Supplementary Figure S1. Secondary structure of the N-terminus of PilA proteins from Desulfuromondales species and other bacteria that possess type IVa pilA genes. The location of alpha helices (represented by red H) and beta strands (represented by yellow E) was predicted with Jpred 4 (Drozdetskiy et al, 2015). Transmembrane helices (green background) were predicted with TmPred (Hofmann & Stoffel, 1993), TMHMM (Krogh et al, 2001), and HMMTOP (Tusnady & Simon, 2001).

G. bemidjiensis (Gbem_2590)

```
MLNKLRSNKGFTLIELLIVVAIIGILAAIAIPQFSAYREKAYNAASNSDLKNFKTGLEAFNADFQTYPAAYVASTN
---HHH----HHHHHHHHHHHHHHHHHHHH----HHHHHHHHHHHHH-----HHHHHHHHHH-------EEEE---
```

G. bremensis (K419DRAFT_00801)

```
MLNKLRSNKGFTLIELLIVVAIIGILAAIAIPQFSAYREKAYNAASNSDLKNWKTGQEAYQADFQAYPAAYDVH
--HHHH----HHHHHHHHHHHHHHHHHHH----HHHHHHHHHH------HHHHHHHHHHHHHHH----------
```

Pelobacter seleniigenes (N909DRAFT_0006)

```
MLKKFRKNEKGFTLIELLIVVAIIGILAAIAIPQFASYRQKAFNSASQSDLKTIKTSLEGYYTDEYYYPY
--HHHHH-----HHHHHHHHHHHHHHHHHHHHH-HHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
```

Geobacter sp. OR-1 (WP_041974243)

```
MLSKLRSNKGFTLIELLIVVAIIGILAAIAIPQFSAYREKAYNTAANADDKNAKTGEEAYNADNQKYPLAYDQH
--HHHHH----HHHHHHHHHHHHHHHHHHH---HHHHHHHHHHHHHHHHHHHHHHHHHHHHH------------
```

Geobacter sp. M18 (GM18_2492)

```
MLNKIRSNKGFTLIELLIVVAIIGILAAIAIPQFSAYRAKAYNAAANSDLKNIKTGMEAYMADRQAYPVSLDER
--HHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------------
```

Geobacter sp. M21

```
MLNKLRSNKGFTLIELLIVVAIIGILAAIAIPQFSAYRAKAYNSAANSDLKNMKTGMEAYMADRQAYPALLDQR
--HHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----------
```

*Desulfuromonas sp. TF (*DTFDRAFT_03630)

```
MLKKFRKNEKGFTLIELLIVVAIIGILAAIAIPQFSSYRQKAFNSAGNSDLKNTKTGFEAFMAETQVYPAALDAR
--HHHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----------
```

*Geoalkalibacter ferrihydriticus (*Ga0056053_00657)

```
MLSKFKKNQKGFTLIELLIVVAIIGILAAIAIPQFASYRERAFNSAAQSDLRTIRTSVEAHYAENYQYPATN
--HHHHHH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH--------
```

*Geoalkalibacter subterraneus (*WP_040199521)

```
MLKKFRLNRNQKGFTLIELLIVVAIIGILAAIAIPQFASYRERAFHSASQSDLRNFKTSMEAYYAENQEYPAAFVDGAN
---HHHHH------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------HHH---
```

*Desulfuromonas thiophila (*Ga0056074_12312)

```
MLSKFRKNEKGFTLIELLIVVAIIGILAAIAIPQFAAYRQKAFNSAAISDIRSTKTNLEAYYTDNNNYPY
--HHHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------
```

Geobacter metallireducens (Gmet_1399)

```
MLQKLRNKKGFTLIELLIVVAIIGILAAIAIPQFAAYRQKAFNSAAESDLKNTKTNLESYYSEHQFYPN
--HHHHH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
Geobacter lovleyi (Glov_2096)
MLNKIRNRKGFTLIELLIVVAIIGILAAVAIPQFTTYRIKGYNSNATSDLRNLKTVLESVFADRQGYPGS
-----------HHHHHHHHHHHHHHHHHHH---HHHHHHHH--------HHHHHHHHHHHHH--------
Geobacter sulfurreducens (GSU1496)
MANYPHTPTQAAKRRKETLMLQKLRNRKGFTLIELLIVVAIIGILAAIAIPQFSAYRVKAYNSAASSDLRNLKTALESAFADDQTYPPES
---------HHHHHHHHHHHHHHHH-----HHHHHHHHHHHHHHHHHHHH--HHHHHHHHHHHHHH--HHHHHHHHHHHHH---------
Geobacter pickeringii (Ga0069007_111762)
MLQKLRSKKGFTLIELLIVVAIIGILAAIAIPQFTAYRAKSYNSAAQSDLRNFKTAMEAAYTDTQSYPNI
--HHHH-----HHHHHHHHHHHHHHHHHHH---HHHHHHHHHHHHHHH-H--HHHHHHHHH---------
Desulfuromusa kysingii (Ga0056096_02700)
MLKMFRKGNQKGFTLIELLIVVAIIGILAAIAIPQFASYRERGFNAQAMSDVRNERTDLEGYYATWFSYPEE
-HHHHHH------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
Geobacter argillaceus (Ga0052872_01800)
MLVNLRSKKGFTLIELLIVVAIIGILAAIAIPQFSAYQAKARNSAANADCKNIKTGWEAFGADNSGVYPAALDIR
---EH-------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------------
Geobacter argillaceus (Ga0052872_01802)
MLAKLRNERGFTLIELLIVVAIIGILAAIAIPQFSAYQAKARNSAANADCKNIKTGWEAFGADNSGVYPAALDIR
--HHH-------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------------
Geobacter soli (WP_039645155)
MLQKLRNRKGFTLIELLIVVAIIGILAAIAIPQFSAYREKAYNSAANSDLKNVKTGMESFMADNQEYPGKVDYAQ
--HHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------------
Geopsychrobacter electrodiphilus (D888DRAFT_2042)
MLKKFRKNEKGFTLIELLIVVAIIGILAAIAIPQFSAYRAKAYNAASNSDLKNIKTGMEAYMADNQAYPSDMSYR
--HHHHHH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----------
Pelobacter propionicus (Ppro_1656)
MLNKLRNRKGFTLIELLIVVAIIGILAAIAIPQFSAYRAKAYNSAANSDLKNIKTGMEAFMADNQQYPGDVDYR
--HHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------------
Desulfuromonas subbituminosa (Ga0064601_106193)
MRRNIRGFSLIELLVVLAILGILMAIAVPMYNQYRRRANRAEGRATLVEAAQIAERSFVRNNTYMNVTIGPNVADDIRDR
--HHH----HHHHHHHHHHHHHHHHHHH-HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH--------------------
Geobacter uraniireducens (Gura_2677)
MLNKLRSNKGFTLIELLIVVAIIGILAAIAIPQFSKYRIQGFNASGNSDLKNIRTSQESLYAEWQHYGLTQGLATVAGLPG
-----------HHHHHHHHHHHHHHHHHH-----HHHHHHH--HHHHHHHHHHHHHHHHHHHHHHHHHHHHH---------
Geobacter daltonii (Geob_3369)
MLNKLRNKEGFTLIELLIVVAIIGILAAIAIPQFSAYRARGFNASAQSDVRGLATSEAALFGDAQVFGATQFIAAPVAPAP
```

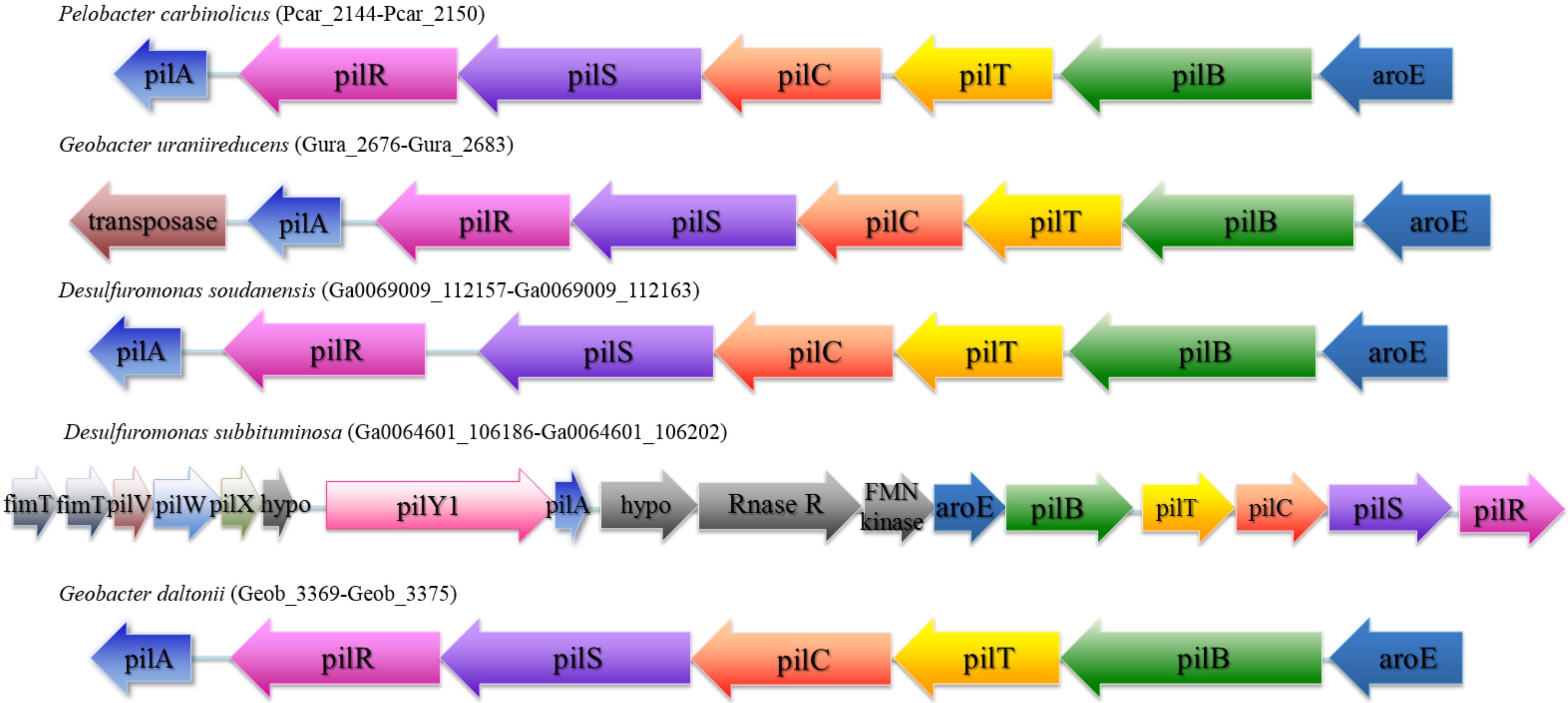
```
-----------HHHHHHHHHHHHHHHHHH---HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
Desulfuromonas soudanensis (Ga0069009_112157)
MLSKFRKSEEGFTLIELLIVVAIIGILAAIAIPQFAAYRIRGYNSAANSDVRNVGTAEEALFADSQGYGSPV
--HHHHH-----HHHHHHHHHHHHHHHHHH----HHHHHHHH---HHHHHHHHHHHHHHHHHHHHH------


Pelobacter carbinolicus (Pcar_2154)
MKTKESGFSLIELLVTVAIIGILSAIAVPIYNQHILRTNRAAAKGLLTEMAQRLERHYTRNNTYAGLDVQDM
---------HHHHHHHHHHHHHHHHHHH-HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------------
Pelobacter carbinolicus (Pcar_2144)
MLKELRKNEKGFTLIELLIVVAIIGILAAIAIPQFAAYRQRAFNSAALTDINNLQKSEAAFFTDWQVFGHSAAA
--HHHHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH---------
Desulfobacterium autotrophicum (HRM2_27700)
MFKRLREKAKNSKGFTLIELMIVIAIIGILAAIAIPQFMTYKAKAYNAGSLSDLHNLRLEFEGYNATWDAYPN
--HHHHHHH------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH---HHHHHHHHHHHHHHHH---------
Myxococcus fulvus (WP_046715654)
MLNRLMKKKGGFTLIELMIVVAIIGILAAIAIPNFIRFQAKSKQSEAKTNLKAIFTAQKAYFGEKDKYVSDFKV
------------HHHHHHHHHHHHHHHHHHHHH-HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH----------
Neisseria gonorrhoeae (AAC38433)
MNTLQKGFTLIELMIVIAIVGILAAVALPAYQDYTARAQVSEAILLAEGQKSAVTGYYLNNGKWPADNGA
---HHHHHHHHHHHHHHHHHHHHHHHHH------HHHHHHHHHHHHHH--HHHHHHHHHHH---------
Escherichia coli (WP_000360901)
MDKQRGFTLIELMVVIGIIAILSAIGIPAYQNYLRKAALTDMLQTFVPYRTAVELCALEHGGLDTCDGGSN
-------HHHHHHHHHHHHHHHHHHH------HHHHHHHHHHHHHHHHHHHHHHHHHHH------------
Hippea maritima (Hipma_0737)
MREFRNKKGFTLIELLVVVAIIAILAAIAIPQYAKYRRSAQDSAALSDLKTIQTTAEAYYADNMHYPY
----H------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------
Hippea alviniae (G415DRAFT_0872)
MKELKGKKGFTLIELLVVVAIIAILAAIAIPQYAKYRQKAYDAAALSDIKNAKTVFEAYFSDNQEYPTIN
----HH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH--------
Deferribacter desulfuricans (DEFDS_1270)
MKKTNKKGFTLIELLVVVAIIGILAAIAIPQFAKYRKNAQDSAALSDLKTIQSTAEAFYADKNHYPY
---HHH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------
Flexistipes sinusarabici (Flexsi_2291)
MKKDTISFTNGRVGFTLIEVLTVIVIIGILAVIAIPQFASYRISAFNSTAQSDLRNAKSHLEAYYSEHGTYPAD
----EEEE-------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
Flexistipes sinusarabici (Flexsi_2288)
```

MVRKSNGKKGFTLIELLVVVAIIGILAAIAIPQFAKYRINAFNSAAQSDLANVKSALESYYAENFTYPSP
-----------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
*Desulfobacula toluolica (*TOL2_21350)
MFNWLKQRRNQKGFTLIELMIVIAIIGILAAIAVPQFSKYRARSFNTQAIADARIIKNETGGYFAEWSKFP
--HHHHHHH------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----

*Desulfobacula phenolica (*Ga0066824_11648)
MFNWLRQKRNQKGFTLIELMIVIAIIGILAAIAVPQFTKYRARSFNTQAISDARNIKNEAGGYYAEYDHFPY
--HHHHHHH-----HHHHHHHHHHHHHHHHHH------HHHHHHHHHHHHHHHHHHHHHHHHHEE-------
*Desulfobacula sp. TS (*Ga0097800_108051)
NWLKKHRNQKGFTLIELMIVIAIIGILAAIAIPQFASYRAKSYNSASISDVRNLRTDLESYYAEWNVYAD
---HHHH-----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH------
*Desulfobotulus alkaliphilus (*LZ24DRAFT_00006)
MLSKVRIRHDQKGFTLIELMIVIAIIGILAAVAIPQFASYRARGYNSQALSDARNLRTDMEGFHATWNTYPGN
---------------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-------
*Desulfobotulus sapovorans (*BR04DRAFT_00394)
MLSKIRMRRNQKGFTLIELMIVIAIIGILAAVAIPQFAKYRQNAFNASAQSDLRNAKSSLEAYFSENFVYP
---HHHHHHHH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH-----
*Thauera linaloolentis (*C666_06285)
MKKIQKGFTLIELMIVVAIIGILAAIAIPQFNEYRAKANDTSAVADAKNGITAIISSLR
--HHHHHHHHHHHHHHHHHHHHHHHH------------------------HHHHHHH—
*Thauera linaloolentis (*C666_05425)
MGKSQGFTLIELMIVIAIIGMLAAVAIPQYSTYVLKGKLAEPRANLSEMRVRMERYFQDNRRYNAVVGV
-------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH----------
*Thauera linaloolentis (*C666_15290)
MKKAQQGFTLIELMIVVAIIGILAAIAIPQYQDYVARSQVSRVMSETASLRTAVETCLMDGKTDIGAGADQ
---H----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH---HHHHHHHHHH-----------
*Thauera terpenica (*M622_11345)
MKKMQKGFTLIELMIVVAIIGILAAIAIPQFSEYTRKSENKVAQTDARNFLTAAIANSN
--HH----HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH---
*Thauera terpenica (*M622_01585)
MKFRKTVAGFSLIELMIALAVISILASIAYPNYMEYLQRARRAECASVLLGQANAMERRFSTTNSYVGAL
----H-----HHHHHHHHHHHHHHHHHHH---HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH--------
*Thauera humireducens (*WP_048709378)
MKRAQGFSLIELMIVVAVIGILAAVAVPQYNQYILKSKLAEARAELSDARVRMERYFQDNRRYNNAAD
-------HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH---------

*Thauera humireducens (*WP_048706629)

```
MKKIQKGFTLIELMIVVAIIGILAAIAIPQFNEYRAKANDTTAIADVKNGITAVISSLR
--HHHHHHHHHHHHHHHHHHHHHHHH----------------EEE-----HHHHHH--
```



Supplementary Figure S2. Distribution of pilin genes within the *pilA* gene cluster in Desulfuromondales genomes harboring long type IVa *pilA* genes.

Supplementary Figure S3. Secondary structure of “PilA-C” proteins from Desulfuromondales species and other bacteria that possess e-pilin genes. The location of alpha helices (red H) and beta strands (yellow E) was predicted with Jpred 4 (Drozdetskiy et al, 2015). Signal peptides (green background) were identified with PSORTb v. 3.0.2 (Yu et al., 2010) and SignalP v. 4.1 (Petersen et al., 2011). Transmembrane helices (turquoise background) were predicted with TmPred (Hofmann & Stoffel, 1993), TMHMM (Krogh et al, 2001), and HMMTOP (Tusnady & Simon, 2001).

*Desulfuromusa kysingii (*Ga0056096_02701): Hydropathicity is -0.086

```
MKKIIILIAVCMIIPSIGMAAVTLGSGTSISDNGDNPTNELSLSPGVFLSYDSDGDDSYALTGANNKGSMCYAVMSGDQGVYQQSIEVADSSDISDTNIIEADDSVDYPDDDDWTQVGG
-HHHHHHHHHHHHHHHHHHHHEE-----------------EE----EEEEE-------EEEE-------EEEEEE-----HHHH-EE-----------EE-------------------
```

*Geopsychrobacter electrodiphilus (*D888DRAFT_2041): Hydropathicity is 0.213

```
MKKILIITIFAVFMTSSAFAATNAITFPTTFDKANTGKTVYGDSTDASATNVNAALIGKTSSGVGCSIKSTTLGYAAVTQHLNGTKAFASSNDSTSIYSKVVTAGTATSNFTNIGTTDFASWTAM
--HHHHHHHHHHHHH---------EE------------EEE------------HHHHHHHH---EEEEE-----EEEEEE--------------HHHHHHHH-----------------------
```

*Pelobacter seleniigenes (*N909DRAFT_0005): Hydropathicity is 0.234

```
MKKIVVLTFCLFLVLPVSGVFAAGDVTSSGGQLTLGSTAGASTNPQLIIGLSPKVVARYVTDGTDTVTAQWYAIGTVHPGGNLGYGTAQNLNNIYFMKYETGAATSTILNELPTTANSASDWSTSWDM
--HHHHHHHHHHHHHH----------------EEE-----------EEEE----EEEEEE------EEEEEEEEEEE----------------EEEEE------HHHHHHH-----------------
```

*Geobacter bemidjiensis (*Gbem_2589): Hydropathicity is 0.095

```
MKKILAAMVVTLSFAGTASAGTLVTAGSGYAIRGGADAATASAAPTPLIKFSTGVWGLINSTPDTTAKTSTGYVIATRHTTGSKDFGTASNRTNIFWKQASAITASVSASQALANDVGSDDETGATFAAGKGWT
-HHHHHHHHHHHH---------EEE----EEEE----------------E------EEE-------------EEEEEE--------EE------EEEEHHH---HHHHHHHHHH-----------EEEE-----
```

*Geobacter bremensis (*K419DRAFT_00800): Hydropathicity is 0.397

```
MKKMALLSSLVVFASTAAFAAPLATHVPTTGGAVAIYGGTGAAEALAAPTSLVKTSTGVNGLVDYPGNTAYLIITKHTTGSKVFGTCNGVNNIYWRQVTSGTLATTMLTGITSGSAATSSFVGNGWTSY
--HHHHHHHHHHHHHHHHHHH----EEEE---EEEEE-----------------------EEEE-----HHEHHHH----------------EEEHHHHHHHHHHHH------------EEE-------
```

*Geobacter sp. OR-1 (*WP_041974245): Hydropathicity is 0.455

```
MKKIIALTALIVISASSYAAAGALATNTVSNAGTAIYGGADATGAGAASSPLFKLSTGVSTIINFDAAGVGYAVFTKHVKGTKVFGTAYDSTAISYFTEAPGTLTTTNTGSATAVPSGWTSM
--HHHHHHHHHHHHHHHHH--------------EEEEE----------------------EEEE-------EEEEEE-----EEEE-------EEEEEE-----------------------
```

*Geobacter sp. M18 (*GM18_2491): Hydropathicity is 0.163

```
MKKIIALSAVVVMLTASLASATSLATGGVSGESKTIYGGISTGDSSGTSATLIGKLSKSVKLGVAYTSGGYALDTKHSSGNTRYGTAHDATAIYKQEIGTTDLAAPTAASYSAFSTWTAM
--HHHHHHHHHHHHHHHHHHHH-----------EEEE-------------EEE-------EEEEE-----EEEEEE-----EE-------HHHHHH---HHHH-------------H---
```

