000994740	not_calculated	0.953	1394	Antarctic bacterium YT0017; AB376088
S001277206	not_calculated	0.934	0960	uncultured Burkholderiales bacterium; GC12m-2-30; EU641707
S001277739	not_calculated	0.976	0892	uncultured Burkholderiales bacterium; LW18m-1-63; EU642240
S001327468	not_calculated	0.944	1397	uncultured bacterium; ZWB4-10; FJ801207
S002067639	not_calculated	1.000	1269	uncultured bacterium; ncd232f04c1; HM262613
S002332952	not_calculated	0.943	0667	uncultured gamma proteobacterium; CM01189X1A09; HM535516
S002973045	not_calculated	0.939	0789	uncultured bacterium; TFAge90; HE659040
S003575148	not_calculated	0.939	0754	uncultured bacterium; W031c9_8924; JQ375387
S003771739	not_calculated	1.000	0750	uncultured bacterium; bacflank_0447; KC606691
S003918272	not_calculated	0.922	1383	Paucibacter toxinivorans; 51_1; HG530244
S003971361	not_calculated	1.000	0762	uncultured bacterium; GS2P_8F_b04; KC711777
S004197669	not_calculated	0.925	0576	uncultured bacterium; 1-8-11-8; KJ613050
S004197690	not_calculated	0.937	0575	uncultured bacterium; 1-8-11-34; KJ613071
S004447365	not_calculated	0.927	1273	Paucibacter sp. CH; KM365439
S004530683	not_calculated	0.936	1307	Paucibacter sp. HP2F; KM187432

unclassified_Burkholderiales (3)

S000886176	not_calculated	0.922	0797	uncultured Roseateles sp.; GASP-MB3W2_E10; EF665936
S003575150	not_calculated	0.922	0752	uncultured bacterium; WIR12Powerb6_8926; JQ375389
S004215236	not_calculated	0.924	1410	Pelomonas sp. 7A-206; KF441637

Lineage:**Results for Query Sequence: LL12, 641 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000966025	not_calculated	0.966	1333	Pseudomonas sp. G3DM-12; EU037274
S000966026	not_calculated	0.966	1363	Pseudomonas sp. G3DM-13; EU037275
S000966040	not_calculated	0.966	1404	Pseudomonas sp. G3DM-86; EU037289
S001002084	not_calculated	0.989	0568	uncultured bacterium; N06Jun-53; EU443003
S001167883	not_calculated	0.966	0719	uncultured bacterium; P3bac_4; FM179028
S001167903	not_calculated	0.966	0732	uncultured bacterium; P3bac_29; FM179048
S001167912	not_calculated	0.966	0777	uncultured bacterium; P3bac_38; FM179057
S001167913	not_calculated	0.966	0701	uncultured bacterium; P3bac_71; FM179058
S001167915	not_calculated	0.966	0675	uncultured bacterium; P3bac_73; FM179060
S001167921	not_calculated	0.966	0716	uncultured bacterium; P3bac_83; FM179066
S001167923	not_calculated	0.966	0767	uncultured bacterium; P3bac_85; FM179068
S001167925	not_calculated	0.966	0765	uncultured bacterium; P3bac_87; FM179070
S001167928	not_calculated	0.966	0732	uncultured bacterium; P3bac_90; FM179073
S001167933	not_calculated	0.966	0757	uncultured bacterium; P3bac_96; FM179078
S002957124	not_calculated	0.975	0660	Pseudomonas sp. PE-R2A-2; JN571350
S004119785	not_calculated	0.970	0797	uncultured bacterium; 56-M13F; KJ483151
S004119786	not_calculated	0.970	0795	uncultured bacterium; 77-M13F; KJ483152
S004593561	not_calculated	0.967	0892	uncultured bacterium; SAB14; KT900430
S004593568	not_calculated	0.967	0892	uncultured bacterium; SAB23; KT900437
S004593572	not_calculated	0.967	0887	uncultured bacterium; SAB29; KT900441

Lineage:**Results for Query Sequence: WG28, 772 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Firmicutes (20)

class Bacilli (20)

order Bacillales (20)

family Bacillaceae 1 (20)

genus Metabacillus (20)

S000366697	not_calculated 0.987 1434	Metabacillus indicus (T); type strain: Sd/3; AJ583158
S000426321	not_calculated 0.987 1421	Bacillus sp. JL-79; AY745815
S000559375	not_calculated 0.987 1339	Bacillus sp. HU28; DQ109578
S001095431	not_calculated 0.994 1364	Bacillus sp. B311Ydz-hh; EU070359
S001610269	not_calculated 0.987 1345	Bacillus sp. HU13.1; FJ897767
S001610270	not_calculated 0.987 1338	Bacillus sp. HU16.1; FJ897768
S001610271	not_calculated 0.987 1344	Bacillus sp. HU19.1; FJ897769
S001610274	not_calculated 0.987 1350	Bacillus sp. HU33.1; FJ897772
S001745350	not_calculated 0.988 1374	Bacillus sp. P10; GU113080
S002222174	not_calculated 0.987 1391	Bacillus sp. M71_S53; FM992830
S002419290	not_calculated 0.987 1376	Bacillus sp. G3(2010); HQ418487
S002913904	not_calculated 0.987 1379	Bacillus indicus; KU12; JF895483
S002913906	not_calculated 0.987 1375	Bacillus indicus; KU14; JF895485
S003315291	not_calculated 0.987 1360	Bacillus sp. DHC04; JQ904715
S003614137	not_calculated 0.994 1334	Bacillus sp. G2(2012); JX293287
S003745652	not_calculated 0.994 1334	Bacillus sp. M2(2012); JX849024
S004077231	not_calculated 0.987 1341	Bacillus sp. 135B221Y11; KC815841
S004080219	not_calculated 0.987 1366	Bacillus indicus; L15; KF791344
S004228529	not_calculated 0.987 1362	Bacillus indicus; JB 174; KJ920924
S004498360	not_calculated 0.990 0974	Bacillus indicus; HQB816; KT758609