*Geobacter sp. M21 (*GM21_1637): Hydropathicity is -0.051

```
MKKIIALSAVAVLLTSSLASAAALTGGVSDESKSIYGGTTTDATTASATLIGKLSKNVKLGANYDTGGYALETRHSSGNTRYGTAFDATAIYKQEGATAVEKPSTTSYSSFSTWTAM
--HHHHHHHHHHHHHHHHHH------------EEEE-----------HHHHHHH----EEEEEE----EEEEEE----------------EE-------------------------
```

*Pelobacter propionicus (*Ppro_1657): Hydropathicity is 0.216

```
MYGDKSTATAATAALIGKTSTGVSVGLLTSSLGYAVVTQHKNGTKAFGSSYDSTSVFSSTVTEGTALLTVPTAITSADFTGTWTSM
------------HHHHHHHH---EEEEE-----EEEEEE-----E--------HHHHHHHHHH-----------------------
```

*Geobacter argillaceus (*Ga0052872_01799): Hydropathicity is 0.112

```
MKRIISLVALMLIVTSGSAFAAAFTSGSTNTNGTGQSIYGGVDATTAAGTTAPMLGRLSKGVQFGAAFSNTTYAHTTKHSGGTKMYGTAQNSTAIYSQDATAIAAPSTSDANAFATGWTAM
--HHHHHHHHHHHHHHHHHHHEEEE-----------EEEE-----------HHHHHHHH---EEEEEE----EEEEEE-----EEE--------E--------------------------
```

*Geobacter argillaceus (*Ga0052872_01801): Hydropathicity is 0.256

```
MKRIISLVALMLIVTSGSAFATAFATGATDTNGTGETVYGGVDATTAAGTTAPVLGRLSKGVHFGAAFSATTYALTTKHSGGTKMYGTAQNSTAIYSQDATAIAAPSTSDANAFATGWTAM
--HHHHHHHHHHHHHHHHHHHHHH------------EEEE-----------HHHHHHHH----EEEEE----EEEEEE-----EEE--------E--------------------------
```

*Desulfuromonas sp. TF (*DTFDRAFT_03629): Hydropathicity is 0.468

```
VKKISILAVLFVFIACNVSFAAALASGGTTTTTGLQVFGGVDADDAAGSSSVLLGKMSKGVYFGAAYTTGGYACATKHTSGSKAYGTAHDSTAIYFQDIGTAALSTVTPSAASNTAFGSAWTAM
```

--HHHHHHHHHHHHHHHHHHHHHHH---------EEEE-----------HHHHHHHHH---EEEEE------EEEEE----------------EE-----------------------------

Geoalkalibacter ferrihydriticus (Ga0056053_00658): Hydropathicity is -0.011

MKKMVVLLAAFVLLFSGHAFGFTKADDDKQITCGTGGPTVPLSPRVEALYLGTATTYAVATRNVQGTRTFGTAHNETGIFWAEGISDDVKPTLNTEFSSDATWNQL

-HHHHHHHHHHHHHH--------------EEEE-------------EEEEE-----EEEE-------EEE-------EEEE-------------------------

Geoalkalibacter subterraneus (WP_040199522): Hydropathicity is -0.291

MKKTLFSIITLGLLLPGSVFAVTHTIGGDGDKQSAYLGDKTGELFRVSTNVVLEINSTTADYAATSGHLQGTKQYGTTSRFNAIFEGAKDKGSGPTEPKSEVALDTSVFTEFPPETDTNGE

--HHHHHHHHHHHH----EEEEEEE---------EEE------EEEE--EEEEEE-------------------------HHHHH----------------EEE--EEE------------

Desulfuromonas thiophila (Ga0056074_12311): Hydropathicity is -0.191

MKKALFLLLILAFAGTAFAAYSEDATATLGEGDNSLKVKLSNQVKLDYAENGDGDTFVIAAYHDKGTRTFMSSSEDASIYYGEETKITMPDAPDVGTSIGTTDDFDKTL

--HHHHHHHHHHHHHHHHHH--------------EEEEE----EEEEEE------EEEEEEEE----EEE-------EEEE-----EE---------------------

Geobacter metallireducens (Gmet_1400): Hydropathicity is -0.198

MKKKIFLTGLCFLSIGSVAFAASKDVTGSGEIGGSNSTPKLAIQTSNQVTLTYDGGTGHTYGIATLHAKGTRKYASTSNDTKIYYNDNTATAAPSAPVGTATIGGSTNWKNAL

---EEHHH-HHHHHH--HHHH------------------EEEEE----EEEEE------EEEEEEEE-----E--------EEEE---------------EEE----------

Geobacter lovleyi (Glov_2095): Hydropathicity is 0.224

MAKKNMLKLAVVVVLSMVAASASYAATLTLSGATSVGGSSFSSSNKVSAYYVSDSGVSTGFAGTAYGIAAAHGQGDKAIASNQSDAKLYFKTTTPGNATSVASAIATNTSFTGTDWTSM

-----HHHHHHHHHHHHHHHH--HHHEEEE----------------EEEEEE-------------EEEE-----------------EEEEEE-------HHHHHH--------------

Geobacter sulfurreducens (GSU1497): Hydropathicity is -0.388

MKKIITIVAMLLAMQGIAIAAGKIPTTTMGGKDFTFKPSTNVSVSYFTTNGATSTAGTVNTDYAVNTKNSSGNRVFTSTNNTSNIWYIENDAWKGKAVSDSDVTALGTGDVGKSDFSGTEWKSQ

--HHHHHHHHHHHH--HHHH-------------EEE-----EEEEEEE--------------EEEE-------EEEE-------EEEEE--------------EEE------------------

Geobacter pickeringii (Ga0069007_111761): Hydropathicity is 0.272

MKNLMVLSFVSVLTIAVGAAAYAAPITTSTTLGTTTTFTPSSNVQVDAWASNSAYAATSQHLSGNRIFFGMNGDSKIYFNTKTAGSQASVSIGSAGAPATTVPTGYTTL

---HHHHHHHHHHHHHH------------------EEE-------EE------------------EEEEEE----EEEE----------EEE-----------------

Desulfobotulus alkaliphilus (LZ24DRAFT_00005): Hydropathicity is -0.322

MKKIWLYMLTAFAAVALSGMAYADTVTTGEGEKIEIGAGHFADDDGIANADFEFQPSPSVSMSVNAERHYFALTAMSVSAKVPQGMVYGIFSDTQGYYQRAKTDEDDEAPSGEVGDLDGEGDVFEDEDEWTYMG

-HHHHHHHHHHHHHHHH---------------EEEE------------------------EEEE----EEEEEEEEE--------EEEEEE------EE-----------------------EE-----EEEE-

Flexistipes sinusarabici (Flexsi_2289): Hydropathicity is 0.190

MQKISLIHHHKEVKMRKITISIIAICLILMGSMVFAAGTDISTITGINTQLSDKVKGVYFANINASGDYVDFAISTANTQGDEVYATGNFVSKIFCKNIAGDTYVSTDLLQSVSNYNSSASFTSWTCK

---HHHHHH----HEEEEHHHHHHHHHHHHHHHHHHH-----EEE----------EEEEEEE-------EEEEE--------EEEE----HHHHHH----------HHHHHHH---------------

Desulfobacterium autotrophicum (HRM2_27710): Hydropathicity is 0.152

MNSLIKIAVISVIITGLSGFAYAGTAVQTGGAGDTVTFAGTKGLATLSFTPSGNTIINGTSTALTYDITSGCSKTDMSNGMEYGMSQDITGYYQKTQGAADAAPPATITPANWTLMGSSS

--HHHHHHHHHHHHH-----------E-------EEEE------EEEEE------EE-----EEEEE----------------------HHHHHH------------------EEE----

Hippea maritima (Hipma_0736): Hydropathicity is 0.053

MKKILALFMSVCSMAFFASGVYAFTLGGTDTTDINLSANVEAGYYGGGDGSLYIADTYNPKGNGKVYGTGSAYSKIYYTTTTSNFVSGSNASGLSSVNFSGWSTLGE

-HHHHHHHHHHHHHHHHHH-HEEEE--------EEEEEE------------EEEEE--------EEEE-----EEEEEE---------------EEEEE--------

Hippea alviniae (G415DRAFT_0873): Hydropathicity is -0.287

MKKNVFLGIIAISLLFATFSTTARAKLFQSGSTIVSGDTFTPSQGVSLVIVSNSNAYTMESDHKQGRYKYATTNNDEVKKAKCTNDPCGTEIDGDKPTAGTLPSWTWVQ

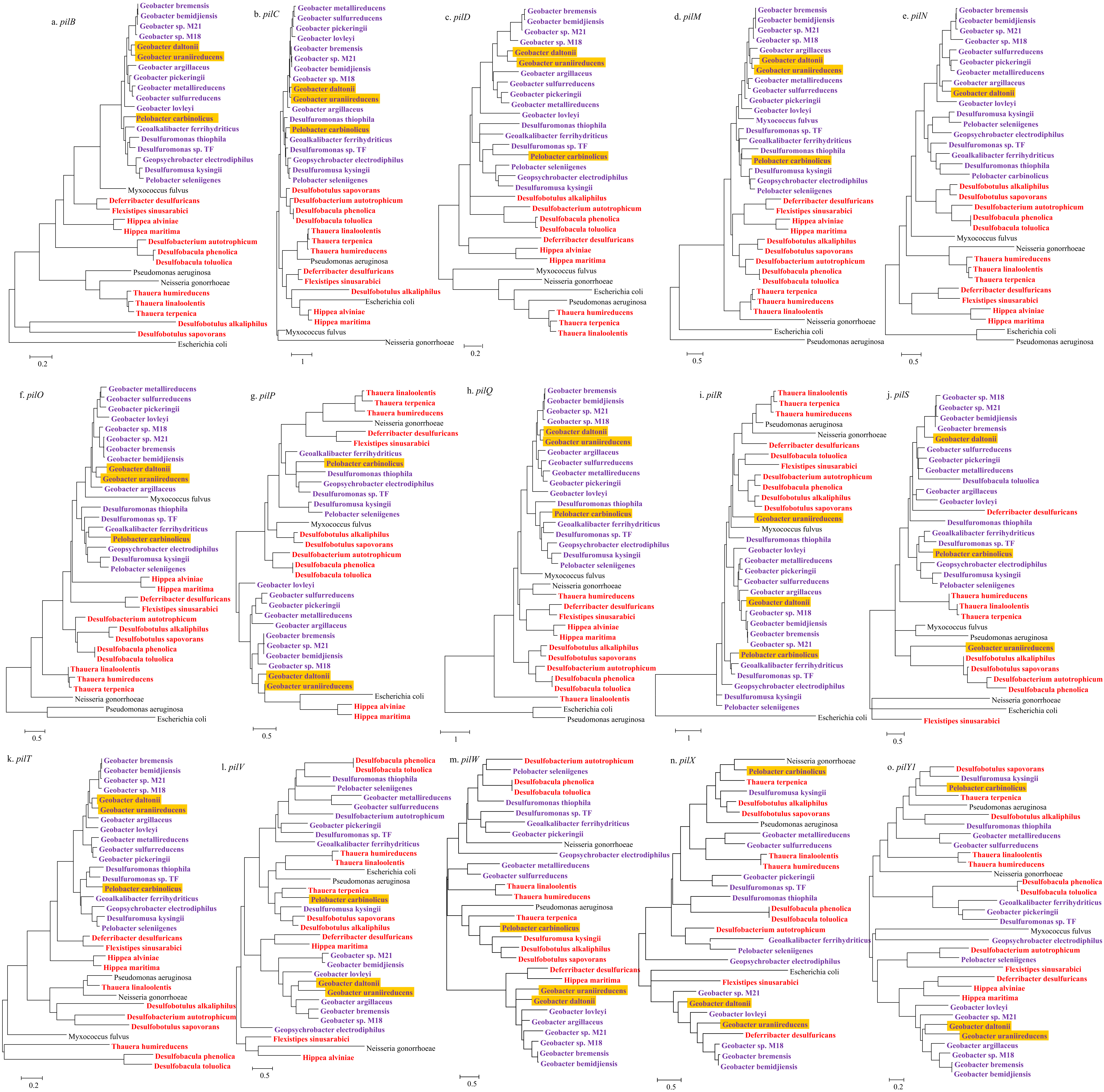
----HHHHHHHHHHHHHHH--HHHHHHHH---EEEE---------EEEEEEE----EEE--------EEEE--------------------------------------

Deferribacter desulfuricans (DEFDS_1271): Hydropathicity is -0.145

MRKLIFLIVILSFASLLFAGDFTLGSTDNETIKLSANVSADYDADTNGNHYVAGTMSSKGTKKYGTADTESVIYYDECTGNDCADDNVTFSGYSSGLSTIQGWTPME

--HHHHHHHHHHHHHHHHH------------EEEEEE------------EEEEE----------------EEEEEE------------EE-----------------

Supplementary Figure S4. Phylogenetic trees generated with the maximum likelihood algorithm showing the relationship of various pilin accessory proteins from the order Desulfuromondales to accessory proteins from other type IVa pilin harboring bacteria. Proteins from Desulfuromondales species are highlighted with purple font. Proteins from Desulfuromondales species with long type IVa pili have an additional orange background. Pilin accessory proteins from e-pili harboring species that are not in the order Desulfuromondales are highlighted in red. The remaining organisms included in the trees have long typeIVa pilin proteins. These phylogenetic trees and identity/similarity matrices outlined in Supplementary Table SX demonstrate that pilin accessory proteins are relatively conserved and that e-pilin harboring species have the same accessory proteins as organisms with long type IVa pilins. In most cases (with the exception of PilV, PilW, PilX, and PilY1), Desulfuromondales proteins form a single monophyletic clade, while accessory proteins from non-Desulfuromondales e-pilin harboring genera such as *Flexistipes, Hippea, Desulfobacterium, Deferribacter, Desulfobacula, Thauera*, and Desulfobotulus fall elsewhere in the phylogenetic trees. Even accessory proteins from Desulfuromondales with long pili cluster with proteins from Desulfuromondales with short e-pilins. E-pilin phylogeny, on the other hand, is unique in that organisms from distant genera such as *Flexistipes, Thauera, Deferribacter, Desulfobacterium, Desulfobacula, Desulfobotulus*, and *Hippea* cluster within the e-pilin clade (Figure 1).



Supplementary Table S1. Breakdown of Desulfuromondales pilin gene clusters and pilin gene clusters from e-pilin harboring species from other bacterial orders. Each pilin gene cluster is shaded in a different color. Genes with GC content +/- 7% of the genome average are highlighted in blue.

A. Pilin gene clusters found in the *Geobacter sulfurreducens* genome. Three different gene clusters were identified and each is highlighted in a different color. Only one gene coding for a horizontal gene transfer protein is present in these gene clusters. Genes from the xap operon and additional glycosyl transferase proteins are located in the vicinity of the e-pilin gene. The overall GC content of *G. sulfurreducens* is 60.94%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Sixteen out of 58 (26%) of the genes have deviant GC values, including *e-pilin, pilA-C, xapA, xapB, xapD, xapH*, and *xapJ.*

Locus ID	Gene	Horizontal transfer gene	GC content
GSU_RF0073	GEMM riboswitch		0.58
GSU1061	aspartate aminotransferase		0.64
GSU1062	cytochrome c, putative		0.66
GSU1063	*pilV*		0.58
GSU1064	*pilW*		0.62
GSU1065	*pilX*		0.6
GSU1066	*pilY1*		0.61
GSU1484	soluble lytic murein transglycosylase		0.62
GSU1485	RNAse R		0.63
GSU1486	*tatC*		0.56
GSU1487	Flavokinase		0.6
GSU1488	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD		0.63
GSU1489	DUF2723 family transferase activity		0.58
GSU1490	*aroE*		0.61
GSU1491	*pilB*		0.59
GSU1492	*pilT*		0.6
GSU1493	*pilC*		0.55
GSU1494	*pilS*		0.59

GSU1495	*pilR*	0.58
GSU1496	**e-pilin**	**0.49**
GSU1497	***pilA*-C**	**0.45**
GSU1498	***xapA*, Tetratricopeptide-like helical**	**0.44**
GSU1499	***xapB*, ABC-2 family transporter protein**	**0.49**
GSU1500	**pili subunit family**	**0.51**
GSU1501	***xapD*, ABC transporter, ATP-binding protein**	**0.49**
GSU1502	*xapE*, 4-hydroxybenzoate polyprenyltransferase	0.54
GSU1503	*xapF*, glycosyl transferase, group 2 family protein	0.56
GSU1504	*xapG*, ABC-type polysaccharide/polyol phosphate export permease	0.56
GSU1505	***xapH*, ABC-type polysaccharide/polyol phosphate transport system, ATPase component**	**0.53**
GSU1506	*xapI*, methyltransferase, FkbM family	0.54
GSU1507	***xapJ*, UDP-Glycosyltransferase/glycogen phosphorylase**	**0.5**
GSU1508	**Glycosyltransferase WbsX**	**0.39**
GSU1509	**glycosyl transferase, group 2 family protein**	**0.38**
GSU1510	**glycosyl transferase, group 2 family protein**	**0.46**
GSU1511	**glycosyl transferase, group 1 family protein**	**0.42**
GSU1512	UDP-galactopyranose mutase	0.58
GSU1513	**S-adenosyl-L-methionine-dependent methyltransferases**	**0.51**
GSU1514	ADP-heptose--lipooligosaccharide heptosyltransferase II	0.6
GSU2019	biotin carboxylase	0.57
GSU2020	biotin carboxyl carrier protein	0.6
GSU2021	xaa-pro dipeptidase	0.6
GSU2022	*aroQ*	0.59
GSU2023	Roadblock/LC7 domain	0.6
GSU2024	TPR repeat	0.58
GSU2025	*aroB*	0.61
GSU2026	*aroK*	0.61

GSU2027	*aroC*		0.61
GSU2028	*pilQ*		0.59
GSU2029	*pilP*		0.58
GSU2030	*pilO*		0.54
GSU2031	***pilN***		**0.53**
GSU2032	*pilM*		0.56
GSU_RF0082	**GEMM riboswitch**		**0.52**
GSU2033	**putative horizontal transfer**	**Lambda repressor-like, DNA-binding domain**	**0.45**
GSU2036	*pilV*		0.56
GSU2037	*fimT*		0.55
GSU2038	*pilY1*		0.59
GSU2043	*pilD*		0.59

B. Pilin gene clusters found in the *Pelobacter carbinolicus* genome. Two different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. This Desulfuromondales species has 2 long type IVa pilin genes. Genes from the xap operon and other glycosyl transferase genes are not present in the *pilA* gene cluster. The overall GC content of *P.carbinolicus* is 55.11%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Nine out of 50 genes (18%) in pilin gene clusters have deviant GC values; these include *pilQ, pilO, pilN, pilM, pilD, pilI*, and *pilC*.

Locus ID	Gene	Horizontal transfer gene	GC content
Pcar_0841	putative horizontal gene transfer protein	Retron-type reverse transcriptase-like	0.59
Pcar_0863	*pihD*, minor pilin protein		0.59
Pcar_0865	*pihP*, minor pilin protein		0.58
Pcar_0866	**pihQ, minor pilin protein**		**0.64**
Pcar_0867	*pilN*		0.6
Pcar_0868	*pilO*		0.55
Pcar_0869	*pihK*, minor pilin protein		0.51
Pcar_0870	*pihL*, minor pilin protein		0.59
Pcar_0871	*pihM*, minor pilin protein		0.62

Pcar_0872	*pilB*		0.6
Pcar_0873	*pilC*		0.59
Pcar_0876	*pihA*, minor pilin protein		0.55
Pcar_0877	*pihH*, minor pilin protein		0.57
Pcar_2121	putative horizontal gene transfer protein	Phage_integrase	0.56
Pcar_2122	hypothetical protein		0.49
Pcar_2123	putative horizontal gene transfer protein	Fic family protein	0.58
Pcar_2124	**putative horizontal gene transfer protein**	**Transposase IS3/IS911family**	**0.44**
Pcar_R0047	tRNA-Leu-TAA		0.62
Pcar_2125	Chorismate dehydratase		0.54
Pcar_2126	outer membrane efflux protein		0.56
Pcar_2127	biotin carboxylase		0.54
Pcar_2128	biotin carboxyl carrier protein		0.56
Pcar_2129	xaa-pro dipeptidase		0.56
Pcar_2130	Roadblock/LC7 domain		0.49
Pcar_2131	Tetratricopeptide repeat		0.55
Pcar_2132	*aroB*		0.5
Pcar_2133	*aroC*		0.56
Pcar_2134	***pilQ***		**0.47**
Pcar_2135	*pilP*		0.48
Pcar_2136	***pilO***		**0.43**
Pcar_2137	***pilN***		**0.44**
Pcar_2138	***pilM***		**0.44**
Pcar_2139	***pilD***		**0.46**
Pcar_2141	**pilI**		**0.45**
Pcar_2142	*xapD*, probable ABC transporter ATP-binding protein		0.5
Pcar_2143	*pilA*-2		0.5
Pcar_2144	*pilA*-1		0.53
Pcar_2145	*pilR*		0.49
Pcar_2146	*pilS*		0.48

Pcar_2147	***pilC***		**0.47**
Pcar_2148	*pilT*		0.54
Pcar_2149	*pilB*		0.54
Pcar_2150	*aroE*		0.56
Pcar_2151	Flavokinase		0.52
Pcar_2152	RNAse R		0.55
Pcar_2154	*pilE*		0.49
Pcar_2155	*pilY1*		0.5
Pcar_2156	*pilX*		0.54
Pcar_2157	*pilW*		0.51
Pcar_2158	*pilV*		0.51
Pcar_2159	*fimT*		0.52

C. Pilin gene clusters found in the *Geobacter metallireducens* genome. Three different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. At least 3 different glycosyl transferase genes and xap operon genes are located in the vicinity of the e-pilin gene. The overall GC content of *G. metallireducens* is 59.49%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twelve out of 64 (19%) of these genes have deviant GC values, including *e-pilin, pilA-C, xapA, xapB, xapD, xapE, xapG*, and *xapH*.

Locus ID	Gene	Horizontal transfer gene	GC content
Gmet_0734	*pilV*		0.55
Gmet_0735	*pilW*		0.57
Gmet_0736	*pilX*		0.59
Gmet_0737	*pilY1*		0.57
Gmet_0738	protein of unknown function DUF294, nucleotidyltransferase putative		0.61
Gmet_0739	transporter, SSS family		0.63
Gmet_0740	Uncharacterized membrane protein, DUF485 family		0.55
Gmet_0741	transcriptional regulator, IclR family		0.61
Gmet_0742	PS51257 Prokaryotic membrane lipoprotein lipid attachment		0.59
Gmet_0743	Transcriptional and/or translational regulatory protein YebC/TACO1		0.6
Gmet_0958	putative horizontal gene transfer protein	IS111A transposase	0.53

Gmet_0959	*pilD*		0.63
Gmet_0960	*pilS*		0.64
Gmet_0961	*pilR*		0.64
Gmet_0962	*pilE*		0.57
Gmet_0963	*fimU*		0.55
Gmet_0964	*pilV*		0.52
Gmet_0965	*pilW*		0.57
Gmet_0966	*pilX*		0.59
Gmet_0967	*pilY1*		0.57
Gmet_0968	hypothetical protein		0.53
Gmet_0969	**hypothetical protein**		**0.51**
Gmet_RF0069	GEMM_riboswitch		0.54
Gmet_0970	putative horizontal transfer gene protein	Lambda repressor-like	0.52
Gmet_0971	*pilM*		0.58
Gmet_0972	*pilN*		0.58
Gmet_0973	*pilO*		0.54
Gmet_0974	*pilP*		0.58
Gmet_0975	*pilQ*		0.57
Gmet_0976	*aroC*		0.65
Gmet_0977	*aroK*		0.6
Gmet_0978	*aroB*		0.63
Gmet_0979	Tetratricopeptide repeat		0.59
Gmet_0980	Roadblock/LC7 domain		0.6
Gmet_0981	*aroQ*		0.57
Gmet_0982	Xaa-Pro aminopeptidase		0.6
Gmet_0983	biotin carboxyl carrier protein		0.61
Gmet_0984	biotin carboxylase		0.6

Gmet_1386	RNAse R		0.65
Gmet_1387	*tatC*		0.6
Gmet_1388	flavokinase		0.61
Gmet_1389	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD		0.63
Gmet_1391	DUF2723 domain protein with transferase activity		0.6
Gmet_1392	*aroE*		0.63
Gmet_1393	*pilB*		0.6
Gmet_1394	*pilT*		0.62
Gmet_1395	*pilC*		0.6
Gmet_1396	*pilS*		0.57
Gmet_1397	*pilR*		0.61
Gmet_1398	putative horizontal gene transfer protein	IS204/IS1001/IS1096/IS1165 transposase	0.54
Gmet_1399	**e-pilin**		**0.45**
Gmet_1400	**_pilA_-C**		**0.46**
Gmet_1401	**_xapB_, ABC-2 family transporter protein**		**0.48**
Gmet_1402	**Type II secretion system protein G**		**0.49**
Gmet_1403	**_xapD_, ABC transporter-related protein**		**0.48**
Gmet_1404	**_xapA_, Tetratricopeptide-like helical**		**0.43**
Gmet_1405	**_xapE_, UbiA prenyltransferase family**		**0.48**
Gmet_1406	**_xapG_, lipopolysaccharide transport system permease protein**		**0.39**
Gmet_1407	**_xapH_, ABC-type polysaccharide/polyol phosphate transport system, ATPase component**		**0.44**
Gmet_1408	**Glycosyl transferase, group 1**		**0.46**
Gmet_1409	**hypothetical protein**		**0.41**
Gmet_1410	*xapJ*, Glycosyl transferase, family 9		0.52

D. Pilin gene clusters found in the *Pelobacter propionicus* genome. Three different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. While some xap genes were detected in the e-pilin gene cluster, no glycosyl transferase genes were present. The overall GC content of *P. propionicus* is 58.48%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Twelve out of 48 (25%) of these genes have deviant GC values, including *pilA-C, xapA, pilX, pilM, pilO*, and *pilP*.

Locus ID	Gene	Horizontal transfer gene	GC content
Ppro_0982	*pilD*		0.58
Ppro_0983	*pilS*		0.61
Ppro_0984	*pilR*		0.61
Ppro_0985	thiol:disulfide interchange protein DsbC		0.57
Ppro_0986	hypothetical protein		0.55
Ppro_0987	*pilY1*		0.56
Ppro_0988	***fimT***		**0.49**
Ppro_0989	*pilV*		0.53
Ppro_0990	*pilW*		0.54
Ppro_0991	***pilX***		**0.47**
Ppro_0992	***pilM***		**0.45**
Ppro_0993	***pilN***		**0.45**
Ppro_0994	***pilO***		**0.42**
Ppro_0995	***pilP***		**0.45**
Ppro_0996	*pilQ*		0.52
Ppro_0997	*pilZ*		0.52
Ppro_0998	Highly conserved protein containing a thioredoxin domain		0.56
Ppro_0999	Transcriptional regulator WYL domain		0.56
Ppro_RF0077	GEMM_RNA_motif		0.54
Ppro_1000	helicase, putative		0.53
Ppro_1001	**putative horizontal gene transfer protein**	**CRISPR-associated protein Cas1**	**0.37**
Ppro_1649	putative horizontal gene transfer protein	transposase, IS4 family	0.56
Ppro_1650	Protein of unknown function DUF2905		0.61
Ppro_1651	Predicted ATPase, Adenine nucleotide alpha hydrolases		0.63
Ppro_1652	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)/GTP cyclohydrolase II		0.61
Ppro_1653	hypothetical protein		0.5
Ppro_1654	enolase		0.61

Ppro_1655	*pilR*		0.59
Ppro_1656	e-pilin		0.54
Ppro_1657	***pilA*-C**		**0.42**
Ppro_1658	***xapA*, Tetratricopeptide-like helical**		**0.44**
Ppro_1659	*xapB*, ABC-2 family transporter protein		0.58
Ppro_1660	Tetratricopeptide-like helical		0.57
Ppro_1661	*xapD*, ABC-2 type transport system ATP-binding protein		0.62
Ppro_1662	methionyl-tRNA synthetase		0.62
Ppro_1663	Cell fate regulator YaaT, PSP1 superfamily		0.64
16 genes			
Ppro_1679	***pilZ***		**0.5**
Ppro_2500	**putative horizontal gene transfer protein**	**transposase, IS4 family**	**0.5**
4 genes			
Ppro_RF0091	GEMM_RNA_motif		0.56
6 genes			
Ppro_2511	*pilS*		0.62
Ppro_2512	*pilC*		0.59
Ppro_2513	*pilT*		0.62
Ppro_2514	*pilB*		0.6
Ppro_2515	DUF2723		0.63
Ppro_2516	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD		0.61
Ppro_2517	Flavokinase		0.62
Ppro_2518	**ATP-dependent DNA helicase RecG**		**0.67**
Ppro_2519	*pilZ*		0.63

E. Pilin gene clusters found in the *Geobacter uraniireducens* genome. Two different gene clusters were identified and each is highlighted in a different color. Fourteen genes coding for horizontal gene transfer proteins were detected in these gene clusters. *G. uraniireducens* has a long type IVa *pilA* gene. Only two homologs from the xap operon (*xapB* and *xapD*) were detected in the *pilA* gene cluster, none of which included glycosyl transferases. The overall GC content of G. uraniireducens is

54.24%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Fifteen out of 80 (19%) of the pilin genes had deviant GC values, including *fimT, pilV, pilM, pilN, pilO*, and *pilP*.

Locus ID	Gene	Horizontal transfer gene	GC content
Gura_1800	*pilD*		0.52
Gura_1801	*pilS*		0.54
Gura_1802	*pilR*		0.52
Gura_1803	Thiol:disulfide interchange protein DsbC		0.52
Gura_1804	*pilY1*		0.52
Gura_1805	***fimT***		**0.46**
Gura_1806	***pilV***		**0.42**
Gura_1807	*pilW*		0.49
Gura_1808	*pilX*		0.45
Gura_RF0078	GEMM_RNA_motif		0.5
Gura_1809	**putative horizontal gene transfer protein**	**Lambda repressor-like, DNA-binding domain**	**0.44**
Gura_1810	***pilM***		**0.43**
Gura_1811	***pilN***		**0.4**
Gura_1812	***pilO***		**0.38**
Gura_1813	***pilP***		**0.42**
Gura_1814	*pilQ*		0.49
Gura_1815	**hypothetical protein**		**0.37**
Gura_1816	Ig family protein		0.5
Gura_1817	**Thiol:disulfide interchange protein DsbC**		**0.38**
Gura_1818	*aroC*		0.55
Gura_1819	*aroK*		0.5
Gura_1820	*aroB*		0.52
Gura_1821	Tetratricopeptide TPR_2 repeat protein		0.49
Gura_1822	Roadblock/LC7 domain		0.5
Gura_1823	*aroQ*		0.48
Gura_1824	Xaa-Pro aminopeptidase		0.52
Gura_1825	biotin carboxyl carrier protein		0.5

Gura_1826	biotin carboxylase	0.51
Gura_2666	Protein of unknown function DUF2950	0.58
Gura_2667	**Protein of unknown function DUF3300**	**0.66**
Gura_2668	putative exported protein	0.58
Gura_2669	Protein of unknown function DUF3313	0.57
Gura_2670	Antibiotic biosynthesis monooxygenase	0.54
Gura_2671	transcriptional regulator, NifA subfamily, Fis Family	0.57
Gura_2672	Lipid-binding SYLF domain	0.53
Gura_2673	**hypothetical protein**	**0.45**
Gura_2674	*xapB*, ABC-2 family transporter protein	0.48
Gura_2675	*xapD*, ABC transporter related	0.53
Gura_2676	putative horizontal gene transfer protein transposase, IS4 family	0.47
Gura_2677	*pilA*	0.49
Gura_2678	*pilR*	0.56
Gura_2679	*pilS*	0.57
Gura_2680	*pilC*	0.54
Gura_2681	*pilT*	0.52
Gura_2682	*pilB*	0.5
Gura_2683	*aroE*	0.51
Gura_2684	DUF2723	0.51
Gura_2685	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD	0.52
Gura_2686	Flavokinase	0.5
Gura_2687	*tatC*	0.52
Gura_2697	*pilR*	0.55
Gura_2698	*pilS*	0.53
Gura_2699	RNAse R	0.58
Gura_2700	Soluble lytic murein transglycosylase	0.56
Gura_2701	**ABC transporter related**	**0.62**
Gura_2702	nucleotidyltransferase	0.58
Gura_2703	transcriptional regulator, MarR family	0.61

Gura_2704	outer membrane efflux protein		0.56
Gura_2705	secretion protein HlyD family protein		0.59
Gura_2706	drug resistance transporter, EmrB/QacA subfamily		0.59
Gura_2707	multi-sensor hybrid histidine kinase		0.57
Gura_2708	putative two component, sigma-54 specific, transcriptional regulator, Fis family		0.6
Gura_2709	hypothetical protein		0.53
Gura_2710	CheY-like superfamily		0.54
Gura_2711	hypothetical protein		0.6
Gura_2712	Cytochrome c family protein		0.6
Gura_2713	cytochrome B561		0.59
Gura_2714	**hypothetical protein**		**0.62**
Gura_2715	putative horizontal gene transfer protein	Programmed cell death antitoxin YdcD	0.57
Gura_2716	putative horizontal gene transfer protein	transcriptional modulator of MazE/toxin, MazF	0.59
Gura_2717	putative horizontal gene transfer protein	Prevent host death protein, Phd antitoxin # D	0.56
Gura_2718	putative horizontal gene transfer protein	addiction module toxin, RelE/StbE family	0.55
Gura_2719	**putative horizontal gene transfer protein**	**CRISPR-associated protein Cas1]**	**0.63**
Gura_2720	putative horizontal gene transfer protein	Transposase IS200-like	0.57
Gura_2721	putative horizontal gene transfer protein	CRISPR-associated protein, Cas2 family	0.49
Gura_2722	putative horizontal gene transfer protein	Very-short-patch-repair endonuclease	0.48
Gura_2723	putative horizontal gene transfer protein	CRISPR-associated exonuclease, Cas4 family	0.58
Gura_2724	hypothetical protein		0.58
Gura_2725	**putative horizontal gene transfer protein**	**CRISPR-associated helicase Cas3**	**0.43**
Gura_2726	putative horizontal gene transfer protein	putative addiction module component, TIGR02574 family	0.5
Gura_2727	putative horizontal gene transfer protein	Death on curing protein, Doc toxin	0.51

F. Pilin gene clusters found in the *Geobacter lovleyi* genome. Two different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. Genes from the xap operon and genes coding for additional glycosyl transferase proteins are present. The overall GC content of *G. lovleyi* is 54.74%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Eighteen out of 39 (46%) of the pilin genes have deviant GC values, including *e-pilin, pilA-C, pilX, xapA, xapB, xapI, pilY1, pilV, pilX, pilM, pilN, pilO, pilP, pilQ*, and *fimT*.

Locus ID	Gene	Horizontal transfer gene	GC content
Glov_1639	**putative horizontal gene transfer protein**	**Lambda repressor-like, DNA-binding domain**	**0.47**
Glov_1640	**_pilM_**		**0.47**
Glov_1641	**_pilN_**		**0.42**
Glov_1642	**_pilO_**		**0.42**
Glov_1643	**_pilP_**		**0.47**
Glov_1644	**_pilQ_**		**0.47**
Glov_1645	PS51257 family protein		0.45
Glov_1646	Aldolase		0.46
Glov_1647	chorismate mutase		0.49
Glov_1648	L-aspartate oxidase		0.51
Glov_1649	Flavokinase		0.51
Glov_1650	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD		0.55
Glov_1651	DUF2723		0.53
Glov_1652	*aroE*		0.54
Glov_1653	*pilB*		0.52
Glov_1654	*pilT*		0.52
Glov_1655	*pilC*		0.5
Glov_1656	*pilS*		0.52
Glov_1657	*pilR*		0.53
Glov_2089	*xapD*, ABC transporter related		0.49
Glov_2090	**hypothetical protein**		**0.46**
Glov_2091	**_xapB_, ABC-2 family transporter protein**		**0.47**
Glov_2092	**_xapI_, Methyltransferase type 11**		**0.4**
Glov_2093	**Glycosyl transferase family 41**		**0.4**
Glov_2094	**_xapA_, Tetratricopeptide-like helical**		**0.36**
Glov_2095	**_pilA_-C**		**0.43**
Glov_2096	**e-pilin**		**0.47**

Glov_2151	***pilX***		**0.45**
Glov_2152	***pilW***		**0.46**
Glov_2153	***pilV***		**0.41**
Glov_2154	***fimT***		**0.41**
Glov_2155	***pilY1***		**0.47**
Glov_2156	PS51257 membrane lipoprotein lipid attachment site		0.49
Glov_2157	thiol:disulfide interchange protein DsbC		0.53
Glov_2158	*pilR*		0.56
Glov_2159	*pilS*		0.57
Glov_2160	*pilD*		0.57
19 genes			
Glov_2179	putative horizontal gene transfer protein	Integrase catalytic region	0.52
Glov_2180	putative horizontal gene transfer protein	IstB domain protein ATP-binding protein	0.51

G. Pilin gene clusters found in the *Geobacter bemidjiensis* genome. Two different gene clusters were identified and each is highlighted in a different color. Only one gene coding for a horizontal gene transfer protein was detected in these gene clusters. Genes from the *xap* operon and additional glycosyl transferase genes were detected in the e-pilin gene cluster. The overall GC content of *G. bemidjiensis* is 60.27%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Three out of 61 (5%) genes had deviant GC values.

Locus ID	Gene	Horizontal transfer gene	GC content
Gbem_1532	*pilD*		0.58
Gbem_1533	*pilS*		0.63
Gbem_1534	*pilR*		0.64
Gbem_1535	Disulphide bond isomerase, DsbC		0.61
Gbem_1536	*pilY1*		0.63
Gbem_1537	*fimU*		0.61
Gbem_1538	*pilV*		0.58
Gbem_1539	*pilW*		0.61
Gbem_1540	*pilX*		0.59

Gbem_1541	*fimU*		0.56
Gbem_1542	*pilV*		0.6
Gbem_1543	*pilW*		0.59
Gbem_1544	*pilX*		0.62
Gbem_1545	putative horizontal transfer gene protein	Lambda repressor-like, DNA-binding domain	0.55
Gbem_1546	*pilM*		0.59
Gbem_1547	*pilN*		0.6
Gbem_1548	*pilO*		0.56
Gbem_1549	*pilP*		0.63
Gbem_1550	*pilQ*		0.62
Gbem_1551	**PS51257 membrane lipoprotein lipid attachment**		**0.49**
Gbem_1552	Ig-family protein		0.61
Gbem_1553	**Disulphide bond isomerase**		**0.51**
Gbem_1554	*aroC*		0.65
Gbem_1555	*aroK*		0.61
Gbem_1556	*aroB*		0.63
Gbem_1557	Tetratricopeptide TPR_2 repeat protein		0.63
Gbem_1558	Roadblock/LC7 domain		0.59
Gbem_1559	*aroQ*		0.61
Gbem_1560	Xaa-Pro aminopeptidase		0.63
Gbem_1561	biotin carboxyl carrier protein		0.59
Gbem_1562	biotin carboxylase		0.61
Gbem_2573	*xapF*, glycosyl transferase family 2		0.58
Gbem_2574	glycosyl transferase family 2		0.58
Gbem_2575	glycosyl transferase group 1		0.55
Gbem_2576	acetyltransferase		0.57
Gbem_2577	DegT/DnrJ/EryC1/StrS aminotransferase		0.59
Gbem_2578	**hypothetical protein**		**0.52**
Gbem_2579	methyltransferase type 12		0.54
Gbem_2580	*xapH*, ABC-type polysaccharide/polyol phosphate transport system, ATPase component		0.58

Gbem_2581	*xapG*, ABC-type polysaccharide/polyol phosphate export permease	0.54
Gbem_2582	glycosyl transferase family 2	0.58
Gbem_2583	glycosyl transferase family 2	0.61
Gbem_2584	*xapE*, UbiA prenyltransferase	0.59
Gbem_2585	*xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase	0.6
Gbem_2586	*xapD*, ABC transporter related protein	0.59
Gbem_2587	Tetratricopeptide-like helical	0.57
Gbem_2588	*xapB*, ABC-2 family transporter protein	0.56
Gbem_2589	*pilA*-C	0.6
Gbem_2590	e-pilin	0.53
Gbem_2591	*pilR*	0.63
Gbem_2592	*pilS*	0.61
Gbem_2593	*pilC*	0.61
Gbem_2594	*pilT*	0.61
Gbem_2595	*pilB*	0.61
Gbem_2596	*aroE*	0.67
Gbem_2597	DUF2723 transferase activity	0.63
Gbem_2598	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD	0.61
Gbem_2599	Flavokinase	0.64
Gbem_2600	*tatC*	0.58
Gbem_2601	RNAse R	0.65
Gbem_2602	Soluble lytic murein transglycosylase	0.63

H. Pilin gene clusters found in the *Geobacter daltonii* genome. Two different gene clusters were identified and each is highlighted in a different color. Nine different genes coding for horizontal gene transfer proteins were detected in these gene clusters. *G. daltonii* does not have an e-pilin gene, rather it has a long type IVa *pilA* gene. No xap or glycosyl transferase genes were detected in the *pilA* gene cluster. The overall GC content of G. daltonii is 53.47%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Eleven out of 67 (16%) of the pilin genes had deviant GC values, including *pilS, pilQ, pilO, pilN*, and *pilM*.