Lineage:**Results for Query Sequence: WG49, 780 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000382845	not_calculated 0.970 0396	Pseudomonas sp. MIS38; AB028923
S001612356	not_calculated 0.966 0500	Pseudomonas sp. Air371; GQ484952
S001872976	not_calculated 0.963 0429	Pseudomonas putida; 2-14 (1); FJ639237
S002884375	not_calculated 0.964 1414	uncultured bacterium; X1-3; JN013931
S003259754	not_calculated 0.958 1397	Pseudomonas sp. BCRC 80328; JQ361087
S004451822	not_calculated 0.956 0545	Pseudomonas sp. C10-2(2015); KM819177
S004451825	not_calculated 0.978 0544	Pseudomonas sp. C10-5; KM819180
S004451835	not_calculated 1.000 0543	Pseudomonas sp. C11-6; KM819190
S004451843	not_calculated 1.000 0543	Pseudomonas sp. C12-6; KM819198
S004451848	not_calculated 1.000 0543	Pseudomonas sp. C1-5; KM819203
S004451896	not_calculated 1.000 0543	Pseudomonas sp. C7-5; KM819251
S004451902	not_calculated 0.991 0544	Pseudomonas sp. C8-3; KM819257
S004451917	not_calculated 0.978 0544	Pseudomonas sp. N10-2; KM819272
S004451943	not_calculated 1.000 0543	Pseudomonas sp. N1-4; KM819298
S004451969	not_calculated 1.000 0543	Pseudomonas sp. N4-6; KM819324
S004451972	not_calculated 1.000 0543	Pseudomonas sp. N5-1; KM819327
S004451974	not_calculated 1.000 0543	Pseudomonas sp. N5-3; KM819329
S004451994	not_calculated 1.000 0543	Pseudomonas sp. N7-8; KM819349
S004451995	not_calculated 0.978 0544	Pseudomonas sp. N8-1; KM819350
S004490876	not_calculated 0.955 1323	Pseudomonas sp. PDD-59b-37; KR922166

Lineage:**Results for Query Sequence: LL18, 695 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Bacteroidetes (20)

class Flavobacteriia (20)

order Flavobacteriales (20)

family Flavobacteriaceae (20)

genus Flavobacterium (20)

S000623924	not_calculated 0.934 1420	Flavobacterium sp. WB 4.3-34; AM177631
S000808137	not_calculated 0.934 0487	uncultured bacterium; MA61_2003T1c_80; EF377797
S000808145	not_calculated 0.924 0515	uncultured bacterium; MA61_2003T1c_72; EF377805
S000808179	not_calculated 0.925 0521	uncultured bacterium; MA61_2003T1c_37; EF377839
S000808181	not_calculated 0.946 0502	uncultured bacterium; MA61_2003T1c_35; EF377841
S000808187	not_calculated 0.925 0521	uncultured bacterium; MA61_2003T1c_28; EF377847
S000808204	not_calculated 0.925 0518	uncultured bacterium; MA61_2003T1c_10; EF377864
S000808210	not_calculated 0.925 0519	uncultured bacterium; MA61_2003T1c_4; EF377870
S000808214	not_calculated 0.928 0499	uncultured bacterium; MA61_2003T1c; EF377874
S000905742	not_calculated 0.938 0650	uncultured Flavobacteriales bacterium; MS003A1_H03; EF695527
S000905760	not_calculated 0.939 0659	uncultured Flavobacteriales bacterium; MS004A1_B01; EF695545
S000905881	not_calculated 0.933 0594	uncultured Flavobacteriales bacterium; MS008A1_E11; EF695666
S000906200	not_calculated 0.925 0630	uncultured Flavobacteriales bacterium; MS018A1_A07; EF695985
S000911359	not_calculated 0.944 0426	uncultured Flavobacteriales bacterium; MS028A1_A07; EF701144
S000911397	not_calculated 0.924 0502	uncultured Flavobacteriales bacterium; MS028A1_F07; EF701182
S000911403	not_calculated 0.956 0499	uncultured Flavobacteriales bacterium; MS028A1_G04; EF701188
S001253276	not_calculated 0.925 0521	uncultured Bacteroidetes bacterium; MA161D06; FJ532837
S001253289	not_calculated 0.926 0528	uncultured Bacteroidetes bacterium; MA161D02; FJ532850
S001253295	not_calculated 0.925 0518	uncultured Bacteroidetes bacterium; MA161A07; FJ532856
S001253300	not_calculated 0.925 0523	uncultured Bacteroidetes bacterium; MA161F08; FJ532861

Lineage:**Results for Query Sequence: WG22, 755 unique oligos**

rootrank Root (20) (match sequences)

domain Bacteria (20)

phylum Bacteroidetes (20)

class Flavobacteriia (20)

order Flavobacteriales (20)

family Flavobacteriaceae (20)

genus Flavobacterium (20)