Locus ID	Gene	Horizontal transfer gene	GC content

Geob_3056	biotin carboxylase	0.49
Geob_3057	biotin carboxyl carrier protein	0.49
Geob_3058	Xaa-Pro aminopeptidase	0.49
Geob_3059	*aroQ*	0.47
Geob_3060	Roadblock/LC7 domain	0.51
Geob_3061	Tetratricopeptide domain protein	0.47
Geob_3062	*aroB*	0.48
Geob_3063	*aroC*	0.54
Geob_3064	PS51257 Prokaryotic membrane lipoprotein lipid attachment	0.46
Geob_3065	PS51257 Prokaryotic membrane lipoprotein lipid attachment	0.48
Geob_3066	***pilQ***	**0.44**
Geob_3067	*pilP*	0.47
Geob_3068	***pilO***	**0.4**
Geob_3069	***pilN***	**0.41**
Geob_3070	***pilM***	**0.4**
Geob_3071	**putative horizontal transfer gene protein Lambda repressor-like, DNA-binding domain**	**0.41**
Geob_3072	**hypothetical protein**	**0.39**
Geob_3073	***pilX***	**0.45**
Geob_3074	*pilW*	0.46
Geob_3075	***pilV***	**0.45**
Geob_3076	*fimT*	0.46
Geob_3077	*pilY1*	0.5
Geob_3078	**pilL**	**0.41**
Geob_3079	*pilR*	0.47
Geob_3080	*pilS*	0.49
Geob_3081	*pilD*	0.5
Geob_3361	phenylalanyl-tRNA synthetase, alpha subunit	0.53
Geob_3362	LSU ribosomal protein L20P	0.53
Geob_3363	LSU ribosomal protein L35P	0.48
Geob_3364	bacterial translation initiation factor 3 (bIF-3)	0.49

Geob_3365	threonyl-tRNA synthetase	0.53
Geob_R0048	**tRNA-Val**	**0.66**
Geob_3366	hypothetical protein	0.46
Geob_3367	ABC-type transport system, putative ATPase subunit	0.47
Geob_3368	*xapD*, ABC transporter related	0.52
Geob_3369	*pilA*	0.54
Geob_3370	*pilR*	0.49
Geob_3371	***pilS***	**0.43**
Geob_3372	*pilC*	0.47
Geob_3373	*pilT*	0.51
Geob_3374	*pilB*	0.51
Geob_3375	*aroE*	0.51
Geob_3376	DUF2723	0.51
Geob_3377	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD	0.51
Geob_3378	Flavokinase	0.51
Geob_3379	*tatC*	0.51
Geob_3380	response regulator receiver modulated CheB methylesterase	0.55
Geob_3381	MCP methyltransferase, CheR-type	0.5
Geob_3382	PBS lyase HEAT domain protein repeat-containing protein	0.56
Geob_3383	MCP methyltransferase, CheR-type	0.51
Geob_3384	methyl-accepting chemotaxis sensory transducer	0.57
Geob_3385	CheW protein	0.56
Geob_3386	CheA signal transduction histidine kinase	0.55
Geob_3387	response regulator CheY	0.51
Geob_3388	response regulator receiver protein	0.52
Geob_3389	two component, sigma54 specific, transcriptional regulator, Fis family	0.56
Geob_3390	PAS/PAC sensor signal transduction histidine kinase	0.52
Geob_3391	RNAse R	0.57
Geob_3392	Soluble lytic murein transglycosylase	0.56
16 genes		

Geob_3409	putative horizontal transfer gene protein	CRISPR-associated protein, Cas2 family	0.51
Geob_3410	putative horizontal transfer gene protein	CRISPR-associated protein, Cas1 family	0.57
Geob_3411	putative horizontal transfer gene protein	CRISPR-associated exonuclease, Cas4 family	0.57
Geob_3412	putative horizontal transfer gene protein	Virulence protein RhuM-like	0.54
Geob_3413	putative horizontal transfer gene protein	CRISPR-associated protein, Csd2 family	0.53
Geob_3414	putative horizontal transfer gene protein	CRISPR-associated protein, Csd1 family	0.52
Geob_3415	putative horizontal transfer gene protein	CRISPR-associated protein, Cas5d family	0.52
Geob_3416	putative horizontal transfer gene protein	CRISPR-associated helicase, Cas3 family	0.52

I. Pilin gene clusters found in the Geobacter sp. M21 genome. Two different gene clusters were identified and each is highlighted in a different color. Two different genes coding for horizontal gene transfer proteins were detected in these gene clusters. Numerous xap and glycosyl transferase genes are found in the e-pilin gene cluster. The overall GC content of strain M21 is 60.47%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Two out of 65 (3%) genes had deviant GC values.

Locus ID	Gene	Horizontal transfer gene	GC content
GM21_1602	**putative horizontal gene transfer protein**	**transposase IS116/IS110/IS902**	**0.51**
GM21_1603	PS51257 membrane lipoprotein lipid attachment		0.55
GM21_1604	drug resistance transporter, EmrB/QacA subfamily		0.61
GM21_1605	secretion protein HlyD family protein		0.65
GM21_1606	Outer membrane protein TolC		0.64
17 genes			
GM21_1624	Soluble lytic murein transglycosylase		0.63
GM21_1625	RNAse R		0.64
GM21_1626	*tatC*		0.57
GM21_1627	Flavokinase		0.65
GM21_1628	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD		0.63
GM21_1629	DUF2723		0.63
GM21_1630	*aroE*		0.67
GM21_1631	*pilB*		0.61

GM21_1632	*pilT*	0.62
GM21_1633	*pilC*	0.61
GM21_1634	*pilS*	0.62
GM21_1635	*pilR*	0.63
GM21_1636	e-pilin	0.55
GM21_1637	*pilA*-C	0.58
GM21_1638	*xapB*, ABC-2 family transporter protein	0.56
GM21_1639	Tetratricopeptide-like helical	0.56
GM21_1640	*xapD*, ABC-2 type transport system ATP-binding protein	0.59
GM21_1641	*xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase	0.61
GM21_1642	*xapE*, UbiA prenyltransferase	0.59
GM21_1643	glycosyl transferase family 2	0.6
GM21_1644	glycosyl transferase family 3	0.65
GM21_1645	*xapF*, glycosyl transferase family 2	0.64
GM21_1646	*xapG*, ABC-2 type transporter	0.6
GM21_1647	*xapH*, ABC transporter related	0.56
GM21_1648	Radical SAM superfamily enzyme YgiQ, UPF0313 family	0.58
GM21_1649	glycosyl transferase family 2	0.62
GM21_1650	glycosyl transferase family 2	0.61
GM21_1651	*xapF*, glycosyl transferase family 2	0.61
GM21_1652	Methyltransferase type 11	0.62
GM21_2654	biotin carboxylase	0.61
GM21_2655	biotin carboxyl carrier protein	0.61
GM21_2656	Xaa-Pro aminopeptidase	0.64
GM21_2657	*aroQ*	0.63
GM21_2658	Roadblock/LC7 domain	0.57
GM21_2659	Tetratricopeptide TPR_2 repeat protein	0.63
GM21_2660	*aroB*	0.63
GM21_2661	*aroK*	0.63
GM21_2662	*aroC*	0.66

GM21_2663	PS51257 membrane lipoprotein lipid attachment		0.56
GM21_2664	**PS51257 membrane lipoprotein lipid attachment**		**0.52**
GM21_2665	*pilQ*		0.62
GM21_2666	*pilP*		0.63
GM21_2667	*pilO*		0.57
GM21_2668	*pilN*		0.6
GM21_2669	*pilM*		0.59
GM21_2670	putative horizontal transfer gene protein	Lambda repressor-like, DNA-binding domain	0.54
GM21_2671	*pilX*		0.64
GM21_2672	*pilW*		0.59
GM21_2673	*pilV*		0.57
GM21_2674	*fimT*		0.56
GM21_2675	hypothetical protein		0.56
GM21_2676	prepilin-type N-terminal cleavage/methylation domain		0.57
GM21_2677	*pilV*		0.53
GM21_2678	*fimT*		0.56
GM21_2679	*pilY1*		0.6
GM21_2680	hypothetical protein		0.61
GM21_2681	Disulphide bond isomerase, DsbC		0.61
GM21_2682	*pilR*		0.64
GM21_2683	*pilS*		0.64
GM21_2684	*pilD*		0.59

J. Pilin gene clusters found in the Geobacter sp. M18 genome. Two different gene clusters were identified and each is highlighted in a different color. One gene coding for a horizontal gene transfer protein was detected in these gene clusters. Numerous xap and glycosyl transferase genes were found in the e-pilin gene cluster. The overall GC content of strain M18 is 61.18%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Three out of 65 (5%) of the genes have deviant GC values.

Locus ID	Gene	Horizontal Transfer Gene	GC content

GM18_1367	*pilD*		0.61
GM18_1368	*pilS*		0.61
GM18_1369	*pilR*		0.64
GM18_1370	Disulphide bond isomerase, DsbC		0.6
GM18_1371	*pilY1*		0.62
GM18_1372	*fimU*		0.58
GM18_1373	*pilV*		0.59
GM18_1374	*pilW*		0.63
GM18_1375	*pilX*		0.62
GM18_1376	*fimT*		0.57
GM18_1377	*pilV*		0.59
GM18_1378	prepilin-type N-terminal cleavage/methylation domain		0.63
GM18_1379	hypothetical protein		0.68
GM18_1380	**putative horizontal transfer gene protein**	**Lambda repressor-like, DNA-binding domain**	**0.51**
GM18_1381	*pilM*		0.61
GM18_1382	*pilN*		0.6
GM18_1383	*pilO*		0.59
GM18_1384	*pilP*		0.63
GM18_1385	*pilQ*		0.63
GM18_1386	PS51257 membrane lipoprotein lipid attachment		0.57
GM18_1387	Ig-like family protein		0.61
GM18_1388	**disulfide bond isomerase, DsbC/G-like protein**		**0.53**
GM18_1389	*aroC*		0.67
GM18_1390	*aroK*		0.63
GM18_1391	*aroB*		0.65
GM18_1392	tetratricopeptide repeat-containing protein		0.63
GM18_1393	Roadblock/LC7 domain		0.62
GM18_1394	*aroQ*		0.66
GM18_1395	Xaa-Pro aminopeptidase		0.63

GM18_1396	biotin carboxyl carrier protein	0.6
GM18_1397	biotin carboxylase	0.62
GM18_2471	hypothetical protein	0.54
GM18_2472	**family 2 glycosyl transferase**	**0.5**
GM18_2473	*xapJ*, glycosyl transferase family 9	0.6
GM18_2474	Nucleotide-diphospho-sugar transferases	0.62
GM18_2475	*xapI*, type 11 methyltransferase	0.59
GM18_2476	*xapF*, family 2 glycosyl transferase	0.58
GM18_2477	group 1 glycosyl transferase	0.59
GM18_2478	group 1 glycosyl transferase	0.6
GM18_2479	hypothetical protein	0.55
GM18_2480	Glycosyl transferases group 1	0.58
GM18_2481	*xapH*, ABC transporter-like protein	0.59
GM18_2482	*xapG*, ABC-2 type transporter	0.58
GM18_2483	family 2 glycosyl transferase	0.62
GM18_2484	family 2 glycosyl transferase	0.64
GM18_2485	family 2 glycosyl transferase	0.62
GM18_2486	*xapE*, UbiA prenyltransferase	0.61
GM18_2487	*xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase	0.64
GM18_2488	*xapD*, ABC transporter-like protein	0.61
GM18_2489	Tetratricopeptide-like helical	0.58
GM18_2490	*xapB*, ABC-2 family transporter protein	0.59
GM18_2491	*pilA*-C	0.61
GM18_2492	e-pilin	0.55
GM18_2493	*pilR*	0.63
GM18_2494	*pilS*	0.61
GM18_2495	*pilC*	0.61
GM18_2496	*pilT*	0.63
GM18_2497	*pilB*	0.62
GM18_2498	*aroE*	0.68

GM18_2499	DUF2723	0.62
GM18_2500	Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD	0.61
GM18_2501	Flavokinase	0.65
GM18_2502	*tatC*	0.59
GM18_2503	RNAse R	0.65
GM18_2504	soluble lytic murein transglycosylase	0.64

K. Pilin gene clusters found in the *Geobacter bremensis* genome. Two different gene clusters were identified and each is highlighted in a different color. One gene coding for a horizontal gene transfer protein was detected in these gene clusters. Numerous xap and glycosyl transferase genes were found in the e-pilin gene cluster. The overall GC content of *G. bremensis* is 60.26%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. One out of 56 (2%) of the genes have deviant GC values.

Locus ID	Gene	Horizontal transfer gene	GC content
K419DRAFT_00152	biotin carboxylase		0.61
K419DRAFT_00153	biotin carboxyl carrier protein		0.6
K419DRAFT_00154	Xaa-Pro aminopeptidase		0.64
K419DRAFT_00155	*aroQ*		0.61
K419DRAFT_00156	Roadblock/LC7 domain		0.6
K419DRAFT_00157	Tetratricopeptide repeat-containing domain		0.64
K419DRAFT_00158	*aroB*		0.64
K419DRAFT_00159	*aroK*		0.62
K419DRAFT_00160	*aroC*		0.66
K419DRAFT_00161	PS51257 Prokaryotic membrane lipoprotein lipid attachment		0.53
K419DRAFT_00162	PS51257 Prokaryotic membrane lipoprotein lipid attachment		0.53
K419DRAFT_00163	*pilQ*		0.63
K419DRAFT_00164	*pilP*		0.65
K419DRAFT_00165	*pilO*		0.57
K419DRAFT_00166	*pilN*		0.6
K419DRAFT_00167	*pilM*		0.6
K419DRAFT_00168	putative horizontal transfer gene protein	Lambda repressor-like, DNA-binding domain	0.54

K419DRAFT_00169	hypothetical protein	0.63
K419DRAFT_00170	*pilW*	0.59
K419DRAFT_00171	*pilV*	0.58
K419DRAFT_00172	*fimT*	0.58
K419DRAFT_00173	*pilX*	0.6
K419DRAFT_00174	*pilW*	0.62
K419DRAFT_00175	*pilV*	0.57
K419DRAFT_00176	*fimU*	0.61
K419DRAFT_00177	*pilY1*	0.63
K419DRAFT_00178	Disulphide bond isomerase, DsbC	0.61
K419DRAFT_00179	*pilR*	0.64
K419DRAFT_00180	*pilS*	0.62
K419DRAFT_00181	*pilD*	0.59
K419DRAFT_00788	radical SAM additional 4Fe4S-binding SPASM domain-containing protein	0.62
K419DRAFT_00789	methyltransferase, FkbM family	0.61
K419DRAFT_00790	Methylase involved in ubiquinone/menaquinone biosynthesis	0.63
K419DRAFT_00791	*xapH*, lipopolysaccharide transport system ATP-binding protein	0.61
K419DRAFT_00792	*xapG*, lipopolysaccharide transport system permease protein	0.57
K419DRAFT_00793	Glycosyltransferases involved in cell wall biogenesis	0.57
K419DRAFT_00794	*xapF*, Glycosyltransferase, GT2 family	0.64
K419DRAFT_00795	*xapE*, 4-hydroxybenzoate polyprenyltransferase	0.58
K419DRAFT_00796	*xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase	0.6
K419DRAFT_00797	*xapD*, ABC-2 type transport system ATP-binding protein	0.58
K419DRAFT_00798	hypothetical protein	0.59
K419DRAFT_00799	*xapB*, ABC-2 family transporter protein	0.58
K419DRAFT_00800	*pilA*-C	0.59
K419DRAFT_00801	e-pilin	0.53
K419DRAFT_00802	*pilR*	0.63
K419DRAFT_00803	*pilS*	0.63
K419DRAFT_00804	*pilC*	0.61

K419DRAFT_00805	*pilT*	0.61
K419DRAFT_00806	*pilB*	0.61
K419DRAFT_00807	***aroE***	**0.68**
K419DRAFT_00808	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family	0.63
K419DRAFT_00809	Lysylphosphatidylglycerol synthase TM region	0.61
K419DRAFT_00810	Flavokinase	0.65
K419DRAFT_00811	*tatC*	0.58
K419DRAFT_00812	RNAse R	0.65
K419DRAFT_00813	lytic murein transglycosylase	0.63

L. Pilin gene clusters found in the *Desulfuromonas sp. TF* genome. Only one pilin gene cluster was identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in this gene cluster. Numerous xap and glycosyl transferase genes were found in the e-pilin gene cluster. The overall GC content of strain TF is 58.66%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Nine out of 62 (15%) of the genes have deviant GC values, including *pilP*, *xapG, pilN*, and *pilO*.

Locus ID	Gene	Horizontal transfer gene	GC content
DTFDRAFT_03587	*aroC*		0.61
DTFDRAFT_03588	*pilQ*		0.55
DTFDRAFT_03589	***pilP***		**0.48**
DTFDRAFT_03590	***pilO***		**0.45**
DTFDRAFT_03591	***pilN***		**0.46**
DTFDRAFT_03592	*pilM*		0.54
DTFDRAFT_03593	putative horizontal transfer gene protein	Lambda repressor-like, DNA-binding domain	0.57
DTFDRAFT_03594	*pilD*		0.58
DTFDRAFT_03595	**lipopolysaccharide heptosyltransferase II**		**0.48**
DTFDRAFT_03596	**hypothetical protein**		**0.42**
DTFDRAFT_03597	Glycosyltransferase involved in cell wall bisynthesis		0.53
DTFDRAFT_03598	**Methyltransferase domain-containing protein**		**0.51**
DTFDRAFT_03599	Nucleotide-diphospho-sugar transferases		0.55

DTFDRAFT_03600	Methyltransferase domain-containing protein	0.51
DTFDRAFT_03601	Glycosyltransferase involved in cell wall bisynthesis	0.54
DTFDRAFT_03602	Glycosyltransferase involved in cell wall bisynthesis	0.56
DTFDRAFT_03603	Glycosyl transferase family 11	0.59
DTFDRAFT_03604	Glycosyl transferase family 2	0.59
DTFDRAFT_03605	UDP-Glycosyltransferase/glycogen phosphorylase	0.63
DTFDRAFT_03606	Glycosyltransferase involved in cell wall bisynthesis	0.63
DTFDRAFT_03607	Glycosyl transferase family 2	0.63
DTFDRAFT_03608	Methyltransferase domain-containing protein	0.61
DTFDRAFT_03609	Glycosyltransferase involved in cell wall bisynthesis	0.55
DTFDRAFT_03610	Glycosyltransferase, GT2 family	0.59
DTFDRAFT_03611	Glycosyltransferase involved in cell wall bisynthesis	0.53
DTFDRAFT_03612	UDP-Glycosyltransferase/glycogen phosphorylase	0.58
DTFDRAFT_03613	**HAD-superfamily phosphatase, subfamily IIIC/FkbH-like domain-containing protein**	**0.4**
DTFDRAFT_03614	N-acylneuraminate cytidylyltransferase	0.6
DTFDRAFT_03615	perosamine synthetase	0.59
DTFDRAFT_03616	Sugar phosphate isomerase/epimerase	0.58
DTFDRAFT_03617	Protein N-acetyltransferase, RimJ/RimL family	0.58
DTFDRAFT_03618	N-acetylneuraminate synthase	0.63
DTFDRAFT_03619	*xapH*, lipopolysaccharide transport system ATP-binding protein	0.6
DTFDRAFT_03620	***xapG*, lipopolysaccharide transport system permease protein**	**0.51**
DTFDRAFT_03621	Glycosyltransferase involved in cell wall bisynthesis	0.56
DTFDRAFT_03622	Glycosyl transferase family 2	0.53
DTFDRAFT_03623	*xapF*, Glycosyltransferase, GT2 family	0.54
DTFDRAFT_03624	*xapE*, 4-hydroxybenzoate polyprenyltransferase	0.52
DTFDRAFT_03625	*xapA*, glycosyltransferase protein	0.55
DTFDRAFT_03626	*xapD*, ABC-2 type transport system ATP-binding protein	0.59
DTFDRAFT_03627	hypothetical protein	0.54

DTFDRAFT_03628	*xapB*, ABC-2 family transporter protein		0.55
DTFDRAFT_03629	*pilA*-C		0.58
DTFDRAFT_03630	e-pilin		0.54
DTFDRAFT_03631	*pilR*		0.59
DTFDRAFT_03632	*pilS*		0.55
DTFDRAFT_03633	*pilC*		0.56
DTFDRAFT_03634	*pilT*		0.59
DTFDRAFT_03635	*pilB*		0.58
DTFDRAFT_03636	Flavokinase		0.56
DTFDRAFT_03637	RNAse R		0.59
DTFDRAFT_03638	putative horizontal transfer gene protein	plasmid segregation protein ParM	0.59
DTFDRAFT_03639	Uncharacterized conserved protein, DUF1015 family		0.57
DTFDRAFT_03640	**hypothetical protein**		**0.51**
DTFDRAFT_03641	*fimT*		0.52
DTFDRAFT_03642	PS51257 membrane lipoprotein lipid attachment		0.56
DTFDRAFT_03643	*pilY1*		0.56
DTFDRAFT_03644	*pilX*		0.56
DTFDRAFT_03645	*pilW*		0.57
DTFDRAFT_03646	*pilV*		0.54
DTFDRAFT_03647	*pilR*		0.59
DTFDRAFT_03648	*pilS*		0.55

M. Pilin gene clusters found in the *Pelobacter seleniigenes* genome. Two pilin gene clusters were identified in this genome. Fourteen genes coding for horizontal gene transfer proteins were detected in these clusters. This genome is incomplete, however, genes for xap and glycosyl transferase proteins were found in the e-pilin gene cluster. The overall GC content of P. seleniigenes is 54.19%. Genes with GC content +/- 7% of this value are highlighted in bold blue. Thirty-three out of 55 (60%) genes in these clusters have deviant GC values, including *e-pilin, pilA-C, pilR, pilS, pilD, pilN, pilO,xapD, xapB, pilP*, and *pilQ*.

Locus ID	Gene	Horizontal transfer gene	GC content
N909DRAFT_0002	***xapB*, ABC-2 family transporter protein**		**0.31**

N909DRAFT_0003	***xapD*, ABC-2 type transport system ATP-binding protein**		**0.39**
N909DRAFT_0004	**O-antigen ligase like membrane protein**		**0.33**
N909DRAFT_0005	***pilA*-C**		**0.43**
N909DRAFT_0006	**e-pilin**		**0.38**
N909DRAFT_0007	***pilR***		**0.44**
N909DRAFT_0008	***pilS***		**0.44**
N909DRAFT_0009	*pilC*		0.47
N909DRAFT_0010	*pilT*		0.5
N909DRAFT_0011	*pilB*		0.49
N909DRAFT_0012	***aroE***		**0.46**
N909DRAFT_0013	Flavokinase		0.48
N909DRAFT_0014	*pilY1*		0.49
N909DRAFT_0015	**hypothetical protein**		**0.46**
N909DRAFT_0016	*pilX*		0.48
N909DRAFT_0017	*pilV*		0.48
N909DRAFT_0018	*pilW*		0.48
N909DRAFT_0019	*fimT*		0.47
N909DRAFT_4146	***pilD***		**0.45**
N909DRAFT_4147	putative horizontal gene transfer protein	Lambda repressor-like, DNA-binding domain	0.47
N909DRAFT_4148	*pilM*		0.47
N909DRAFT_4149	***pilN***		**0.42**
N909DRAFT_4150	***pilO***		**0.43**
N909DRAFT_4151	***pilP***		**0.44**
N909DRAFT_4152	***pilQ***		**0.46**
N909DRAFT_4153	***aroB***		**0.46**
N909DRAFT_4154	**Flp pilus assembly protein TadD, contains TPR repeats**		**0.46**
N909DRAFT_4155	**Roadblock/LC7 domain**		**0.43**
N909DRAFT_4156	**Xaa-Pro aminopeptidase**		**0.46**
N909DRAFT_4157	**biotin carboxyl carrier protein**		**0.45**

N909DRAFT_4158	Biotin carboxylase		0.49
N909DRAFT_4159	chorismate dehydratase		0.48
N909DRAFT_4160	**PS51257 membrane lipoprotein lipid attachment**		**0.46**
N909DRAFT_4161	tRNA_Leu_TAA		0.6
N909DRAFT_4162	**hypothetical protein**		**0.36**
N909DRAFT_4163	**putative horizontal gene transfer protein**	**RepA plasmid replication protein**	**0.45**
N909DRAFT_4164	**putative horizontal gene transfer protein**	**mobilisation protein (MobC)**	**0.44**
N909DRAFT_4165	putative horizontal gene transfer protein	Relaxase/Mobilisation nuclease domain-containing protein	0.49
N909DRAFT_4166	**hypothetical protein**		**0.46**
N909DRAFT_4167	**hypothetical protein**		**0.46**
N909DRAFT_4168	**putative horizontal gene transfer protein**	**P-type conjugative transfer protein TrbJ**	**0.43**
N909DRAFT_4169	putative horizontal gene transfer protein	P-type conjugative transfer protein TrbL	0.47
N909DRAFT_4170	putative horizontal gene transfer protein	RNA(fMet)-specific endonuclease VapC	0.47
N909DRAFT_4171	**putative horizontal gene transfer protein**	**antitoxin VapB**	**0.44**
N909DRAFT_4172	hypothetical protein		0.56
N909DRAFT_4173	**hypothetical protein**		**0.3**
N909DRAFT_4174	**putative horizontal gene transfer protein**	**HTH-type transcriptional regulator / antitoxin HigA**	**0.44**
N909DRAFT_4175	**Predicted nucleic-acid-binding protein, contains PIN domain**		**0.45**
N909DRAFT_4176	putative horizontal gene transfer protein	Antidote-toxin recognition MazE	0.5
N909DRAFT_4177	putative horizontal gene transfer protein	KfrA_N replication region DNA-binding N-term	0.52
N909DRAFT_4178	putative horizontal gene transfer protein	putative transposase	0.53
N909DRAFT_4179	**hypothetical protein**		**0.35**
N909DRAFT_4180	**hypothetical protein**		**0.37**
N909DRAFT_4181	**putative horizontal gene transfer protein**	**HNH endonuclease**	**0.44**
N909DRAFT_4182	putative horizontal gene transfer protein	Site-specific recombinase XerC	0.48

N. Pilin gene clusters found in the *Geobacter argillaceus* genome. Two pilin gene clusters were identified in this genome. One gene coding for a horizontal gene transfer protein was detected in these clusters. Numerous genes for xap and glycosyl transferase proteins were detected in the e-pilin gene cluster. The overall GC content of *G. argillaceus* is 58.2%. Genes that had

GC contents +/- 7% of this value are highlighted in bold blue. Seven out of 51 genes (14%) in these clusters have deviant GC values, including *pilM, pilN, xapB, pilO*, and *pilP*.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0052872_00748	*aroQ*		0.56
Ga0052872_00749	Roadblock/LC7 domain		0.53
Ga0052872_00750	Tetratricopeptide repeat-containing protein		0.57
Ga0052872_00751	*aroB*		0.61
Ga0052872_00752	*aroC*		0.61
Ga0052872_00753	**hypothetical protein**		**0.43**
Ga0052872_00754	*pilQ*		0.55
Ga0052872_00755	***pilP***		**0.49**
Ga0052872_00756	***pilO***		**0.49**
Ga0052872_00757	***pilN***		**0.47**
Ga0052872_00758	***pilM***		**0.47**
Ga0052872_00759	**putative horizontal gene transfer**	**Lambda repressor-like, DNA-binding domain**	**0.48**
Ga0052872_00761	*pilW*		0.54
Ga0052872_00762	*pilV*		0.52
Ga0052872_00763	*fimU*		0.54
Ga0052872_00764	*pilY1*		0.56
Ga0052872_00765	*pilR*		0.57
Ga0052872_00766	*pilS*		0.61
Ga0052872_00767	*pilD*		0.59
Ga0052872_01782	Glycosyltransferase involved in cell wall bisynthesis	ccc	0.61
Ga0052872_01783	Nucleotide-diphospho-sugar transferases		0.56
Ga0052872_01784	Glycosyltransferase involved in cell wall bisynthesis		0.6
Ga0052872_01785	Methyltransferase domain-containing protein		0.58
Ga0052872_01786	Glycosyltransferase involved in cell wall bisynthesis		0.57
Ga0052872_01787	*xapF*, Glycosyltransferase involved in cell wall bisynthesis		0.57

Ga0052872_01788	Nucleotide-diphospho-sugar transferases	0.57
Ga0052872_01789	S-adenosyl-L-methionine-dependent methyltransferases	0.6
Ga0052872_01790	*xapH*, lipopolysaccharide transport system ATP-binding protein	0.59
Ga0052872_01791	*xapG*, lipopolysaccharide transport system permease protein	0.57
Ga0052872_01792	Glycosyltransferase involved in cell wall bisynthesis	0.57
Ga0052872_01793	Glycosyltransferase, GT2 family	0.56
Ga0052872_01794	*xapE*, 4-hydroxybenzoate polyprenyltransferase	0.56
Ga0052872_01795	*xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase	0.58
Ga0052872_01796	*xapD*, ABC-2 type transport system ATP-binding protein	0.57
Ga0052872_01797	Pili subunit family protein	0.54
Ga0052872_01798	***xapB*, ABC-2 family transporter protein**	**0.44**
Ga0052872_01799	*pilA*-C	0.55
Ga0052872_01800	e-pilin	0.56
Ga0052872_01801	*pilA*-C	0.57
Ga0052872_01802	e-pilin	0.56
Ga0052872_02385	*pilR*	0.61
Ga0052872_02386	*pilS*	0.59
Ga0052872_02387	*pilC*	0.57
Ga0052872_02388	*pilT*	0.61
Ga0052872_02389	*pilB*	0.58
Ga0052872_02390	DUF2723	0.58
Ga0052872_02391	Lysylphosphatidylglycerol synthase TM region	0.6
Ga0052872_02392	Flavokinase	0.61
Ga0052872_02393	*tatC*	0.56
Ga0052872_02394	RNAse R	0.66
Ga0052872_02395	soluble lytic murein transglycosylase	0.61

O. Pilin gene clusters found in the *Desulfuromusa kysingii* genome. Two pilin gene clusters were identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in these clusters. This genome is incomplete and the e-pilin gene was located near the end of a contig, however, xap genes and glycosyltransferase genes were detected in the e-pilin gene cluster. The overall GC content of *D. kysingii* is 46.43%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Six out of 50 genes (12%) in these clusters had GC content that was > 7% from the overall average, but only one pilin gene (*pilA-C*) had a deviant GC value.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0056096_02700	e-pilin		0.42
Ga0056096_02701	***pilA-C***		**0.38**
Ga0056096_02702	*xapD*, ABC-2 type transport system ATP-binding protein		0.46
Ga0056096_02703	*xapB*, ABC-type transport system, permease component		0.42
Ga0056096_02704	hypothetical protein		0.44
Ga0056096_02705	*xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase		0.44
Ga0056096_02706	*xapE*, 4-hydroxybenzoate polyprenyltransferase		0.44
Ga0056096_02707	ABC transporter		0.49
Ga0056096_02708	hypothetical protein		0.46
Ga0056096_02709	hypothetical protein		0.39
Ga0056096_02710	**putative horizontal gene transfer protein**	**putative addiction module component, TIGR02574 family**	**0.38**
Ga0056096_02711	**CDP-alcohol phosphatidyltransferase**		**0.35**
Ga0056096_02712	phosphoenolpyruvate mutase		0.41
Ga0056096_02713	phosphonopyruvate decarboxylase		0.39
Ga0056096_02714	**phosphonate metabolism-associated iron-containing alcohol dehydrogenase**		**0.36**
Ga0056096_02715	CDP-alcohol phosphatidyltransferase		0.42
Ga0056096_02716	**hypothetical protein**		**0.35**
Ga0056096_02717	*xapJ*, lipopolysaccharide heptosyltransferase II		0.46
Ga0056096_02718	phosphoheptose isomerase		0.44
Ga0056096_02719	D-alpha,beta-D-heptose 7-phosphate 1-kinase		0.47
Ga0056096_02720	D-alpha,beta-D-heptose 1,7-bisphosphate phosphatase		0.42
Ga0056096_02721	*pilD*		0.45
Ga0056096_02722	putative horizontal gene transfer	Lambda repressor-like, DNA-binding domain	0.46
Ga0056096_02723	*pilM*		0.44
Ga0056096_02724	*pilN*		0.41
Ga0056096_02725	*pilO*		0.41

Ga0056096_02726	*pilP*	0.44
Ga0056096_02727	*pilQ*	0.42
Ga0056096_02728	*aroB*	0.4
Ga0056096_02729	Tetratricopeptide repeat-containing protein	0.45
Ga0056096_02730	Roadblock/LC7 domain	0.41
Ga0056096_02731	*aroQ*	0.46
Ga0056096_02732	Xaa-Pro aminopeptidase	0.44
Ga0056096_02733	biotin carboxyl carrier protein	0.43
Ga0056096_02734	biotin carboxylase	0.44
Ga0056096_03266	*pilR*	0.43
Ga0056096_03267	*pilS*	0.45
Ga0056096_03268	*pilC*	0.44
Ga0056096_03269	*pilT*	0.45
Ga0056096_03270	*pilB*	0.45
Ga0056096_03271	*aroE*	0.47
Ga0056096_03272	Flavokinase	0.48
Ga0056096_03273	*fimT*	0.44
Ga0056096_03274	pilE	0.47
Ga0056096_03275	*pilY1*	0.46
Ga0056096_03276	**hypothetical**	**0.35**
Ga0056096_03277	*pilX*	0.46
Ga0056096_03278	*pilW*	0.47
Ga0056096_03279	*pilV*	0.47
Ga0056096_03280	*fimT*	0.46

P. Pilin gene clusters found in the *Desulfuromonas thiophila* genome. Three pilin gene clusters were identified in this genome. One gene coding for a horizontal gene transfer protein was detected in these clusters. Genes coding for *xap* and glycosyltransferase proteins were detected in the e-pilin gene cluster. The overall GC content of *D. thiophila* is 60.71%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Twenty out of 59 genes (34%) in these clusters had GC content that was > 7% from the overall average, including *pilQ, pilO, pilN, pilM, pilC, pilR, xapF, xapD, xapA, e-pilin*, and *pilA-C*.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0056074_101100	*pihD*, minor pilin protein		0.64
Ga0056074_101103	*pihP*, minor pilin protein		0.58
Ga0056074_101105	pihQ, minor pilin protein		0.67
Ga0056074_101107	*pilO*, minor pilin protein		0.64
Ga0056074_101115	pihA, minor pilin protein		0.61
Ga0056074_101116	pihH, minor pilin protein		0.6
Ga0056074_104180	biotin carboxylase		0.54
Ga0056074_104181	**biotin carboxyl carrier protein**		**0.52**
Ga0056074_104182	Xaa-Pro aminopeptidase		0.59
Ga0056074_104183	*aroQ*		0.55
Ga0056074_104184	Roadblock/LC7 domain		0.55
Ga0056074_104185	Tetratricopeptide repeat-containing protein		0.58
Ga0056074_104186	*aroB*		0.55
Ga0056074_104187	*aroK*		0.54
Ga0056074_104188	***pilQ***		**0.52**
Ga0056074_104189	*pilP*		0.58
Ga0056074_104190	***pilO***		**0.49**
Ga0056074_104191	***pilN***		**0.49**
Ga0056074_104192	***pilM***		**0.52**
Ga0056074_104193	*pilD*		0.55
Ga0056074_104194	Peroxiredoxin		0.57
Ga0056074_104195	[LSU ribosomal protein L11P]-lysine N-methyltransferase		0.55
Ga0056074_104196	*pilR*		0.58
Ga0056074_104197	*pilS*		0.57
Ga0056074_104198	***pilC***		**0.53**
Ga0056074_104199	*pilT*		0.55
Ga0056074_104200	*pilB*		0.56

Ga0056074_104201	*aroE*		0.63
Ga0056074_104202	Flavokinase		0.61
Ga0056074_104203	RNAse R		0.62
Ga0056074_104204	DUF1015 family		0.62
Ga0056074_104219	putative horizontal gene transfer protein	Integrase core domain-containing protein	0.54
Ga0056074_11717	*pilS*		0.68
Ga0056074_11718	***pilR***		**0.7**
Ga0056074_11719	diguanylate cyclase (GGDEF) domain-containing protein		0.66
Ga0056074_11720	**4'-phosphopantetheinyl transferase**		**0.7**
Ga0056074_11721	*fimT*		0.54
Ga0056074_11722	*pilW*		0.57
Ga0056074_11723	***pilV***		**0.52**
Ga0056074_11724	***pilX***		**0.51**
Ga0056074_11725	*pilY1*		0.54
Ga0056074_1236	*xapE*, 4-hydroxybenzoate polyprenyltransferase		0.61
Ga0056074_1237	***xapA*, glycosyltransferase**		**0.44**
Ga0056074_1238	***xapD*, ABC-2 type transport system ATP-binding protein**		**0.53**
Ga0056074_1239	Pili subunit family protein		0.55
Ga0056074_12310	*xapB*, ABC-2 family transporter protein		0.54
Ga0056074_12311	***pilA*-C**		**0.43**
Ga0056074_12312	**e-pilin**		**0.49**
Ga0056074_12313	PD-(D/E)XK nuclease superfamily protein		0.58
Ga0056074_12314	Putative *xapG*, ABC-type multidrug transport system, ATPase and permease component		0.64
Ga0056074_12315	glucose-1-phosphate thymidylyltransferase		0.6
Ga0056074_12316	lipopolysaccharide heptosyltransferase II		0.63
Ga0056074_12317	CDP-alcohol phosphatidyltransferase		0.54
Ga0056074_12318	**2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase**		**0.49**
Ga0056074_12319	**CDP-alcohol phosphatidyltransferase**		**0.46**
Ga0056074_12320	***xapF*, Glycosyltransferase, GT2 family**		**0.44**
Ga0056074_12321	**Glycosyltransferase involved in cell wall biosynthesis**		**0.42**

Ga0056074_12322	**Glycosyltransferase involved in cell wall bisynthesis**		**0.4**
Ga0056074_12323	**S-adenosyl-L-methionine-dependent methyltransferases**		**0.35**

Q. Pilin gene clusters found in the *Geobacter pickeringii* genome. Two pilin gene clusters were identified in this genome. Seven genes coding for horizontal gene transfer proteins were detected in these clusters. Genes coding for *xap* and glycosyltransferase proteins were detected in the e-pilin gene cluster. The overall GC content of *G. pickeringii* is 62.27%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Sixteen out of 56 genes (13%) in these clusters had GC content that was > 7% from the overall average, including *pilO, pilN, pilM, e-pilin*, *xapA, xapB, xapD, xapE*, and *pilA-C*.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0069007_111117	*pilD*		0.63
Ga0069007_111118	*pilS*		0.67
Ga0069007_111119	*pilR*		0.63
Ga0069007_111120	*fimT*		0.56
Ga0069007_111121	*pilV*		0.58
Ga0069007_111122	*pilW*		0.57
Ga0069007_111123	*pilX*		0.59
Ga0069007_111124	*pilY1*		0.6
Ga0069007_111125	PS51257		0.58
Ga0069007_111126	***fimT***		**0.43**
Ga0069007_111127	GEMM cis-regulatory element		0.6
Ga0069007_111128	**putative horizontal gene transfer protein**	**Lambda repressor-like, DNA-binding domain**	**0.48**
Ga0069007_111129	***pilM***		**0.5**
Ga0069007_111130	***pilN***		**0.52**
Ga0069007_111131	***pilO***		**0.5**
Ga0069007_111132	***pilP***		**0.54**
Ga0069007_111133	*pilQ*		0.57
Ga0069007_111134	*aroC*		0.6
Ga0069007_111135	*aroK*		0.6
Ga0069007_111136	*aroB*		0.63
Ga0069007_111137	TPR-like		0.6

Ga0069007_111138	Roadblock/LC7 domain		0.58
Ga0069007_111139	*aroQ*		0.57
Ga0069007_111140	Peptidase_M24		0.59
Ga0069007_111142	biotin carboxylase		0.59
Ga0069007_111141	biotin carboxyl carrier protein		0.6
Ga0069007_111751	**UDP-galactopyranose mutase**		**0.54**
Ga0069007_111752	Glycosyltransferase involved in cell wall bisynthesis		0.56
Ga0069007_111753	**Glycosyltransferase involved in cell wall bisynthesis**		**0.51**
Ga0069007_111754	Glycosyltransferase involved in cell wall bisynthesis		0.55
Ga0069007_111755	***xapF*, Glycosyl transferase family 2**		**0.54**
Ga0069007_111756	***xapE*, 4-hydroxybenzoate polyprenyltransferase**		**0.46**
Ga0069007_111757	***xapD*, ABC-2 type transport system ATP-binding protein**		**0.47**
Ga0069007_111758	**hypothetical protein**		**0.45**
Ga0069007_111759	***xapB*, ABC-2 family transporter protein**		**0.44**
Ga0069007_111760	***xapA*, Tetratricopeptide repeat-containing domain**		**0.43**
Ga0069007_111761	***pilA*-C**		**0.52**
Ga0069007_111762	**e-pilin**		**0.48**
Ga0069007_111763	*pilR*		0.57
Ga0069007_111764	*pilS*		0.55
Ga0069007_111765	*pilC*		0.55
Ga0069007_111766	*pilT*		0.58
Ga0069007_111767	*pilB*		0.57
Ga0069007_111768	*aroE*		0.62
Ga0069007_111769	DUF2723		0.59
Ga0069007_111771	UPF0104 family		0.62
Ga0069007_111772	Flavokinase		0.61
Ga0069007_111773	*tatC*		0.58
Ga0069007_111774	RNAse R		0.61
Ga0069007_111775	lytic transglycosylase		0.61
Ga0069007_111798	putative horizontal gene transfer protein	phage integrase	0.6

Ga0069007_111799	putative horizontal gene transfer protein	phage related Site-specific DNA recombinase	0.57
Ga0069007_111802	putative horizontal gene transfer protein	phage related transcriptional regulator, AlpA family	0.58
Ga0069007_111804	putative horizontal gene transfer protein	phage/plasmid primase	0.61
Ga0069007_111806	putative horizontal gene transfer protein	putative transposase	0.6
Ga0069007_111807	putative horizontal gene transfer protein	transposase	0.58

R. Pilin gene clusters found in the *Geoalkalibacter ferrihydriticus* genome. One pilin gene cluster was identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in these clusters. Genes from the *xap* operon and proteins involved in LPS biosynthesis were detected in the e-pilin gene cluster. The overall GC content of *G. ferrihydriticus* is 57.87%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Zero out of 40 genes (0%) in these clusters had GC content that was > 7% from the overall average.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0056053_00633	*pilS*		0.6
Ga0056053_00634	*pilR*		0.62
Ga0056053_00635	*pilV*		0.56
Ga0056053_00636	*pilW*		0.6
Ga0056053_00642	*pilV*		0.6
Ga0056053_00643	*pilW*		0.58
Ga0056053_00644	*pilX*		0.6
Ga0056053_00645	*pilY1*		0.58
Ga0056053_00646	hypothetical protein		0.65
Ga0056053_00647	DUF1015		0.56
Ga0056053_00648	putative horizontal transfer gene protein	plasmid segregation protein ParM	0.58
Ga0056053_00649	RNAse R		0.6
Ga0056053_00650	Flavokinase		0.59
Ga0056053_00651	*aroE*		0.61
Ga0056053_00652	*pilB*		0.57
Ga0056053_00653	*pilT*		0.58
Ga0056053_00654	*pilC*		0.6
Ga0056053_00655	*pilS*		0.58

Ga0056053_00656	*pilR*		0.58
Ga0056053_00657	e-pilin		0.53
Ga0056053_00658	*pilA*-C		0.51
Ga0056053_00659	0-antigen ligase		0.55
Ga0056053_00660	*xapD*, ABC-2 type transport system ATP-binding protein		0.6
Ga0056053_00661	*xapB*, ABC-2 family transporter protein		0.57
Ga0056053_00662	Type II secretion system (T2SS), protein G		0.61
Ga0056053_00663	putative horizontal gene transfer protein	REP element-mobilizing transposase RayT	0.51
Ga0056053_00664	*pilD*		0.58
Ga0056053_00665	*pilM*		0.53
Ga0056053_00666	*pilN*		0.55
Ga0056053_00667	*pilO*		0.54
Ga0056053_00668	*pilP*		0.58
Ga0056053_00669	*pilQ*		0.6
Ga0056053_00670	*aroK*		0.59
Ga0056053_00671	*aroB*		0.59
Ga0056053_00672	TPR-like		0.6
Ga0056053_00673	Roadblock/LC7 domain		0.57
Ga0056053_00674	*aroQ*		0.58
Ga0056053_00675	Peptidase_M24		0.59
Ga0056053_00676	biotin carboxyl carrier protein		0.54
Ga0056053_00677	biotin carboxylase		0.57

S. Pilin gene clusters found in the *Geopsychrobacter electrodiphilus* genome. Two pilin gene clusters were identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in these clusters. Genes coding for xap and glycosyltransferase proteins were detected in the e-pilin gene cluster. The overall GC content of *G. electrodiphilus* is 53.2%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty-four out of 62 genes (39%) in these clusters had GC content that was > 7% from the overall average, including *pilA-C, pilF, pilN, pilO, pilP, xapA, xapB, xapD*, and *xapF*.