S000722064	not_calculated 0.954 1330	Flavobacterium sp. YO15; DQ778311
S000808137	not_calculated 0.961 0487	uncultured bacterium; MA61_2003T1c_80; EF377797
S000808202	not_calculated 0.947 0491	uncultured bacterium; MA61_2003T1c_12; EF377862
S000911403	not_calculated 0.960 0499	uncultured Flavobacteriales bacterium; MS028A1_G04; EF701188
S001292015	not_calculated 0.952 0858	Flavobacterium sp. AKB-2008-JO31; AM988916
S001292018	not_calculated 0.952 0858	Flavobacterium sp. AKB-2008-JO41; AM988919
S001326249	not_calculated 0.954 0718	uncultured bacterium; MA00094F03; FJ772295
S001326347	not_calculated 0.954 0719	uncultured bacterium; MA00070G12; FJ772393
S002223149	not_calculated 0.952 0815	Flavobacterium sp. B183; FR696343
S002223161	not_calculated 0.962 0782	Flavobacterium sp. B257; FR696355
S003919245	not_calculated 0.950 1311	Flavobacterium sp. T14L.07.B.CHS.SRW.W.Kidney.D; JX287797
S004005996	not_calculated 0.947 0681	Flavobacterium sp. T13.07.B.CHS.SRW.W.Kidney.D; JX287543
S004005997	not_calculated 0.962 0679	Flavobacterium sp. T14.07.B.CHS.SRW.W.Kidney.D; JX287544
S004005999	not_calculated 0.962 0679	Flavobacterium sp. T16.07.C.CHS.SRW.W.Kidney.D; JX287546
S004006057	not_calculated 0.954 0676	Flavobacterium sp. T123.10.PLAT.SE.H.Kidney.N; JX287604
S004006058	not_calculated 0.954 0676	Flavobacterium sp. T124.10.PLAT.SE.H.Kidney.N; JX287605
S004006147	not_calculated 0.962 0679	Flavobacterium sp. S23.05.B.CHS.LM.W.Kidney.D; JX287694
S004006151	not_calculated 0.961 0673	Flavobacterium sp. S22.05.B.CHS.LM.W.Kidney.N; JX287698
S004006162	not_calculated 0.961 0673	Flavobacterium sp. S27.05.B.CHS.MI.LM.W.Kidney.N; JX287709
S004006240	not_calculated 0.948 1319	Flavobacterium spartansii (T); T16F.07.C.CHS.SRW.W.Kidney.D; JX287799

Lineage:**Results for Query Sequence: WG481, 781 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Bacteroidetes (20)

class Flavobacteriia (20)

order Flavobacteriales (20)

family Flavobacteriaceae (20)

genus Flavobacterium (20)

S000808136	not_calculated 0.965 0521	uncultured bacterium; MA61_2003T1c_81; EF377796
S000808143	not_calculated 0.946 0481	uncultured bacterium; MA61_2003T1c_74; EF377803
S000808145	not_calculated 0.950 0515	uncultured bacterium; MA61_2003T1c_72; EF377805
S000808148	not_calculated 0.954 0568	uncultured bacterium; MA61_2003T1c_69; EF377808
S000808150	not_calculated 0.949 0513	uncultured bacterium; MA61_2003T1c_67; EF377810
S000808162	not_calculated 0.948 0499	uncultured bacterium; MA61_2003T1c_54; EF377822
S000808163	not_calculated 0.949 0506	uncultured bacterium; MA61_2003T1c_53; EF377823
S000808164	not_calculated 0.950 0515	uncultured bacterium; MA61_2003T1c_52; EF377824
S000808167	not_calculated 0.946 0502	uncultured bacterium; MA61_2003T1c_49; EF377827
S000808172	not_calculated 0.950 0515	uncultured bacterium; MA61_2003T1c_44; EF377832
S000808179	not_calculated 0.950 0521	uncultured bacterium; MA61_2003T1c_37; EF377839
S000808187	not_calculated 0.950 0521	uncultured bacterium; MA61_2003T1c_28; EF377847
S000808188	not_calculated 0.949 0511	uncultured bacterium; MA61_2003T1c_27; EF377848
S000808190	not_calculated 0.949 0514	uncultured bacterium; MA61_2003T1c_25; EF377850
S000808200	not_calculated 0.948 0503	uncultured bacterium; MA61_2003T1c_14; EF377860
S000808204	not_calculated 0.950 0518	uncultured bacterium; MA61_2003T1c_10; EF377864
S000808210	not_calculated 0.950 0519	uncultured bacterium; MA61_2003T1c_4; EF377870
S001155309	not_calculated 0.951 1398	Flavobacterium johnsoniae; A3; EU860081
S001253520	not_calculated 0.946 0501	uncultured Bacteroidetes bacterium; MA00164E10; FJ533081
S001318506	not_calculated 0.955 0244	uncultured bacterium; 11-2_341f; FJ652075

Lineage:**Results for Query Sequence: WG14, 581 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Aeromonadales (20)

family Aeromonadaceae (20)

genus Aeromonas (20)

S000014207	not_calculated 0.983 1374	Aeromonas sobria; ATCC 43979T; X74683
S000030055	not_calculated 0.987 0552	Aeromonas sobria; S2M10; AF472502
S000030064	not_calculated 0.987 0552	Aeromonas sobria; S1J6; AF472500
S000030066	not_calculated 0.987 0552	Aeromonas veronii; S3M31; AF472503
S000030068	not_calculated 0.987 0552	Aeromonas sobria; S1J10; AF472501
S000634026	not_calculated 0.983 1425	Vibrio sp. V606; DQ146986
S001156443	not_calculated 0.983 1388	Aeromonas sobria; 2r; EU916710
S001548460	not_calculated 0.983 1333	Aeromonas sobria; JCM 2139; AB472942
S001548462	not_calculated 0.983 1335	Aeromonas sobria; JCM 2141; AB472944
S001548470	not_calculated 0.983 1335	Aeromonas sobria; JCM 2137; AB472952
S001589168	not_calculated 0.983 1329	bacterium C1(2009); GQ398333
S002155982	not_calculated 0.983 1417	Aeromonas sobria; 2CCH202; GU187060
S002179130	not_calculated 0.983 1386	uncultured bacterium; SINO519; HM129731
S002354895	not_calculated 0.983 1417	Aeromonas sobria; type strain: NCIMB 12065; X60412
S002956892	not_calculated 0.985 1366	Aeromonas sobria; YZQ-GL; JN555613
S003302942	not_calculated 0.983 1370	Aeromonas sobria; QY1; JX164206
S003313985	not_calculated 0.983 1364	Aeromonas sobria; M-T-TSA 15; JQ795756
S003313986	not_calculated 0.983 1364	Aeromonas sobria; M-T-TSA 98; JQ795757
S003470548	not_calculated 0.983 1424	uncultured bacterium; C1; JX262557
S004045511	not_calculated 0.988 0877	Aeromonas sobria; P-Q-1; KC991311

Lineage:**Results for Query Sequence: WG16, 683 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)
order Sphingomonadales (20)
family Sphingomonadaceae (20)
genus Sphingobium (20)