Locus ID	Gene	Horizontal transfer gene	GC content
D888DRAFT_0269	*pilV*		0.56
D888DRAFT_0270	*pilW*		0.53
D888DRAFT_0271	*pilX*		0.58
D888DRAFT_0272	*pilY1*		0.58
D888DRAFT_0273	type II secretion system protein H		0.58
D888DRAFT_0274	HAMP domain-containing protein		0.51
D888DRAFT_0275	*fimT*		0.56
D888DRAFT_0276	*pilV*		0.54
D888DRAFT_0277	*pilW*		0.52
D888DRAFT_0278	*pilX*		0.56
D888DRAFT_0279	*pilY1*		0.53
D888DRAFT_0280	pilE		0.47
D888DRAFT_1999	**polysaccharide chain length determinant protein**		**0.45**
D888DRAFT_2000	polysaccharide export outer membrane protein		0.47
D888DRAFT_2001	sugar transferase		0.46
D888DRAFT_2002	Tetratricopeptide repeat-containing domain, FimV		0.48
D888DRAFT_2003	*pilZ*		0.48
D888DRAFT_2004	**LuxR family transcriptional regulator**		**0.43**
D888DRAFT_2005	**CAAX prenyl protease-related protein**		**0.45**
D888DRAFT_2006	**PEP-CTERM protein-sorting domain**		**0.4**
D888DRAFT_2007	horizontal gene transfer	transposase, IS4 family	0.55
D888DRAFT_2008	**PEP-CTERM protein-sorting domain**		**0.41**
D888DRAFT_2009	tRNA_Leu_TAA		0.6
D888DRAFT_2010	chorismate dehydratase		0.47
D888DRAFT_2011	biotin carboxylase		0.49
D888DRAFT_2012	**biotin carboxyl carrier protein**		**0.44**
D888DRAFT_2013	Xaa-Pro aminopeptidase		0.47
D888DRAFT_2014	***aroQ***		**0.44**

D888DRAFT_2015	**Roadblock/LC7 domain**	**0.42**
D888DRAFT_2016	**pilF**	**0.45**
D888DRAFT_2017	***aroB***	**0.43**
D888DRAFT_2018	*pilQ*	0.47
D888DRAFT_2019	***pilP***	**0.43**
D888DRAFT_2020	***pilO***	**0.45**
D888DRAFT_2021	***pilN***	**0.41**
D888DRAFT_2022	*pilM*	0.46
D888DRAFT_2023	Predicted transcriptional regulator with C-terminal CBS domains	0.49
D888DRAFT_2024	*pilD*	0.48
D888DRAFT_2025	lipopolysaccharide heptosyltransferase II	0.5
D888DRAFT_2026	**Glycosyltransferases, probably involved in cell wall biogenesis**	**0.36**
D888DRAFT_2027	putative horizontal gene transfer protein transposase, IS4 family	0.48
D888DRAFT_2028	**polysaccharide transporter, PST family**	**0.44**
D888DRAFT_2029	dTDP-4-amino-4,6-dideoxygalactose transaminase	0.52
D888DRAFT_2030	**Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase**	**0.37**
D888DRAFT_2031	**Glycosyltransferase, GT2 family**	**0.39**
D888DRAFT_2032	**rhamnosyltransferase**	**0.39**
D888DRAFT_2033	**Glycosyltransferase, GT2 family**	**0.38**
D888DRAFT_2034	*xapF*, Glycosyltransferase, GT2 family	0.49
D888DRAFT_2035	*xapE*, 4-hydroxybenzoate polyprenyltransferase	0.49
D888DRAFT_2036	**Dolichyl-phosphate-mannose-protein mannosyltransferase**	**0.4**
D888DRAFT_2037	*xapD*, ABC-2 type transport system ATP-binding protein	0.46
D888DRAFT_2038	**pili subunit superfamily**	**0.42**
D888DRAFT_2039	***xapB*, ABC-2 family transporter protein**	**0.42**
D888DRAFT_2040	***xapA*, TPR-like**	**0.45**
D888DRAFT_2041	***pilA*-C**	**0.43**
D888DRAFT_2042	e-pilin	0.46
D888DRAFT_2043	*pilR*	0.54
D888DRAFT_2044	*pilS*	0.52

D888DRAFT_2045	*pilC*	0.51
D888DRAFT_2046	*pilT*	0.49
D888DRAFT_2047	*pilB*	0.5
D888DRAFT_2048	*aroE*	0.53

T. Pilin gene clusters found in the *Desulfuromonas soudanensis* genome. One pilin gene cluster was identified in this genome. Two genes coding for horizontal gene transfer proteins were present in this cluster. A short e-pilin gene is not present in this Desulfuromondales species but a long type IVa *pilA* gene was detected. Only a couple of putative xap operon genes (*xapB* and *xapD*) were detected in the *pilA* gene cluster. The overall GC content of *D. soudanensis* is 61.19%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Seven out of 49 genes (14%) in these clusters have GC content that is > 7% from the overall average, including *pilC, pilM, pilN, pilO*, and *pilP*.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0069009_112132	GEMM cis-regulatory		0.55
Ga0069009_112133	tRNA_Leu_TAA		0.62
Ga0069009_112134	chorismate dehydratase		0.63
Ga0069009_112135	Outer membrane protein TolC		0.65
Ga0069009_112136	hypothetical protein		0.59
Ga0069009_112137	Lipoate--protein ligase		0.67
Ga0069009_112138	biotin carboxylase		0.62
Ga0069009_112139	biotin carboxyl carrier protein		0.58
Ga0069009_112140	Xaa-Pro aminopeptidase		0.65
Ga0069009_112141	*aroQ*		0.63
Ga0069009_112142	Roadblock/LC7/MglB family		0.56
Ga0069009_112143	Tetratricopeptide repeat-containing protein		0.64
Ga0069009_112144	*aroB*		0.63
Ga0069009_112145	*aroK*		0.64
Ga0069009_112146	*aroC*		0.65
Ga0069009_112147	*pilQ*		0.57
Ga0069009_112148	***pilP***		**0.53**
Ga0069009_112149	***pilO***		**0.49**

Ga0069009_112150	***pilN***		**0.47**
Ga0069009_112151	***pilM***		**0.46**
Ga0069009_112152	**putative horizontal transfer gene protein**	**Lambda repressor-like, DNA-binding domain**	**0.53**
Ga0069009_112153	*pilD*		0.6
Ga0069009_112154	pili subunit family protein		0.55
Ga0069009_112155	*xapB*, ABC-2 family transporter protein		0.56
Ga0069009_112156	*xapD*, ABC-2 type transport system ATP-binding protein		0.6
Ga0069009_112157	*pilA*		0.59
Ga0069009_112158	*pilR*		0.59
Ga0069009_112159	*pilS*		0.6
Ga0069009_112160	***pilC***		**0.53**
Ga0069009_112161	*pilT*		0.61
Ga0069009_112162	*pilB*		0.6
Ga0069009_112163	*aroE*		0.64
Ga0069009_112164	flavokinase		0.61
Ga0069009_112165	RNAse R		0.63
Ga0069009_112166	*pilY1*		0.54
Ga0069009_112167	*pilX*		0.56
Ga0069009_112168	*pilW*		0.56
Ga0069009_112169	*fimT*		0.56
Ga0069009_112170	*pilR*		0.65
Ga0069009_112171	*pilS*		0.62
Ga0069009_112172	ferredoxin		0.64
Ga0069009_112173	Predicted arabinose efflux permease, MFS family		0.66
Ga0069009_112174	PS51257 Prokaryotic membrane lipoprotein lipid attachment		0.62
Ga0069009_112175	heavy metal efflux pump, CzcA family		0.62
Ga0069009_112176	membrane fusion protein, multidrug efflux system		0.66
Ga0069009_112177	transcriptional regulator, TetR family		0.65
Ga0069009_112178	uncharacterized protein		0.66
Ga0069009_112179	**putative horizontal transfer gene protein**	**IS4 transposase**	**0.53**

Ga0069009_112180	Undecaprenyl-diphosphate phosphatase		0.65

U. Pilin gene clusters found in the *Desulfuromonas subbituminosa* genome. One pilin gene cluster was identified in this genome. No genes coding for horizontal gene transfer proteins were present in this cluster. A short e-pilin gene is not present in this Desulfuromondales species but a long type IVa *pilA* gene was detected. Only a couple of putative xap operon genes (*xapB* and *xapD*) were detected in the *pilA* gene cluster. The overall GC content of *D. subbituminosa* is 60.27%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Three out of 40 genes (8%) in these clusters have GC content that is > 7% from the overall average, including *pilW*.

Locus ID	Gene	Horizontal transfer gene	GC content
Ga0064601_106184	*pilS*		0.66
Ga0064601_106185	*pilR*		0.63
Ga0064601_106186	*fimT*		0.63
Ga0064601_106187	*fimT*		0.56
Ga0064601_106188	*pilV*		0.6
Ga0064601_106189	***pilW***		**0.52**
Ga0064601_106190	*pilX*		0.53
Ga0064601_106191	**hypothetical protein**		**0.34**
Ga0064601_106192	*pilY1*		0.55
Ga0064601_106193	pilE		0.6
Ga0064601_106194	Uncharacterized conserved protein, DUF1015 family		0.55
Ga0064601_106195	RNAse R		0.62
Ga0064601_106196	flavokinase		0.58
Ga0064601_106197	*aroE*		0.64
Ga0064601_106198	*pilB*		0.59
Ga0064601_106199	*pilT*		0.62
Ga0064601_106200	*pilC*		0.59
Ga0064601_106201	*pilS*		0.62
Ga0064601_106202	*pilR*		0.62
Ga0064601_106203	*xapD*, ABC-2 type transport system ATP-binding protein		0.57
Ga0064601_106204	*xapB*, ABC-type transport system, permease component		0.6

Ga0064601_106205	pili subunit family	0.59
Ga0064601_106206	*pilD*	0.61
Ga0064601_106207	*pilM*	0.57
Ga0064601_106208	*pilN*	0.58
Ga0064601_106209	*pilO*	0.56
Ga0064601_106210	*pilP*	0.58
Ga0064601_106211	*pilQ*	0.61
Ga0064601_106212	*aroC*	0.64
Ga0064601_106213	*aroB*	0.6
Ga0064601_106214	Tetratricopeptide repeat-containing protein	0.63
Ga0064601_106215	Roadblock/LC7	0.59
Ga0064601_106216	*aroQ*	0.59
Ga0064601_106217	Xaa-Pro aminopeptidase	0.63
Ga0064601_106218	biotin carboxyl carrier protein	0.6
Ga0064601_106219	biotin carboxylase	0.6
Ga0064601_106220	Outer membrane protein TolC	0.65
Ga0064601_106221	Chorismate dehydratase	0.61
Ga0064601_106222	**tRNA_Leu_TAA**	**0.71**
Ga0064601_106223	hypothetical protein	0.58

V. Pilin gene clusters found in the *Desulfobacterium autotrophicum* genome. Six pilin gene clusters were identified in this genome. Twenty-three genes coding for horizontal gene transfer proteins were present in this cluster. Several *xap* operon genes (*xapA, xapB*, and *xapD*) and O-antigen ligase, which is involved in LPS biosynthesis, are present in the e-pilin gene cluster. The overall GC content of *D. autotrophicum* is 48.76%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Eleven out of 158 (7%) genes in these clusters have GC content that is > 7% from the overall average, none of which included pilin genes.

Locus ID	Gene	Horizontal transfer gene	GC content
HRM2_04990	*pilT*		0.53
HRM2_05000	*pilT*		0.51
HRM2_05010	CheY-like superfamily		0.49

HRM2_05020	putative 4-hydroxybutyrate CoA-transferase		0.54
HRM2_05030	pantothenate kinase		0.52
HRM2_05040	YbbR-like		0.51
HRM2_05050	Dihydropteroate synthase		0.54
HRM2_05060	membrane protease FtsH		0.53
HRM2_05070	tRNA(Ile)-lysidine synthetase-like protein		0.55
HRM2_05080	DHH phosphoesterases		0.51
HRM2_05090	carbohydrate ABC transporter ATP-binding protein, UgpC		0.52
HRM2_05100	carbohydrate ABC transporter substrate-binding protein, UgpB		0.51
HRM2_05110	carbohydrate ABC transporter membrane protein, UgpA		0.5
HRM2_05120	carbohydrate ABC transporter membrane protein, UgpE		0.52
HRM2_05130	putative MlaD protein		0.5
HRM2_05140	DUF1178		0.5
HRM2_05150	Na / Phosphate-cotransporter family		0.52
HRM2_05160	putative methyltransferase		0.53
HRM2_05170	putative horizontal gene transfer protein	phage like HTH domain protein	0.53
HRM2_05180	**methylthioribose-1-phosphate isomerase**		**0.57**
HRM2_05190	5'-methylthioadenosine phosphorylase		0.54
HRM2_05200	adenine phosphoribosyltransferase		0.49
HRM2_05210	Drug/metabolite transporter		0.53
HRM2_05220	glutamate racemase		0.56
HRM2_05230	erythrose 4-phosphate dehydrogenase		0.54
HRM2_05240	putative horizontal gene transfer protein	phage-like Winged helix-turn-helix transcription repressor	0.49
HRM2_05250	putative horizontal gene transfer protein	phage-like Winged helix-turn-helix transcription repressor	0.56
HRM2_05260	Small-conductance mechanosensitive channel		0.55
HRM2_05270	Aldehyde ferredoxin oxidoreductase		0.56
HRM2_05280	cytoplasmic protein RtcB		0.54
HRM2_05290	putative 2'-5' RNA ligase		0.53
HRM2_05300	DUF342		0.53
HRM2_05310	YehS, DUF1456 family		0.5

HRM2_05320	uracil permease UraA		0.53
HRM2_05330	uracil phosphoribosyltransferase		0.53
HRM2_05340	putative horizontal gene transfer protein	replication restart DNA helicase PriA	0.54
HRM2_05350	hypothetical protein		0.5
HRM2_05360	sigma-54 dependent DNA-binding response regulator		0.52
HRM2_05370	Cys-tRNA(Pro) deacylase, prolyl-tRNA editing enzyme YbaK/EbsC		0.55
HRM2_05380	succinyl-CoA synthetase, beta subunit SucC2		0.55
HRM2_05390	L-glutamine ABC transporter ATP-binding protein		0.5
HRM2_05400	amino acid ABC transporter membrane protein 2		0.55
HRM2_05410	amino acid ABC transporter membrane protein 1		0.51
HRM2_05420	Extracellular solute-binding protein, family 3		0.5
HRM2_05430	Extracellular solute-binding protein, family 3		0.52
HRM2_05440	putative horizontal gene transfer protein	phage-like HTH-transcription repressor	0.43
HRM2_05450	putative horizontal gene transfer protein	CRISPR-associated protein, Cas1 family	0.44
HRM2_05460	putative horizontal gene transfer protein	CRISPR-associated protein, Cas2 family	0.44
HRM2_05470	putative DNA repair protein		0.45
HRM2_05480	**putative horizontal gene transfer protein**	**csh1 CRISPR-associated protein Csh1**	**0.41**
HRM2_05490	**hypothetical protein**		**0.38**
HRM2_05500	putative horizontal gene transfer protein	CRISPR-associated protein, Csh2 family	0.42
HRM2_05510	**putative horizontal gene transfer protein**	**putative CRISPR-associated protein Cas5**	**0.4**
HRM2_05520	**putative horizontal gene transfer protein**	**CRISPR-associated helicase, Cas3 family**	**0.37**
HRM2_05530	**putative horizontal gene transfer protein**	**CRISPR-associated exonuclease, Cas4 family**	**0.33**
HRM2_10740	putative horizontal gene transfer protein	phage-like transcriptional regulator, XRE family	0.49
HRM2_10750	Branched-chain-amino-acid transaminase		0.52
HRM2_10760	hypothetical protein		0.51
HRM2_10770	putative horizontal gene transfer protein	HNH endonuclease	0.52
HRM2_10780	GTP-binding protein Era		0.51
HRM2_10790	Probable GTP-binding protein EngB		0.49
HRM2_10800	aspartate aminotransferase AspC		0.5

HRM2_10810	ATP phosphoribosyltransferase		0.52
HRM2_10820	phosphoribosyl-AMP cyclohydrolase		0.47
HRM2_10830	Membrane carboxypeptidase		0.51
HRM2_10840	radical SAM domain family protein		0.52
HRM2_10850	metal-dependent phosphoesterase / ribonuclease III		0.52
HRM2_10860	putative horizontal gene transfer protein	phage-like transcriptional regulator	0.47
HRM2_10870	glutamyl-tRNA reductase		0.51
HRM2_10880	cytochrome c assembly protein CcmC		0.53
HRM2_10890	precorrin-2 dehydrogenase		0.53
HRM2_10900	putative metal-dependent hydrolase		0.51
HRM2_10910	dihydrouridine synthase family protein		0.56
HRM2_10920	ferric uptake regulation protein		0.54
HRM2_10930	Fe2+ transport system protein FeoB		0.52
HRM2_10940	DUF1058		0.5
HRM2_10950	Tetratricopeptide-like helical		0.49
HRM2_10960	hypothetical protein		0.46
HRM2_10970	*pilR*		0.51
HRM2_10980	*pilS*		0.46
HRM2_10990	*PilM*		0.48
HRM2_11000	*pilN*		0.43
HRM2_11010	*pilO*		0.44
HRM2_11020	*pilP*		0.52
HRM2_11030	*pilQ*		0.48
HRM2_11040	pilF		0.48
HRM2_11050	hypothetical protein		0.49
HRM2_11060	L-threonine synthase		0.51
HRM2_11070	seryl-tRNA synthetase		0.5
HRM2_11080	5-formyltetrahydrofolate cyclo-ligase		0.45
HRM2_11090	potassium channel protein		0.5
HRM2_11100	protein-L-isoaspartate O-methyltransferase		0.52

HRM2_11110	Uncharacterized membrane protein YqaA		0.49
HRM2_11120	Fe-S-cluster containining protein		0.5
HRM2_11130	putative horizontal gene transfer protein	phage-like Winged helix-turn-helix transcription repressor	0.52
HRM2_11140	Phosphopantetheine adenylyltransferase		0.46
HRM2_11150	putative small methyltransferase		0.48
HRM2_11160	transcriptional regulator (FIS family protein)		0.49
HRM2_11170	PAS/PAC sensor signal transduction histidine kinase		0.5
HRM2_11180	DUF4390		0.47
HRM2_11190	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase		0.53
HRM2_11200	Mg chelatase-related protein		0.55
HRM2_11210	homolog of heat shock protein 33		0.52
HRM2_11220	hypothetical protein		0.46
HRM2_11230	indolepyruvate:ferredoxin oxidoreductase, alpha subunit IorA1		0.53
HRM2_11240	indolepyruvate ferredoxin oxidoreductase, subunit iorB		0.56
HRM2_11250	general secretion pathway protein F		0.52
HRM2_11260	Zinc finger, SWIM-type		0.49
HRM2_11270	putative horizontal gene transfer protein	phage-like helicase	0.51
HRM2_27610	putative horizontal gene transfer protein	phage-like site-specific recombinase XerD	0.54
HRM2_27620	putative horizontal gene transfer protein	predicted phage SPO1 DNA polymerase-related protein	0.52
HRM2_27630	CoaBC		0.53
HRM2_27640	putative lipoprotein		0.48
HRM2_27650	*pilY1*		0.45
HRM2_27660	*pilX*		0.48
HRM2_27670	*pilV*		0.44
HRM2_27680	*pilW*		0.45
HRM2_27690	***fimT***		**0.4**
HRM2_27700	e-pilin		0.46
HRM2_27710	*pilA*-C		0.45
HRM2_27720	*xapD*, ABC-type transport system, ATP-binding protein		0.48

HRM2_27730	*xapB*, ABC-type transport system, permease component		0.49
HRM2_27740	*xapA*, Tetratricopeptide-like helical		0.48
HRM2_27750	**O-antigen ligase like membrane protein**		**0.4**
HRM2_27760	*pilR*		0.51
HRM2_22330	*pilC*		0.46
HRM2_22340	*pilS*		0.51
HRM2_30410	*pilD*		0.51
HRM2_30420	CheX1		0.5
HRM2_30430	Hbp		0.45
HRM2_30440	hypothetical protein		0.45
HRM2_30450	Exodeoxyribonuclease I subunit C		0.49
HRM2_30460	SSU ribosomal protein S9P		0.51
HRM2_30470	LSU ribosomal protein L13P		0.44
HRM2_30490	hypothetical protein		0.46
HRM2_30500	putative ErfK family protein		0.5
HRM2_30510	putative horizontal gene transfer	Holliday junction ATP-dependent DNA helicase ruvB	0.54
HRM2_30520	putative horizontal gene transfer	ruvA holliday junction DNA helicase RuvA	0.52
HRM2_30530	putative horizontal gene transfer	Holliday junction endonuclease RuvC	0.53
HRM2_30540	putative aspartyl/asparaginyl beta-hydroxylase		0.49
HRM2_30550	peptidoglycan-associated lipoprotein		0.51
HRM2_30560	periplasmic component of the TolB complex		0.48
HRM2_30570	Cell division and transport-associated protein TolA		0.52
HRM2_30580	Cell division and transport-associated protein TolR		0.53
HRM2_30590	Cell division and transport-associated protein TolQ		0.5
HRM2_30600	GroEL		0.5
HRM2_30610	GroES		0.47
HRM2_30620	putative FmdB family protein		0.48
HRM2_30630	hypothetical protein		0.45
HRM2_30640	**DUF1713**		**0.4**
HRM2_30650	protease FtsH subunit HflC		0.5

HRM2_30660	protease FtsH subunit HflK		0.49
HRM2_30670	putative horizontal gene transfer	transposase (IS4 element)	0.46
HRM2_22780	**putative horizontal gene transfer**	**integrase (catalytic domain)**	**0.34**
HRM2_22790	hypothetical protein		0.53
HRM2_22800	**putative horizontal gene transfer**	**transposase for insertion sequences IS116, IS110 and IS902**	**0.39**
HRM2_23080	*pilB*		0.5

W. Pilin gene clusters found in the *Desulfobotulus sapovorans* genome. Six pilin gene clusters were identified in this genome. Ten genes coding for horizontal gene transfer proteins were present in these pilin clusters. Several *xap* operon genes (*xapB* and *xapD*) and O-antigen ligase, which is involved in LPS biosynthesis, are present in the e-pilin gene cluster. The overall GC content of *D. sapovorans* is 53.52%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Six out of 54 genes (11%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin, xapB*, O-antigen ligase, and *pilN*.