S000127496	not_calculated 0.993 1333	Sphingobium yanoikuyae; KF706; AB109749
S000130603	not_calculated 0.993 1341	Sphingomonas sp.; B1; X94099
S000130607	not_calculated 0.993 1345	Sphingobium yanoikuyae; PAH-degrading; X85023
S000379067	not_calculated 0.993 1227	Sphingobium yanoikuyae; DD109; AY574367
S000391716	not_calculated 0.993 1316	Sphingobium yanoikuyae; AF331661
S000437529	not_calculated 0.993 1336	Sphingobium yanoikuyae; B1; U37524
S000538425	not_calculated 0.993 1258	estrogen-degrading bacterium KC14; DQ066444
S000568813	not_calculated 0.993 1001	Sphingomonas sp. 14DN-61; AB200352
S000605852	not_calculated 0.993 1331	Sphingomonas sp. PF-D; DQ202285
S000751080	not_calculated 0.993 1356	Sphingomonas sp. H-1; EF012277
S000752101	not_calculated 0.993 1356	Sphingomonas sp. ZnH-1; EF061133
S000905547	not_calculated 0.993 1249	uncultured delta proteobacterium; COREB41; EF562226
S000907643	not_calculated 1.000 0568	uncultured alpha proteobacterium; MS072A1_H04; EF697428
S001034313	not_calculated 0.993 1174	uncultured Sphingomonas sp.; 1P-1-C04; EU704732
S001183889	not_calculated 1.000 0414	uncultured bacterium; DGGE gel band EU77; FJ217234
S001183898	not_calculated 1.000 0414	uncultured bacterium; DGGE gel band EU102; FJ217243
S001183902	not_calculated 1.000 0414	uncultured bacterium; DGGE gel band EU114; FJ217247
S001183910	not_calculated 1.000 0414	uncultured bacterium; DGGE gel band EU137; FJ217255
S001188774	not_calculated 0.993 1260	groundwater planktonic bacterium Y2; FJ204471
S001873580	not_calculated 1.000 0596	Sphingobium sp. FB4; GU223137

Lineage:**Results for Query Sequence: LLX3, 663 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Mycobacteriales (20)

family Nocardiaceae (20)

genus Rhodococcus (20)

S000098216	not_calculated 0.991 1364	Rhodococcus sp. V4.ME.27; V4.ME.27 = MM_2341; AJ244659
S000432130	not_calculated 0.991 1408	bacterium CAGY6; AF538745
S000503459	not_calculated 0.955 0944	Rhodococcus sp. RG-14; AY561580
S001154143	not_calculated 0.986 1354	Rhodococcus cercidiphylli; DS30; EU834254
S001419310	not_calculated 1.000 0532	uncultured bacterium; C2_E2M13f; AB482566
S001487046	not_calculated 0.980 1275	uncultured bacterium; nbw08g02c1; GQ060982
S001537228	not_calculated 0.961 1271	uncultured bacterium; nbw621f07c1; GQ111164
S001550357	not_calculated 0.950 1412	Rhodococcus sp. HLSBA34; FJ999587
S001550358	not_calculated 0.950 1318	Rhodococcus sp. HLSBA15; FJ999588
S001550360	not_calculated 0.950 1434	Rhodococcus fascians; HLSBA48; FJ999590
S002081869	not_calculated 0.962 1275	uncultured bacterium; ncd529e11c1; HM276843
S002230512	not_calculated 0.989 0732	Rhodococcus sp. sm460-14; HM537186
S002445738	not_calculated 0.989 0732	Rhodococcus sp. Desert14; HQ711535
S002449179	not_calculated 0.991 1312	Rhodococcus sp. 28-JH4M; JF722669
S002655154	not_calculated 0.968 1273	uncultured bacterium; ncd1556b09c1; JF135221
S002954793	not_calculated 0.989 1311	Rhodococcus sp. SS04-04; JN120916
S003315049	not_calculated 0.991 1322	Rhodococcus sp. Pp2; JQ861537
S004008625	not_calculated 0.986 0682	Rhodococcus sp. I11A-02587; KC550139
S004219015	not_calculated 0.989 0775	Rhodococcus sp. JSM 221S126; KJ685842
S004486051	not_calculated 1.000 0627	Rhodococcus sp. I13A-01690; KR184637

Lineage:**Results for Query Sequence: Methanosarcina, 1292 unique oligos****rootrank** Root (20) (match sequences)

domain Archaea (20)

phylum Euryarchaeota (20)

class Methanomicrobia (20)

order Methanosarcinales (20)

family Methanosarcinaceae (20)

genus Methanosarcina (20)

S000436500	not_calculated 1.000 1292	Methanosarcina acetivorans (T); DSM 2834; M59137
S000642553	not_calculated 0.990 1343	Methanosarcina acetivorans C2A; AE010299
S000642555	not_calculated 0.995 1345	Methanosarcina acetivorans C2A; AE010299
S000642559	not_calculated 0.995 1345	Methanosarcina acetivorans C2A; AE010299
S001272122	not_calculated 0.956 0681	unidentified archaeon LMA134; U87515
S001390345	not_calculated 0.951 0384	Methanosarcina sp. enrichment culture clone MSC-3; FJ984744
S001449131	not_calculated 0.950 0402	uncultured methanogenic archaeon; SMPFLSS58m(2)_7; FJ982731
S001571279	not_calculated 0.957 0532	uncultured archaeon; VE07-04-ARC; GQ340375
S002915301	not_calculated 0.989 0977	Methanosarcina acetivorans; GRAU-9; JN020914
S002935479	not_calculated 0.958 0527	uncultured archaeon; A0610R001_E17; AB651912
S002937750	not_calculated 0.953 0532	uncultured archaeon; A1001R001_E12; AB654194
S002973522	not_calculated 0.946 0496	uncultured Methanosarcina sp.; MFC-3barc; HM043286
S003208650	not_calculated 0.961 0639	uncultured archaeon; C6; JN596403
S003764635	not_calculated 0.955 0534	uncultured archaeon; Gr13_H01; JX865737
S004071290	not_calculated 0.990 1384	Methanosarcina acetivorans C2A; AE010299
S004071291	not_calculated 0.995 1386	Methanosarcina acetivorans C2A; AE010299
S004071292	not_calculated 0.995 1386	Methanosarcina acetivorans C2A; AE010299
S004207966	not_calculated 0.947 0495	uncultured archaeon; AEtH4P12C01; LK026070
S004343079	not_calculated 0.971 0729	uncultured archaeon; A-OTU9-XH9; KM221190
S004599141	not_calculated 0.947 0525	uncultured Methanosarcinales archaeon; JN413085; LN796110