Locus ID	Gene	Horizontal transfer gene	GC content
BR04DRAFT_00387	**putative horizontal gene transfer protein**	**putative transposase or invertase**	**0.46**
BR04DRAFT_00388	hypothetical protein		0.49
BR04DRAFT_00389	Ribosome-binding ATPase YchF, GTP1/OBG family		0.54
BR04DRAFT_00390	**Tetratricopeptide-like**		**0.45**
BR04DRAFT_00391	***xapB*, ABC-2 family transporter protein**		**0.43**
BR04DRAFT_00392	*xapD*, ABC-2 type transport system ATP-binding protein		0.49
BR04DRAFT_00393	**O-antigen ligase**		**0.43**
BR04DRAFT_00394	**e-pilin**		**0.45**
BR04DRAFT_00395	hypothetical protein		0.49
BR04DRAFT_00396	prolipoprotein diacylglyceryl transferase		0.54
BR04DRAFT_00397	Nitroreductase		0.54
BR04DRAFT_00398	homoserine kinase type II		0.55
BR04DRAFT_00399	methionine aminopeptidase, type I		0.53
BR04DRAFT_00400	SEC-C motif-containing protein		0.57
BR04DRAFT_00401	1,4-dihydroxy-6-naphthoate synthase		0.56
BR04DRAFT_00402	YHS domain-containing protein		0.49

BR04DRAFT_00403	putative horizontal gene transfer protein	phage integrase/recombinase XerD	0.57
BR04DRAFT_00210	*pilT*		0.57
BR04DRAFT_00211	*pilT*		0.57
BR04DRAFT_00102	*pilT*		0.52
BR04DRAFT_00103	*pilT*		0.52
BR04DRAFT_02125	putative horizontal gene transfer protein	plasmid segregation protein	0.49
47 genes			
BR04DRAFT_02173	pilE		0.51
BR04DRAFT_02174	*pilY1*		0.52
BR04DRAFT_02175	hypothetical protein		0.47
BR04DRAFT_02176	*pilX*		0.55
BR04DRAFT_02177	*pilW*		0.53
BR04DRAFT_02178	*pilV*		0.51
BR04DRAFT_02179	*pilY1*		0.52
BR04DRAFT_02180	*pilX*		0.51
BR04DRAFT_02181	prepilin-type N-terminal cleavage/methylation domain-containing protein		0.55
BR04DRAFT_02182	prepilin-type N-terminal cleavage/methylation domain-containing protein		0.52
BR04DRAFT_02183	*fimT*		0.5
BR04DRAFT_02184	*pilT*		0.57
7 genes			
BR04DRAFT_02192	*pilC*		0.56
BR04DRAFT_02193	*pilB*		0.59
BR04DRAFT_02194	Type II secretory pathway, component ExeA		0.57
BR04DRAFT_02195	putative horizontal gene transfer protein	transposase, IS605 OrfB family, central region	0.52
BR04DRAFT_02578	**putative horizontal gene transfer protein**	**phage related GEMM cis-regulatory element**	**0.65**
33 genes			
BR04DRAFT_02613	*pilS*		0.55
BR04DRAFT_02614	*pilC*		0.51
6 genes			
BR04DRAFT_02621	putative horizontal gene transfer protein	phage related Site-specific recombinase XerD	0.47

BR04DRAFT_02622	putative horizontal gene transfer protein	phage related HicB_like antitoxin	0.51
BR04DRAFT_02623	putative horizontal gene transfer protein	phage related Site-specific DNA recombinase	0.54
3 genes			
BR04DRAFT_02627	putative horizontal gene transfer protein	Phage integrase family protein	0.55
BR04DRAFT_01789	*pilQ*		0.49
BR04DRAFT_01790	*pilP*		0.51
BR04DRAFT_01791	*pilO*		0.51
BR04DRAFT_01792	***pilN***		**0.44**
BR04DRAFT_01793	*pilM*		0.49
BR04DRAFT_01794	*pilS*		0.48
BR04DRAFT_01795	*pilR*		0.53
24 genes			
BR04DRAFT_01821	putative horizontal gene transfer protein	phage-like PIN domain nuclease, toxin-antitoxin system	0.51

X. Pilin gene clusters found in the *Desulfobotulus alkaliphilus* genome. Seven pilin gene clusters were identified in this genome. 18 genes coding for horizontal gene transfer proteins were present in these pilin clusters. Only two *xap* operon genes (*xapB* and *xapD*) are present in the e-pilin gene cluster. The overall GC content of *D. alkaliphilus* is 50.78%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 77 genes (5%) in these clusters have GC content that is > 7% from the overall average.

Locus ID	Gene	Horizontal transfer gene	GC content
LZ24DRAFT_00001	**putative horizontal gene transfer protein**	**PIN domain-like**	**0.37**
LZ24DRAFT_00002	pili subunit family protein		0.49
LZ24DRAFT_00003	*xapB*, ABC-2 family transporter protein		0.49
LZ24DRAFT_00004	*xapD*, ABC-2 type transport system ATP-binding protein		0.51
LZ24DRAFT_00005	*pilA*-C		0.46
LZ24DRAFT_00006	e-pilin		0.5
LZ24DRAFT_00007	hypothetical protein		0.47
LZ24DRAFT_00008	Putative transcriptional regulator, AlgH/UPF0301 family		0.56
LZ24DRAFT_00009	mcp methyl-accepting chemotaxis protein		0.53
LZ24DRAFT_00010	gspF general secretion pathway protein F		0.56

LZ24DRAFT_00011	Uncharacterized membrane protein YdjX		0.51
LZ24DRAFT_00012	hypothetical protein		0.49
LZ24DRAFT_00013	hypothetical protein		0.5
LZ24DRAFT_00014	ATP-binding cassette, subfamily B		0.54
LZ24DRAFT_00015	ATP-binding cassette, subfamily B		0.55
LZ24DRAFT_00016	putative horizontal gene transfer protein	phage Site-specific recombinase	0.54
LZ24DRAFT_00340	*pilN*		0.56
LZ24DRAFT_00341	hypothetical protein		0.52
LZ24DRAFT_00342	hypothetical protein		0.57
LZ24DRAFT_00343	hypothetical protein		0.51
LZ24DRAFT_00344	*pilD*		0.54
LZ24DRAFT_00345	*pilT*		0.56
LZ24DRAFT_00346	*pilB*		0.56
LZ24DRAFT_00347	*pilC*		0.54
LZ24DRAFT_00348	PPIC-type PPIASE domain-containing protein		0.51
LZ24DRAFT_00349	hypothetical protein		0.52
LZ24DRAFT_00350	hypothetical protein		0.49
LZ24DRAFT_00351	putative horizontal gene transfer protein	phage related antitoxin RelB	0.5
LZ24DRAFT_00352	putative horizontal gene transfer protein	phage related antitoxin RelB	0.45
LZ24DRAFT_00938	*pilZ*		0.44
LZ24DRAFT_00939	*pilB*		0.46
14 genes			
LZ24DRAFT_00955	*pilZ*		0.5
8 genes			
LZ24DRAFT_00964	putative horizontal gene transfer protein	phage related Site-specific recombinase XerD	0.47
LZ24DRAFT_00965	hypothetical protein		0.5
LZ24DRAFT_00966	putative horizontal gene transfer protein	phage Predicted nuclease of the RNAse H fold, HicB family	0.49
LZ24DRAFT_00967	putative horizontal gene transfer protein	phage Site-specific DNA recombinase	0.52
LZ24DRAFT_00968	hypothetical protein		0.47
LZ24DRAFT_00969	putative horizontal gene transfer protein	Phage integrase family protein	0.51

LZ24DRAFT_01035	**putative horizontal gene transfer protein**	**addiction module antidote protein, HigA family**	**0.41**
8 genes			
LZ24DRAFT_01045	putative horizontal gene transfer protein	antitoxin YefM	0.54
10 genes			
LZ24DRAFT_01056	putative horizontal gene transfer protein	Invasin/intimin cell-adhesion	0.5
LZ24DRAFT_01057	*pilQ*		0.47
LZ24DRAFT_01058	*pilP*		0.48
LZ24DRAFT_01059	*pilO*		0.52
LZ24DRAFT_01060	*pilN*		0.49
LZ24DRAFT_01061	*pilM*		0.51
LZ24DRAFT_01062	**hypothetical protein**		**0.39**
LZ24DRAFT_01063	*pilS*		0.47
LZ24DRAFT_01064	*pilR*		0.54
LZ24DRAFT_01796	putative horizontal gene transfer protein	crossover junction endodeoxyribonuclease RuvC	0.54
LZ24DRAFT_01797	tol-pal system protein YbgF		0.48
LZ24DRAFT_01798	outer membrane protein OmpA		0.54
26 genes			
LZ24DRAFT_01825	putative horizontal gene transfer protein	LysM domain-containing protein	0.53
LZ24DRAFT_01826	*fimT*		0.5
LZ24DRAFT_01827	pilE		0.47
LZ24DRAFT_01828	*pilY1*		0.45
LZ24DRAFT_01829	**pilY2**		**0.36**
LZ24DRAFT_01830	*pilX*		0.48
LZ24DRAFT_01831	*pilW*		0.44
LZ24DRAFT_01832	*pilV*		0.49
LZ24DRAFT_01833	*pilY1*		0.51
LZ24DRAFT_01979	*pilD*		0.5
7 genes			
LZ24DRAFT_01987	*pilT*		0.52

LZ24DRAFT_01988	*pilT*		0.53
LZ24DRAFT_01989	TRAP transporter, DctM subunit		0.5
LZ24DRAFT_01990	hypothetical protein		0.48
LZ24DRAFT_01991	putative horizontal gene transfer protein	single-stranded-DNA-specific exonuclease	0.56
38 genes			
LZ24DRAFT_02040	putative horizontal gene transfer protein	competence protein ComEC	0.55
5 genes			
LZ24DRAFT_02046	*pilB*		0.51
LZ24DRAFT_02700	*pilT*		0.53
LZ24DRAFT_02701	*pilT*		0.53
96 genes			
LZ24DRAFT_02798	putative horizontal gene transfer protein	LysM domain-containing protein	0.54
6 genes			
LZ24DRAFT_02805	*pilB*		0.49
8 genes			
LZ24DRAFT_02814	putative horizontal gene transfer protein	Phage integrase family protein	0.52
LZ24DRAFT_02815	hypothetical protein		0.55
LZ24DRAFT_02816	putative horizontal gene transfer protein	phage related KilA-N domain-containing protein	0.52

Y. Pilin gene clusters found in the *Thauera linaloolentis* genome. Seven pilin gene clusters were identified in this genome. Seventeen genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes coding for xap and glycosyltransferase or LPS biosynthesis proteins were not detected in the e-pilin gene cluster. The overall GC content of *T. linaloolentis* is 66.58%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Thirteen out of 64 genes (20%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin, pilE*, a long type IVa *pilA* gene, *pilX, pilV, pilW*, and *pilY1*.

Locus ID	Gene	Horizontal transfer gene	GC content
C666_06255	putative horizontal transfer	Endonuclease, Uma2 family	0.63
C666_06260	ABC-2 type transport system ATP-binding protein		0.67
C666_06265	**Nucleotidyltransferase substrate binding subunit/domain**		**0.59**
C666_06270	Nucleotidyltransferase domain		0.62

C666_06275	hypothetical protein		0.69
C666_06280	ABC-2 family transporter protein		0.62
C666_06285	**e-pilin**		**0.48**
C666_06290	**putative horizontal transfer gene**	**endonuclease VapC**	**0.59**
C666_06295	**putative horizontal transfer gene**	**antitoxin VapB**	**0.58**
C666_06300	putative horizontal transfer gene	Winged helix" DNA-binding domain	0.67
C666_06305	Glutaredoxin		0.62
C666_06310	hypothetical protein		0.64
C666_06315	NADPH-glutathione reductase		0.7
C666_06320	molybdopterin-guanine dinucleotide biosynthesis protein A		0.71
C666_06325	diguanylate cyclase (GGDEF) domain-containing protein		0.7
C666_06330	putative horizontal transfer gene	putative N6-adenine-specific DNA methylase	0.69
C666_06335	pilU		0.64
C666_06340	*pilT*		0.65
C666_06345	pyridoxal phosphate enzyme, YggS family		0.71
C666_06350	pyrroline-5-carboxylate reductase		0.73
C666_06355	YggT family protein		0.68
C666_06360	putative horizontal transfer gene	Endonuclease, Uma2 family	0.68
C666_06365	dihydroorotase		0.69
C666_06370	aspartate carbamoyltransferase		0.6
C666_06375	uracil phosphoribosyltransferase		0.69
C666_06380	putative horizontal transfer gene	Holliday junction resolvase-like protein	0.71
C666_06385	Putative transcriptional regulator, AlgH/UPF0301 family		0.67
C666_06390	deoxyribodipyrimidine photo-lyase		0.69
C666_06395	cystathione beta-lyase		0.72
C666_06400	Acyl-CoA N-acyltransferase		0.64
C666_06405	chemosensory pili system protein ChpA		0.71
C666_06410	pilJ		0.7
C666_06415	**pilI**		**0.75**
C666_06420	pilH		0.65

C666_06425	pilG		0.65
C666_05425	**pilE**		**0.58**
C666_05430	***fimT***		**0.61**
C666_05435	***pilV***		**0.55**
C666_05440	***pilW***		**0.57**
C666_05445	***pilX***		**0.58**
C666_05450	***pilY1***		**0.57**
C666_15290	**long *pilA***		**0.53**
C666_15295	D-alanyl-D-alanine carboxypeptidase		0.67
C666_15300	Peptidoglycan/LPS O-acetylase OafA/YrhL,		0.66
C666_15305	Transketolase		0.68
C666_15310	putative horizontal transfer gene	Putative restriction endonuclease	0.68
C666_15315	putative horizontal transfer gene	mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system	0.6
C666_15320	putative horizontal transfer gene	Lambda repressor-like, DNA-binding domain	0.68
C666_15325	putative horizontal transfer gene	plasmid stability protein	0.6
C666_15330	**putative horizontal transfer gene**	**plasmid stabilization protein**	**0.57**
C666_15335	putative horizontal transfer gene	LysR family transcriptional regulator,	0.73
C666_04815	putative horizontal transfer gene	phage integrase/recombinase XerD	0.66
15 genes			
C666_04895	*pilB*		0.64
C666_04900	*pilC*		0.63
C666_04905	*pilD*		0.65
C666_00255	*pilR*		0.67
C666_00260	*pilS*		0.69
10 genes			
C666_00310	putative horizontal transfer gene	DNA-binding transcriptional regulator, LysR family	0.68
C666_08630	*pilM*		0.65
C666_08635	*pilN*		0.63
C666_08640	*pilO*		0.63

C666_08645	*pilP*		0.64
17 genes			
C666_08730	putative horizontal transfer gene	DNA-binding transcriptional regulator, LysR family	0.68
C666_15955	*pilQ*		0.7

Z. Pilin gene clusters found in the *Thauera terpenica* genome. Five pilin gene clusters were identified in this genome. Thirteen genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes coding for *xap*, glycosyltransferase and LPS biosynthesis proteins were not detected in the e-pilin gene cluster. The overall GC content of *T. terpenica* is 64.3%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Eight out of 55 genes (15%) in these clusters had GC content that was > 7% from the overall average, including *e-pilin*, *pilQ, pilX, pilV, pilW*, and *pilY1*.

Locus ID	Gene	Horizontal transfer gene	GC content
M622_11220	pilG		0.6
M622_11225	pilH		0.62
M622_11230	pilI		0.66
M622_11235	pilJ		0.67
M622_11240	chemosensory pili system protein ChpA		0.69
M622_11245	cystathione beta-lyase		0.69
M622_11250	deoxyribodipyrimidine photo-lyase		0.65
M622_11255	Putative transcriptional regulator, AlgH/UPF0301 family		0.65
M622_11260	putative horizontal transfer gene	putative transcription antitermination factor YqgF	0.69
M622_11265	uracil phosphoribosyltransferase		0.68
M622_11270	aspartate carbamoyltransferase		0.66
M622_11275	dihydroorotase		0.68
M622_11280	putative horizontal transfer gene	Endonuclease, Uma2 family	0.67
M622_11285	YggT family protein		0.65
M622_11290	pyrroline-5-carboxylate reductase		0.71
M622_11295	pyridoxal phosphate enzyme, YggS family		0.69
M622_11300	*pilT*		0.63
M622_11305	pilU		0.63
M622_11310	putative horizontal transfer gene	putative N6-adenine-specific DNA methylase	0.69

M622_11315	molybdopterin-guanine dinucleotide biosynthesis protein A		0.71
M622_11320	NADPH-glutathione reductase		0.67
M622_11325	hypothetical protein		0.63
M622_11330	putative horizontal transfer gene	Resolvase, N terminal domain	0.61
M622_11335	putative horizontal transfer gene	prevent-host-death family protein	0.57
M622_11340	*pilT*		0.61
M622_11345	**e-pilin**		**0.54**
M622_11350	hypothetical protein		0.58
M622_11355	ABC-2 family transporter protein		0.67
M622_11360	hypothetical protein		0.64
M622_11365	putative horizontal transfer gene	prevent-host-death family protein	0.64
M622_11370	putative horizontal transfer gene	ParE toxin of type II toxin-antitoxin system, parDE	0.63
M622_11375	*xapD*		0.68
M622_01585	long *PilA*		0.58
M622_01590	hypothetical protein		0.57
M622_01595	***pilY1***		**0.55**
M622_01600	***pilX***		**0.53**
M622_01605	***pilW***		**0.5**
M622_01610	***pilV***		**0.56**
M622_01615	***fimT***		**0.56**
18 genes			
M622_01705	*pilZ*		0.66
M622_11650	putative horizontal transfer gene	Helix-turn-helix domain of transposase family ISL3	0.65
M622_11655	putative horizontal transfer gene	RES domain-containing protein	0.6
17 genes			
M622_11740	*pilB*		0.62
M622_11745	*pilC*		0.62
M622_11750	*pilD*		0.65
M622_13925	*pilR*		0.65
M622_13930	*pilS*		0.66

16 genes			
M622_14010	horizontal gene transfer	excinuclease ABC subunit A	0.65
M622_00030	***pilQ***		**0.52**
M622_00035	**hypothetical protein**		**0.42**
M622_00040	*pilP*		0.59
M622_00045	*pilO*		0.6
M622_00050	*pilN*		0.63
M622_00055	*pilM*		0.63
37 genes			
M622_00240	horizontal gene transfer	LysR family transcriptional regulator	0.64
8 genes			
M622_00280	horizontal gene transfer	TraT complement resistance protein	0.61

AA. Pilin gene clusters found in the *Thauera humireducens* genome. Five pilin gene clusters were identified in this genome. Five genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes coding for *xap*, glycosyltransferase and LPS biosynthesis proteins were not detected in the e-pilin gene cluster. The overall GC content of *T. humireducens* is 66.4%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 28 genes (14%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin*, long type IVa *pilA, pilV*, and *pilY1*.

Locus ID	Gene	Horizontal transfer gene	GC content
WP_048706603.1	horizontal transfer gene	crossover junction endodeoxyribonuclease RuvA	0.71
6 genes			
WP_038012416	pilU		0.64
WP_048706607.1	*pilT*		0.64
14 genes			
WP_048706619	prevent-host-death protein		0.63
WP_048706621	relE toxin		0.6
3 genes			
WP_048706629.1	**epilin**		**0.51**
WP_048710114.1	hypothetical protein		0.59
WP_048706631.1	hypothetical protein		0.66

WP_048706634	horizontal gene transfer-prophage	prevent-host-death family protein	0.61
WP_004252063.1	horizontal transfer	phasin family protein	0.63
5 genes			
WP_004252011.1	*pilZ*		0.65
8 genes			
WP_048709378	**long *pilA***		**0.58**
WP_048709380.1	*fimT*		0.62
WP_048709381.1	***pilV***		**0.57**
WP_048709383.1	*pilW*		0.6
WP_048710599.1	*pilX*		0.59
WP_048709385.1	***pilY1***		**0.58**
WP_048705994	*pilB*		0.63
WP_038011757.1	*pilC*		0.62
WP_048705996.1	*pilD*		0.66
WP_048706143.1	*pilR*		0.69
WP_048706145.1	*pilS*		0.69
4 genes			
WP_048706172.1	horizontal gene transfer	LysR family transcriptional regulator	0.7
WP_004253778	*pilM*		0.62
WP_004253781.1	*pilN*		0.6
WP_038010918.1	*pilO*		0.6
WP_004253787.1	*pilP*		0.6
WP_048710322.1	*pilQ*		0.6

AB. Pilin gene clusters found in the *Flexistipes sinusarabici* genome. Four pilin gene clusters were identified in this genome. Thirty-four genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon were not detected, but O-antigen ligase, which is involved in LPS biosynthesis, is present in the e-pilin gene cluster. The overall GC content of *F. sinusarabici* is 38.29%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 89 genes (5%) in these clusters have GC content that is > 7% from the overall average.