Lineage:**Results for Query Sequence: WG74, 678 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Bacteroidetes (20)

class Flavobacteriia (20)

order Flavobacteriales (20)

family Flavobacteriaceae (20)

genus <i>Flavobacterium</i> (20)		
S000623910	not_calculated 0.991 1421	<i>Flavobacterium</i> sp. WB 3.3.27; AM177617
S000623921	not_calculated 0.982 1423	<i>Flavobacterium</i> sp. WB 4.3-15; AM177628
S000769495	not_calculated 0.973 1211	<i>Bacteroidetes bacterium</i> RBE2CD-132; EF111262
S000911359	not_calculated 0.953 0426	uncultured <i>Flavobacteriales bacterium</i> ; MS028A1_A07; EF701144
S000911403	not_calculated 0.950 0499	uncultured <i>Flavobacteriales bacterium</i> ; MS028A1_G04; EF701188
S001243446	not_calculated 0.959 1205	<i>Flavobacterium</i> sp. CS43; FJ479766
S001258861	not_calculated 0.958 0497	uncultured <i>Bacteroidetes bacterium</i> ; A19YO15RM; FJ568606
S002075586	not_calculated 0.973 1290	uncultured <i>bacterium</i> ; ncd267g02c1; HM270560
S002515977	not_calculated 0.991 1403	uncultured <i>bacterium</i> ; Dianchi-26; HQ324872
S003919239	not_calculated 0.969 1285	<i>Flavobacterium</i> sp. T6L.06.LWF.W.Swimbladder.D; JX287791
S004005991	not_calculated 0.969 0682	<i>Flavobacterium</i> sp. T6.06.LWF.W.Swimbladder.D; JX287538
S004006088	not_calculated 0.991 0679	<i>Flavobacterium</i> sp. S126.08.BKT.W.Gill.N; JX287635
S004006093	not_calculated 0.989 0645	<i>Flavobacterium</i> sp. S149.08.SCU.W.Gill.N; JX287640
S004006094	not_calculated 0.991 0679	<i>Flavobacterium</i> sp. S190.08.BNT.W.Gill.N; JX287641
S004006101	not_calculated 0.976 0679	<i>Flavobacterium</i> sp. S161.08.SCU.W.Gill.N; JX287648
S004006105	not_calculated 0.991 0679	<i>Flavobacterium</i> sp. S130.08.BNT.W.Gill.N; JX287652
S004006110	not_calculated 0.989 0645	<i>Flavobacterium</i> sp. S163.08.SCU.W.Gill.N; JX287657
S004006137	not_calculated 0.991 0679	<i>Flavobacterium</i> sp. S166.08.SCU.W.Gill.N; JX287684
S004006139	not_calculated 0.957 0679	<i>Flavobacterium</i> sp. S43.04.PCOS.MI.H.Brain.D.M; JX287686
S004218528	not_calculated 0.984 1338	<i>Flavobacterium</i> sp. FLX-4; KJ660953

Lineage:**Results for Query Sequence: LL41A, 769 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Caulobacterales (20)

family Caulobacteraceae (20)

genus *Brevundimonas* (20)

S000016026	not_calculated 1.000 1321	<i>Brevundimonas vesicularis</i> ; ATCC 11426 (T); AJ007801
S000017941	not_calculated 1.000 1219	alpha proteobacterium VUN10077; AF137356
S000112396	not_calculated 1.000 1344	<i>Brevundimonas vesicularis</i> ; LMG 2350 (T); AJ227780
S000112771	not_calculated 1.000 1344	<i>Brevundimonas vesicularis</i> ; LMG 11141; AJ227781
S000112773	not_calculated 1.000 1344	<i>Brevundimonas</i> sp. V4.BO.07; AJ227800
S000128774	not_calculated 1.000 1373	thin bent rods; AJ001345
S000254305	not_calculated 1.000 0538	<i>Brevundimonas vesicularis</i> ; ICS11202; AY456200
S000271297	not_calculated 1.000 0593	<i>Brevundimonas vesicularis</i> ; 2.5; AJ626987
S000274136	not_calculated 1.000 0598	<i>Brevundimonas vesicularis</i> ; 5.6; AJ627402
S000334613	not_calculated 1.000 1353	<i>Brevundimonas nasdae</i> (T); GTC1043; AB071954
S000369427	not_calculated 1.000 0931	uncultured <i>bacterium</i> ; FB34-10; AY527799
S000371153	not_calculated 1.000 0544	uncultured <i>bacterium</i> ; Kazan-MN12BT3-285; AY593393
S000382443	not_calculated 1.000 1315	alpha proteobacterium MBIC3965; 94-115; AB019037
S000399535	not_calculated 1.000 1328	<i>Brevundimonas vesicularis</i> ; 28; AY169433
S000470963	not_calculated 1.000 1344	<i>Brevundimonas</i> sp. LMG 9567t1; AJ244647
S000470967	not_calculated 1.000 1345	<i>Brevundimonas</i> sp. V4.BO.05; V4.BO.05 = MM_2802; AJ244704
S000538423	not_calculated 1.000 1195	estrogen-degrading <i>bacterium</i> KC12; DQ066442
S000575369	not_calculated 1.000 0807	<i>bacterium</i> PSB-1-28; AY822564
S000584111	not_calculated 1.000 1193	<i>Brevundimonas vesicularis</i> ; O283; DQ111026
S000616931	not_calculated 1.000 0639	<i>Brevundimonas</i> sp. 52AD23; AB242678

Lineage:**Results for Query Sequence: LL41B, 806 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus *Pseudomonas* (20)

S000878828	not_calculated 0.973 1418	uncultured <i>bacterium</i> ; Hua-w-88; EF632861
S001002084	not_calculated 0.989 0568	uncultured <i>bacterium</i> ; N06Jun-53; EU443003
S001139769	not_calculated 0.992 0733	uncultured <i>bacterium</i> ; Fin_CL-050626_OTU-44; EU808374
S001163839	not_calculated 0.973 0633	uncultured <i>bacterium</i> ; 071020-ONK-PVA3-3; FJ037675
S001163842	not_calculated 0.980 0615	uncultured <i>bacterium</i> ; 071020-ONK-PVA3-12; FJ037678
S001167903	not_calculated 0.970 0732	uncultured <i>bacterium</i> ; P3bac_29; FM179048
S001167921	not_calculated 0.971 0716	uncultured <i>bacterium</i> ; P3bac_83; FM179066
S001167928	not_calculated 0.978 0732	uncultured <i>bacterium</i> ; P3bac_90; FM179073
S001167941	not_calculated 0.978 0732	uncultured <i>bacterium</i> ; P3bac_106; FM179086
S001167958	not_calculated 0.978 0726	uncultured <i>bacterium</i> ; P3bac_162; FM179103
S001167962	not_calculated 0.970 0702	uncultured <i>bacterium</i> ; P3bac_166; FM179107
S002957124	not_calculated 1.000 0660	<i>Pseudomonas</i> sp. PE-R2A-2; JN571350
S003261491	not_calculated 0.981 1316	<i>Pseudomonas</i> sp. HKF-3; AB633201
S003548454	not_calculated 0.970 0759	uncultured <i>bacterium</i> ; Cyp1_50; JQ766566
S003548461	not_calculated 0.970 0766	uncultured <i>bacterium</i> ; Cyp1_58; JQ766573
S003548464	not_calculated 0.970 0759	uncultured <i>bacterium</i> ; Cyp1_61; JQ766576
S003548471	not_calculated 0.970 0759	uncultured <i>bacterium</i> ; Cyp1_68; JQ766583
S003548474	not_calculated 0.970 0759	uncultured <i>bacterium</i> ; Cyp1_71; JQ766586
S004593579	not_calculated 0.974 0893	uncultured <i>bacterium</i> ; SAB37; KT900448
S004593625	not_calculated 0.974 0895	uncultured <i>bacterium</i> ; WB14; KT900494

Lineage:**Results for Query Sequence: LL43F, 415 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Mycobacteriales (20)

family Gordoniaceae (20)

genus *Williamsia* (20)

S000019126	not_calculated 0.952 1375	<i>Williamsia murale</i> ; MA140-96T; Y17384
S000576763	not_calculated 0.952 1370	<i>Williamsia marianensis</i> (T); MT8; AY894336

S000577395	not_calculated	0.952	1355	Williamsia muralis; 500/04; AY986734
S000624861	not_calculated	0.952	1385	Williamsia sp. KTR4; DQ068382
S001152798	not_calculated	0.952	1312	Williamsia sp. SY3; EU073114
S001406931	not_calculated	0.952	1265	uncultured bacterium; nbw819g10c1; GQ015991
S001490264	not_calculated	0.952	1268	uncultured bacterium; nbw68b02c1; GQ064200
S001492774	not_calculated	0.952	1267	uncultured bacterium; nbw728a08c1; GQ066710
S001492803	not_calculated	0.952	1268	uncultured bacterium; nbw728d04c1; GQ066739
S001493088	not_calculated	0.952	1267	uncultured bacterium; nbw731g01c1; GQ067024
S001493490	not_calculated	0.952	1266	uncultured bacterium; nbw1128f12c1; GQ067426
S001523154	not_calculated	0.952	1268	uncultured bacterium; nbw393g11c1; GQ097090
S001523172	not_calculated	0.952	1267	uncultured bacterium; nbw394a09c1; GQ097108
S002134488	not_calculated	0.952	1267	uncultured bacterium; ncd966f06c1; HM329462
S002136570	not_calculated	0.952	1267	uncultured bacterium; ncd967f11c1; HM331544
S002143079	not_calculated	0.952	1268	uncultured bacterium; ncd1114b01c1; HM338053
S002228194	not_calculated	0.952	1390	Williamsia sp. 0713C5-1; HM222683
S002628113	not_calculated	0.952	1267	uncultured bacterium; ncd1317d05c1; JF108180
S002669373	not_calculated	0.952	1263	uncultured bacterium; ncd1703e11c1; JF149440
S004159179	not_calculated	0.954	1269	uncultured bacterium; ncm20b10c1; KF086397

Lineage:

Results for Query Sequence: WG56, 669 unique oligos

rootrank Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Sphingomonadales (20)

family Sphingomonadaceae (20)

genus Sphingomonas (20)

S000022290	not_calculated	0.994	1364	Sphingomonas pituitosa (T); EDIV; AJ243751
S000322922	not_calculated	0.994	1320	Sphingomonas sp. ATCC 53159; AF503283
S000395523	not_calculated	0.994	1308	Sphingomonas sp. ATCC 21423; AF503277
S000395524	not_calculated	0.994	1353	Sphingomonas elodea; ATCC 31461; AF503278
S000395525	not_calculated	0.994	1351	Sphingomonas sp. ATCC 31554; AF503279
S000395527	not_calculated	0.994	1336	Sphingomonas sp. ATCC 31961; AF503281
S000395528	not_calculated	0.994	1341	Sphingomonas sp. ATCC 31853; AF503282
S000627321	not_calculated	0.994	1338	Sphingomonas azotifigens; NBRC 15496; Y22; AB217473
S000640151	not_calculated	0.994	1372	Sphingomonas sp. BR12187; DQ340850
S000640152	not_calculated	0.994	1320	Sphingomonas sp. BR12188; DQ340851
S000640153	not_calculated	0.994	1377	Sphingomonas sp. BR12189; DQ340852
S000640154	not_calculated	0.994	1351	Sphingomonas sp. BR12190; DQ340853
S000640157	not_calculated	0.994	1373	Sphingomonas sp. BR12193; DQ340856
S000640158	not_calculated	0.994	1367	Sphingomonas sp. BR12194; DQ340857
S000640163	not_calculated	0.996	1363	Sphingomonas sp. BR12199; DQ340862
S000751149	not_calculated	1.000	0474	Sphingomonas sp. 47; EF016512
S000841780	not_calculated	0.995	0634	Sphingomonas sp. SNRW7-1; AB299762
S001744415	not_calculated	1.000	0635	Sphingomonas sp. FO211; GQ849293
S003556467	not_calculated	1.000	0534	uncultured bacterium; AETSB2_E03; AB718129
S003784924	not_calculated	0.999	0972	Sphingomonas sp. L6-3; AB819407

Lineage:

Results for Query Sequence: WG34B, 647 unique oligos

rootrank Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000751166	not_calculated	1.000	0473	bacterium F2; EF016529
S000805644	not_calculated	1.000	0932	Pseudomonas fluorescens; D18; EF204232
S001152156	not_calculated	1.000	1356	Pseudomonas jessenii; FB18; AM933510
S001169975	not_calculated	1.000	1357	Pseudomonas sp. S01; FJ002582
S001188882	not_calculated	1.000	1357	Pseudomonas sp. OTUC1; FJ210842
S001267980	not_calculated	1.000	1285	uncultured Pseudomonas sp.; ARN35; AM936588
S001553047	not_calculated	1.000	1300	uncultured Pseudomonas sp.; OTUM7; EU826658
S001794880	not_calculated	1.000	1408	Pseudomonas fluorescens; LMG 14577; GU198122
S002166950	not_calculated	1.000	0579	Pseudomonas sp. SA014; GU989373
S002166988	not_calculated	1.000	0653	Pseudomonas sp. SA062; GU989421
S002912398	not_calculated	1.000	0696	Pseudomonas sp. S1IP15; JF743675
S002912408	not_calculated	1.000	0696	Pseudomonas sp. S1ID9; JF743685
S002912410	not_calculated	1.000	0696	Pseudomonas sp. S1ID14; JF743687
S003277992	not_calculated	1.000	1431	Pseudomonas sp. HC1-12; JF312924
S003278003	not_calculated	1.000	1417	Pseudomonas sp. HC1-23; JF312935
S003278007	not_calculated	1.000	1412	Pseudomonas sp. HC1-27; JF312939
S003278025	not_calculated	1.000	1430	Pseudomonas sp. HC2-18; JF312957
S003305516	not_calculated	1.000	0680	Pseudomonas sp. SF-1-07; HE794902
S003314008	not_calculated	1.000	1348	Pseudomonas fluorescens; M-T-TSA_84; JQ795779
S003562427	not_calculated	1.000	0518	uncultured Pseudomonas sp.; B3_0_022; JN866195

Lineage:

Results for Query Sequence: WG36, 757 unique oligos

rootrank Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Enterobacteriales (20)

family Yersiniaceae (20)

genus Rouxiella (20)

S000721442	not_calculated	1.000	0860	Rahnella aquatilis; SF1-34; AM268335
S000721444	not_calculated	1.000	0839	Rahnella aquatilis; SF2-49; AM268337
S000721445	not_calculated	1.000	0861	Rahnella sp. SF2-58; AM268338
S001524953	not_calculated	1.000	1286	uncultured bacterium; nbw503d11c1; GQ098889
S001524960	not_calculated	1.000	1288	uncultured bacterium; nbw503e08c1; GQ098896

S001524969	not_calculated	1.000	1290	uncultured bacterium; nbw503f10c1; GQ098905
S001524987	not_calculated	1.000	1288	uncultured bacterium; nbw503h08c1; GQ098923
S001524993	not_calculated	1.000	1287	uncultured bacterium; nbw504a02c1; GQ098929
S001525011	not_calculated	1.000	1289	uncultured bacterium; nbw504c03c1; GQ098947
S001525059	not_calculated	1.000	1285	uncultured bacterium; nbw504h09c1; GQ098995
S001525063	not_calculated	1.000	1289	uncultured bacterium; nbw505a03c1; GQ098999
S001525134	not_calculated	1.000	1289	uncultured bacterium; nbw505g09c1; GQ099070
S001525149	not_calculated	1.000	1288	uncultured bacterium; nbw506a01c1; GQ099085
S001525161	not_calculated	1.000	1286	uncultured bacterium; nbw506b01c1; GQ099097
S001525173	not_calculated	1.000	1288	uncultured bacterium; nbw506c01c1; GQ099109
S001525179	not_calculated	1.000	1287	uncultured bacterium; nbw506c09c1; GQ099115
S001525187	not_calculated	1.000	1291	uncultured bacterium; nbw506d05c1; GQ099123
S001525242	not_calculated	1.000	1288	uncultured bacterium; nbw507b01c1; GQ099178
S001525255	not_calculated	1.000	1288	uncultured bacterium; nbw507c08c1; GQ099191
S001525273	not_calculated	1.000	1287	uncultured bacterium; nbw507e12c1; GQ099209

Lineage:**Results for Query Sequence: LL46, 632 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Actinobacteria (20)

class Actinobacteria (20)

order Propionibacteriales (20)

family Nocardiodaceae (20)

genus Aeromicrobium (20)

S000027750	not_calculated	0.889	0632	Nocardioides sp. 2.20; AJ299233
S000028280	not_calculated	0.907	0603	Nocardioides sp. 2.14; AJ299232
S000433700	not_calculated	0.912	0442	uncultured actinomycete; ACT-A2; AJ427636
S000605629	not_calculated	0.886	1244	Nocardiodaceae bacterium SM2; DQ195813
S000860070	not_calculated	0.984	1342	Aeromicrobium sp. 1_C7_65; EF540459
S000860077	not_calculated	0.913	1336	Aeromicrobium sp. 1/4_C7/16_31; EF540466
S000893634	not_calculated	0.889	1315	Aeromicrobium kwangyangensis; CW35; EF693740
S000968355	not_calculated	0.984	0492	bacterium EP1.29; EU279889
S001154138	not_calculated	0.888	1337	Aeromicrobium kwangyangensis; DS23; EU834249
S001199074	not_calculated	0.884	1286	Aeromicrobium sp. I_Gauze_W_12_4; FJ267536
S001255820	not_calculated	0.907	0751	uncultured bacterium; C042; FJ561558
S002973444	not_calculated	0.894	0740	uncultured bacterium; A083_BATS; HM032273
S002973478	not_calculated	0.916	0741	uncultured bacterium; A171_BATS; HM032307
S003537983	not_calculated	0.884	1368	uncultured bacterium; AC1C2BD02; JQ428031
S003789365	not_calculated	0.892	1332	Aeromicrobium sp. Es15; JQ977434
S004231673	not_calculated	0.902	1306	Aeromicrobium sp. W-NaCl-1; KM083518
S004492037	not_calculated	0.908	0690	Aeromicrobium sp. VO38-3; KT152266
S004492038	not_calculated	0.916	0680	Aeromicrobium sp. VO41-3; KT152267
S004531243	not_calculated	0.918	1319	Aeromicrobium sp. VO40-3; KM406763
S004596305	not_calculated	0.888	0561	uncultured bacterium; TB-A-1_H04; LC024200

Lineage:**Results for Query Sequence: LL24, 687 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Alphaproteobacteria (20)

order Caulobacteriales (20)

family Caulobacteraceae (20)

genus Brevundimonas (20)

S000271297	not_calculated	1.000	0593	Brevundimonas vesicularis; 2.5; AJ626987
S000274136	not_calculated	1.000	0598	Brevundimonas vesicularis; 5.6; AJ627402
S000371153	not_calculated	1.000	0544	uncultured bacterium; Kazan-MN12BT3-285; AY593393
S000703344	not_calculated	1.000	0443	uncultured alpha proteobacterium; PA-B06; DQ295368
S000841756	not_calculated	1.000	0574	Brevundimonas sp. SSRS4-5; AB299738
S001420253	not_calculated	1.000	0505	uncultured bacterium; C2_65H09f; AB483509
S001420254	not_calculated	1.000	0505	uncultured bacterium; C2_65J21f; AB483510
S001420341	not_calculated	1.000	0505	uncultured bacterium; C2_S4A01f; AB483597
S001420342	not_calculated	1.000	0505	uncultured bacterium; C2_S4D12f; AB483598
S001420343	not_calculated	1.000	0505	uncultured bacterium; C2_S4H10f; AB483599
S001420344	not_calculated	1.000	0505	uncultured bacterium; C2_S4I05f; AB483600
S001421083	not_calculated	1.000	0505	uncultured bacterium; N2_12B20f; AB484339
S001421084	not_calculated	1.000	0505	uncultured bacterium; N2_12F08f; AB484340
S001421085	not_calculated	1.000	0505	uncultured bacterium; N2_12P07f; AB484341
S001422066	not_calculated	1.000	0505	uncultured bacterium; N2_S4F03f; AB485322
S002341426	not_calculated	1.000	0586	uncultured alpha proteobacterium; CR011C2; HQ532501
S002352459	not_calculated	1.000	0672	alpha proteobacterium PM35; HQ607641
S002411029	not_calculated	1.000	0536	Brevundimonas sp. CB1-1; HQ876726
S003321035	not_calculated	1.000	0574	uncultured Brevundimonas sp.; No. 8; AB695098
S003614866	not_calculated	1.000	0511	Brevundimonas sp. TW_LB_DL4; JX402644

Lineage:**Results for Query Sequence: WG59, 724 unique oligos****rootrank** Root (20) (match sequences)

domain Bacteria (20)

phylum Proteobacteria (20)

class Gammaproteobacteria (20)

order Pseudomonadales (20)

family Pseudomonadaceae (20)

genus Pseudomonas (20)

S000734902	not_calculated	0.991	0576	Pseudomonas putida; C-1; AB236664
S001419646	not_calculated	1.000	0539	uncultured bacterium; C2_13J13f; AB482902
S003260799	not_calculated	0.991	0564	Pseudomonas sp. StFLB093; AB628303
S003260812	not_calculated	0.991	0564	Pseudomonas sp. StFLB106; AB628316
S003260813	not_calculated	0.991	0564	Pseudomonas sp. StFLB107; AB628317
S003260814	not_calculated	0.991	0564	Pseudomonas sp. StFLB109; AB628318
S003260822	not_calculated	0.991	0564	Pseudomonas sp. StFLB118; AB628326
S003260823	not_calculated	0.991	0564	Pseudomonas sp. StFLB119; AB628327

S003260825	not_calculated 0.991 0564	Pseudomonas sp. StFLB121; AB628329
S003260826	not_calculated 0.991 0564	Pseudomonas sp. StFLB122; AB628330
S003260827	not_calculated 0.991 0564	Pseudomonas sp. StFLB123; AB628331
S003260828	not_calculated 0.991 0564	Pseudomonas sp. StFLB124; AB628332
S003260829	not_calculated 0.991 0564	Pseudomonas sp. StFLB125; AB628333
S003261017	not_calculated 1.000 0564	Pseudomonas sp. StFRB034; AB628521
S003261084	not_calculated 1.000 0564	Pseudomonas sp. StFRB104; AB628588
S003261416	not_calculated 0.991 0565	Pseudomonas sp. StFRB452; AB628920
S003261421	not_calculated 1.000 0564	Pseudomonas sp. StFRB457; AB628925
S003747331	not_calculated 0.992 0624	Burkholderia sp. EECC-564; JX909225
S003747356	not_calculated 0.993 0561	Pseudomonas sp. EECC-36; JX909250
S004485609	not_calculated 0.992 0615	Pseudomonas sp. I15B-00826; KR184195

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