Locus ID	Gene	Horizontal transfer gene	GC content

Flexsi_0510	*pilM*		0.37
Flexsi_0511	*pilN*		0.34
Flexsi_0512	*pilO*		0.34
Flexsi_0513	*pilP*		0.34
Flexsi_0514	*pilQ*		0.37
14 genes			
Flexsi_0529	putative horizontal gene transfer protein	Transposase	0.39
21 genes			
Flexsi_0551	putative horizontal gene transfer protein	Transposase	0.39
Flexsi_0552	putative horizontal gene transfer protein	Transposase DDE domain-containing protein	0.39
Flexsi_0553	**putative horizontal gene transfer protein**	**TraT complement resistance protein**	**0.47**
6 genes			
Flexsi_0560	putative horizontal gene transfer protein	transposase, IS5 family	0.38
Flexsi_0561	putative horizontal gene transfer protein	transposase, IS5 family	0.38
Flexsi_0562	putative horizontal gene transfer protein	Transposase DDE domain group 1	0.36
Flexsi_0563	PAS domain S-box-containing protein		0.38
Flexsi_0564	ABC-2 type transport system ATP-binding protein		0.38
Flexsi_0565	Type II secretion system (T2SS), protein G		0.36
Flexsi_0566	*xapD*		0.37
Flexsi_0807	putative horizontal gene transfer protein	Transposase	0.39
7 genes			
Flexsi_0814	putative horizontal gene transfer protein	transposase, IS5 family	0.38
7 genes			
Flexsi_0822	putative horizontal gene transfer protein	transposase IS4 family protein	0.36
Flexsi_0823	putative horizontal gene transfer protein	virulence factor lipase N-terminal	0.4
4 genes			
Flexsi_0828	putative horizontal gene transfer protein	Transposase	0.36
Flexsi_0829	putative horizontal gene transfer protein	integrase/recombinase XerD	0.35
Flexsi_0830	hypothetical protein		0.34

Flexsi_0831	**hypothetical protein**		**0.25**
Flexsi_0832	putative horizontal gene transfer protein	Transposase	0.42
Flexsi_0833	putative horizontal gene transfer protein	IstB_IS21	0.44
4 genes			
Flexsi_0838	**putative horizontal gene transfer protein**	**CAAX amino terminal protease**	**0.3**
3 genes			
Flexsi_0842	*pilC*		0.39
Flexsi_0843	putative horizontal gene transfer protein	Transposase	0.36
Flexsi_0844	two component transcriptional regulator, winged helix family		0.39
Flexsi_0845	ATP-binding region ATPase domain protein		0.35
Flexsi_0846	**hypothetical protein**		**0.25**
Flexsi_0847	*pilY1*		0.37
Flexsi_0848	prepilin-type N-terminal cleavage/methylation domain-containing protein		0.35
Flexsi_0849	*pilV*		0.32
Flexsi_0850	*pilW*		0.33
Flexsi_0851	*pilX*		0.36
Flexsi_0852	hypothetical protein		0.33
Flexsi_0853	putative horizontal gene transfer protein	IstB domain protein ATP-binding protein	0.41
Flexsi_0854	putative horizontal gene transfer protein	Transposase	0.41
Flexsi_0855	putative horizontal gene transfer protein	transposase, IS5 family	0.4
4 genes			
Flexsi_0860	putative horizontal gene transfer protein	integrase/recombinase XerD	0.37
8 genes			
Flexsi_0869	putative horizontal gene transfer protein	transposase, IS5 family	0.37
Flexsi_1189	putative horizontal gene transfer protein	DNA-binding protein HU-beta	0.38
Flexsi_1190	putative horizontal gene transfer protein	transcriptional regulator, XRE family	0.36
23 genes			
Flexsi_1214	*pilS*		0.32
Flexsi_1215	*pilR*		0.35

Flexsi_1216	dihydroorotate oxidase B, catalytic subunit		0.38
Flexsi_1217	dihydroorotate dehydrogenase electron transfer subunit		0.39
Flexsi_1218	carbamoyl-phosphate synthase large subunit		0.4
Flexsi_1219	*pilS*		0.35
Flexsi_1220	*pilC*		0.42
Flexsi_1221	*pilT*		0.42
Flexsi_1222	*pilB*		0.4
Flexsi_1223	*aroE*		0.35
Flexsi_2256	putative horizontal gene transfer protein	Retron-type reverse transcriptase	0.38
Flexsi_2257	putative horizontal gene transfer protein	Transposase	0.36
6 genes			
Flexsi_2264	putative horizontal gene transfer protein	Transposase	0.42
Flexsi_2265	putative horizontal gene transfer protein	IstB-like ATP binding protein	0.41
Flexsi_2266	putative horizontal gene transfer protein	Transposase DDE domain-containing protein	0.35
Flexsi_2267	hypothetical protein		0.38
Flexsi_2268	putative horizontal gene transfer protein	Transposase DDE domain group 1	0.36
Flexsi_2269	putative horizontal gene transfer protein	Transposase	0.38
Flexsi_2270	putative horizontal gene transfer protein	transposase, IS4 family protein	0.35
Flexsi_2271	small redox-active disulfide protein 2		0.43
Flexsi_2272	Protein of unknown function DUF318, transmembrane		0.44
Flexsi_2273	arsenite transporter, ACR3 family		0.39
Flexsi_2274	arsenate reductase		0.38
Flexsi_2275	sulfoxide reductase catalytic subunit YedY		0.4
Flexsi_2276	GCN5-related N-acetyltransferase		0.43
Flexsi_2277	pyridoxamine 5'-phosphate oxidase-related FMN-binding		0.35
Flexsi_2278	transcriptional regulator, GntR family with aminotransferase domain		0.38
Flexsi_2279	Predicted arabinose efflux permease, MFS family		0.36
Flexsi_2280	putative horizontal gene transfer protein	transposase, IS4 family protein	0.35

Flexsi_2281	putative horizontal gene transfer protein	Transposase	0.38
Flexsi_2282	enoyl-CoA hydratase		0.41
Flexsi_2283	2-aminoadipate transaminase		0.36
Flexsi_2284	DinB family protein		0.33
Flexsi_2285	Threonine/homoserine efflux transporter RhtA		0.41
Flexsi_2286	PAS domain S-box-containing protein		0.41
Flexsi_2287	two-component system, NtrC family, sensor histidine kinase HydH		0.41
Flexsi_2288	e-pilin		0.42
Flexsi_2289	*pilA*-C		0.33
Flexsi_2290	O-antigen ligase		0.31
Flexsi_2291	e-pilin		0.4
Flexsi_2292	PS51257 Prokaryotic membrane lipoprotein lipid attachment		0.33
Flexsi_R0054	tRNA_SeC		0.68
Flexsi_2293	ribulose-5-phosphate 3-epimerase		0.41
Flexsi_2294	DUF1858		0.39
Flexsi_2295	NAD(P)-dependent dehydrogenase, short-chain alcohol		0.38
Flexsi_2296	hypothetical protein		0.4
Flexsi_2297	putative horizontal gene transfer protein	membrane-bound lytic murein transglycosylase F	0.39
Flexsi_2298	putative horizontal gene transfer protein	Transposase	0.36

AC. Pilin gene clusters found in the *Hippea maritima* genome. Three pilin gene clusters were identified in this genome. Twenty-nine genes coding for horizontal gene transfer proteins were present in these pilin clusters. Two xap operon genes (*xapB* and *xapD*) and O-antigen ligase can be found in the e-pilin gene cluster. The overall GC content of *H. maritima* is 37.47%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Fifteen out of 134 genes (11%) in these clusters have GC content that is > 7% from the overall average, including *pilV* and *pilT*.

Locus ID	Gene	Horizontal transfer gene	GC content
Hipma_0474	*pilC*		0.38
Hipma_0475	*pilT*		0.4
Hipma_0476	*pilB*		0.36

Hipma_0477	*aroE*		0.35
Hipma_0610	*pilD*		0.36
	20 genes		
Hipma_0631	putative horizontal gene transfer protein	conjugal transfer mating pair stabilization protein TraN	0.43
Hipma_0632	putative horizontal gene transfer protein	Possible phage DNA methylase	0.41
Hipma_0633	hypothetical protein		0.4
Hipma_0634	putative horizontal gene transfer protein	phage M3 protein	0.42
Hipma_0635	**hypothetical protein**		**0.46**
Hipma_0636	putative horizontal gene transfer protein	Type IV conjugative transfer system, protein TraL	0.37
Hipma_0637	putative horizontal gene transfer protein	conjugal transfer pilus assembly protein TraE	0.39
Hipma_0638	putative horizontal gene transfer protein	TraK protein	0.39
Hipma_0639	**putative horizontal gene transfer protein**	**conjugal transfer pilus assembly protein TraB**	**0.45**
Hipma_0640	putative horizontal gene transfer protein	conjugal transfer pilus assembly protein TraV	0.36
Hipma_0641	Thiol:disulfide interchange protein DsbC		0.41
Hipma_0642	hypothetical protein		0.39
Hipma_0643	hypothetical protein		0.4
Hipma_0644	hypothetical protein		0.4
Hipma_0645	OmpA family protein		0.36
Hipma_0646	putative horizontal gene transfer protein	conjugative transfer signal peptidase TraF	0.35
Hipma_0647	putative horizontal gene transfer protein	conjugal transfer pilus assembly protein TraF	0.38
Hipma_0648	**putative cytoplasmic protein**		**0.47**
Hipma_0649	putative horizontal gene transfer protein	conjugal transfer pilus assembly protein TraW	0.39
Hipma_0650	putative horizontal gene transfer protein	conjugal transfer pilus assembly protein TraU	0.44
Hipma_0651	putative horizontal gene transfer protein	type-F conjugative transfer system pilin assembly protein TrbC	0.35
Hipma_0652	trichohyalin		0.33
Hipma_0653	hypothetical protein		0.39
Hipma_0654	putative horizontal gene transfer protein	CRISPR-associated exonuclease Cas4	0.38
Hipma_0655	hypothetical protein		0.36

Hipma_0656	hypothetical protein		0.31
Hipma_0657	hypothetical protein		0.37
Hipma_0658	putative horizontal gene transfer protein	exodeoxyribonuclease V alpha subunit	0.43
Hipma_0665	putative horizontal gene transfer protein	DNA-binding protein HU/Integration host factor	0.38
Hipma_0667	putative horizontal gene transfer protein	conjugal transfer mating pair stabilization protein TraG	0.43
Hipma_0669	putative horizontal gene transfer protein	conjugative transfer pilus assembly protein TraH	0.42
Hipma_0670	**putative horizontal gene transfer protein**	**putative transposase**	**0.29**
Hipma_0671	**putative horizontal gene transfer protein**	**putative transposase**	**0.28**
Hipma_0675	**putative horizontal gene transfer protein**	**TraT complement resistance protein**	**0.45**
Hipma_0676	**hypothetical protein**		**0.47**
Hipma_0677	P-loop containing nucleoside triphosphate hydrolases		0.35
Hipma_0678	hypothetical protein		0.38
Hipma_0679	putative horizontal gene transfer protein	plasmid segregation protein ParM	0.41
Hipma_0680	**putative horizontal gene transfer protein**	**single stranded DNA-binding protein**	**0.45**
Hipma_0681	**hypothetical protein**		**0.5**
Hipma_0682	hypothetical protein		0.38
Hipma_0683	hypothetical protein		0.44
Hipma_0684	putative horizontal gene transfer protein	conjugal transfer ATP-binding protein TraC	0.4
Hipma_0685	hypothetical protein		0.34
Hipma_0686	putative horizontal gene transfer protein	Replicative DNA helicase	0.41
Hipma_0687	hypothetical protein		0.38
Hipma_0688	hypothetical protein		0.43
Hipma_0690	putative horizontal gene transfer protein	Helix-turn-helix domain-containing protein	0.39
Hipma_0695	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.39
Hipma_0696	2-dehydropantoate 2-reductase		0.33
Hipma_0697	Enoyl-CoA hydratase/carnithine racemase		0.42
Hipma_R0026	**tRNA_Pro**		**0.73**
Hipma_0698	Xaa-Pro aminopeptidase		0.37

Hipma_0699	diguanylate cyclase (GGDEF) domain		0.33
Hipma_0700	Signal transduction histidine kinase		0.34
Hipma_0701	tryptophanyl-tRNA synthetase		0.39
Hipma_0702	GGDEF domain-containing protein, diguanylate cyclase		0.33
Hipma_0703	biotin carboxylase		0.42
Hipma_0704	biotin carboxyl carrier protein		0.39
Hipma_0705	PAS domain S-box-containing protein/diguanylate cyclase (GGDEF) domain		0.32
Hipma_0706	DUF763		0.4
Hipma_0707	acetolactate synthase, large subunit		0.4
Hipma_0708	acetolactate synthase, small subunit		0.35
Hipma_0709	ketol-acid reductoisomerase		0.41
Hipma_0710	phosphatidylserine decarboxylase		0.37
Hipma_0711	CDP-diacylglycerol---serine O-phosphatidyltransferase		0.36
Hipma_0712	2-isopropylmalate synthase		0.39
Hipma_0713	hypothetical protein		0.33
Hipma_0714	DisA checkpoint controller nucleotide-binding		0.36
Hipma_0715	methylenetetrahydrofolate dehydrogenase (NADP+)		0.38
Hipma_0716	ribosome maturation factor RimP		0.38
Hipma_0717	putative horizontal gene transfer protein	NusA antitermination factor	0.39
Hipma_0718	translation initiation factor IF-2		0.39
Hipma_0719	DUF503		0.34
Hipma_0720	ribosome-binding factor A		0.34
Hipma_0721	phosphoesterase RecJ domain-containing protein		0.38
Hipma_0722	tRNA pseudouridine55 synthase		0.34
Hipma_0723	poly-beta-hydroxybutyrate-responsive repressor		0.36
Hipma_0724	HD-GYP domain, c-di-GMP phosphodiesterase class II		0.36
Hipma_0725	2-octaprenylphenol hydroxylase		0.36
Hipma_0726	4-hydroxy-3-polyprenylbenzoate decarboxylase		0.36

Hipma_0727	flagella basal body P-ring formation protein FlgA	0.33
Hipma_0728	**flagellar basal-body rod protein FlgG**	**0.45**
Hipma_0729	flagellar basal-body rod protein FlgG	0.36
Hipma_0730	*xapB*, ABC-2 family transporter protein	0.34
Hipma_0731	hypothetical protein	0.35
Hipma_0732	*xapD*, ABC-2 type transport system ATP-binding protein	0.37
Hipma_0733	**hypothetical protein**	**0.28**
Hipma_0734	***pilT***	**0.28**
Hipma_0735	O-antigen ligase	0.3
Hipma_0736	*pilA*-C	0.38
Hipma_0737	e-pilin	0.37
Hipma_0738	OmpA family protein	0.34
Hipma_0739	hypothetical protein	0.34
Hipma_0740	osmoprotectant transport system permease protein	0.39
Hipma_0741	osmoprotectant transport system ATP-binding protein	0.36
Hipma_0742	osmoprotectant transport system permease protein	0.34
Hipma_0743	osmoprotectant transport system substrate-binding protein	0.35
Hipma_0744	Multimeric flavodoxin WrbA	0.4
Hipma_0745	copper-translocating P-type ATPase	0.38
Hipma_0746	DNA-binding transcriptional regulator, FrmR family	0.33
Hipma_0747	hypothetical protein	0.35
Hipma_0748	Protein of unknown function DUF2078, membrane	0.3
Hipma_0749	cation:H+ antiporter	0.34
Hipma_R0027	**tRNA_Leu**	**0.66**
Hipma_0750	peroxiredoxin	0.4
Hipma_0751	LemA family protein	0.32
Hipma_0752	Protein of unknown function DUF2207, membrane	0.34
Hipma_0753	Gamma-glutamyl cyclotransferase-like	0.31

Hipma_0754	hypothetical protein		0.38
Hipma_0755	diguanylate cyclase (GGDEF) domain-containing protein		0.3
Hipma_0756	putative horizontal gene transfer protein	Transposase	0.37
Hipma_0768	putative horizontal gene transfer protein	integrase/recombinase XerD	0.35
Hipma_1079	putative horizontal gene transfer protein	Integrase, catalytic core; Helix-turn-helix	0.38
Hipma_1080	pyrroline-5-carboxylate reductase		0.42
Hipma_1081	heat shock protein HspR		0.35
Hipma_1082	curved DNA-binding protein		0.39
Hipma_1083	HSP20 family protein		0.41
Hipma_1084	ATP-dependent Clp protease ATP-binding subunit ClpB		0.42
Hipma_1085	hypothetical protein		0.34
Hipma_1086	*pilW*		0.33
Hipma_1087	***pilV***		**0.29**
Hipma_1088	N_methyl_3 domain protein		0.33
Hipma_1089	*pilY1*		0.35
Hipma_1185	*pilQ*		0.36
Hipma_1186	*pilP*		0.34
Hipma_1187	*pilO*		0.31
Hipma_1188	*pilN*		0.34
Hipma_1189	*pilM*		0.33

AD. Pilin gene clusters found in the *Hippea alviniae* genome. Four pilin gene clusters were identified in this genome. Three genes coding for horizontal gene transfer proteins were present in these pilin clusters. The *xap* operon (*xapA-J*) can be found in the e-pilin gene cluster. The overall GC content of *H. alviniae* is 37.03%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 53 genes (8%) in these clusters have GC content that is > 7% from the overall average.

Hippea alviniae	GC content is 37.03%	horizontal transfer gene	GC content
G415DRAFT_0150	flagellar basal-body rod protein FlgB		0.34
G415DRAFT_0151	flagellar basal-body rod protein FlgC		0.38
G415DRAFT_0152	flagellar hook-basal body complex protein FliE		0.39

G415DRAFT_0153	flagellar M-ring protein FliF	0.38
G415DRAFT_0154	lagellar motor switch protein FliG	0.41
G415DRAFT_0155	flagellar assembly protein FliH	0.38
G415DRAFT_0156	type III secretion system ATPase, FliI/YscN	0.41
G415DRAFT_0157	flagellar FliJ protein	0.35
G415DRAFT_0158	MgtE N-terminal domain-like	0.37
G415DRAFT_0159	amino acid/amide ABC transporter substrate-binding protein, HAAT family	0.4
G415DRAFT_0160	Uncharacterized conserved protein, contains tandem ACT domains	0.37
G415DRAFT_0161	phenylacetate-CoA ligase	0.39
G415DRAFT_0162	Glutaredoxin-like protein, YruB-family	0.39
G415DRAFT_0163	L-threonine ammonia-lyase	0.37
G415DRAFT_0164	**tRNA_Ala_CGC**	**0.6**
G415DRAFT_0165	DUF302	0.38
G415DRAFT_0166	methyl-accepting chemotaxis sensory transducer with Cache sensor	0.36
G415DRAFT_0167	dgcB diguanylate cyclase	0.32
G415DRAFT_0168	hypothetical protein	0.34
G415DRAFT_0169	*pilM*	0.34
G415DRAFT_0170	*pilN*	0.34
G415DRAFT_0171	*pilO*	0.33
G415DRAFT_0172	*pilP*	0.32
G415DRAFT_0173	*pilQ*	0.34
G415DRAFT_0790	*pilW*	0.35
G415DRAFT_0791	*pilV*	0.34
G415DRAFT_0792	*fimT*	0.33
G415DRAFT_0793	*pilY1*	0.35
20 genes		
G415DRAFT_0814	putative horizontal gene transfer protein putative transposase or invertase	0.33
G415DRAFT_0867	aspartyl-tRNA synthetase	0.4
G415DRAFT_0868	**tRNA_Val_CAC**	**0.62**
G415DRAFT_0869	P-loop containing nucleoside triphosphate hydrolase	0.34

G415DRAFT_0870	hypothetical protein		0.41
G415DRAFT_0871	putative horizontal gene transfer protein	Transposase	0.36
G415DRAFT_0872	e-pilin		0.36
G415DRAFT_0873	*pilA*-C		0.38
G415DRAFT_0874	**hypothetical protein**		**0.25**
G415DRAFT_0875	*xapA*, Tetratricopeptide repeat-containing protein		0.3
G415DRAFT_0876	ATPase		0.33
G415DRAFT_0877	*xapE*, 4-hydroxybenzoate polyprenyltransferase		0.33
G415DRAFT_0878	CDP-alcohol phosphatidyltransferase		0.32
G415DRAFT_0879	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase		0.35
G415DRAFT_0880	**CDP-glycerol glycerophosphotransferase**		**0.26**
G415DRAFT_0881	*xapH*, lipopolysaccharide transport system ATP-binding protein		0.33
G415DRAFT_0882	*xapG*, lipopolysaccharide transport system permease protein		0.35
G415DRAFT_0883	hypothetical protein		0.31
G415DRAFT_0884	putative horizontal gene transfer protein	prevent-host-death family protein	0.34
G415DRAFT_0885	hypothetical protein		0.33
G415DRAFT_0886	**ATPase**		**0.28**
G415DRAFT_0887	*xapJ*		0.35
G415DRAFT_0888	*xapH*		0.33
G415DRAFT_0889	*xapD*		0.35
G415DRAFT_0890	*xapB*		0.33
G415DRAFT_0936	*pilC*		0.35
G415DRAFT_0937	*pilT*		0.4
G415DRAFT_0938	*pilB*		0.36
G415DRAFT_0939	*aroE*		0.35
58 genes			
G415DRAFT_0998	*pilD*		0.36

AE. Pilin gene clusters found in the *Deferribacter desulfuricans* genome. Five pilin gene clusters were identified in this genome. Two genes coding for horizontal gene transfer proteins were present in these pilin clusters. Several xap operon genes (*xapA*, *xapB*, and *xapD*) were detected in the e-pilin gene cluster. The overall GC content of D. desulfuricans is 30.31%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Two out of 50 genes (4%) in these clusters had GC content that was > 7% from the overall average, including *pilN.*

Locus ID	Gene	Horiontal transfer gene	GC content
DEFDS_0111	Putative chemotaxis protein CheX		0.33
DEFDS_0112	*pilD*		0.3
DEFDS_0113	tyrosyl-tRNA synthetase		0.34
DEFDS_0858	*pilX*		0.28
DEFDS_0859	*pilW*		0.31
DEFDS_0860	*pilV*		0.31
DEFDS_0861	Type II secretory pathway, pseudopilin PulG		0.28
DEFDS_0862	*pilY1*		0.3
9 genes			
DEFDS_0873	putative horizontal gene transfer protein	transposase IS654 family	0.33
DEFDS_1090	putative horizontal gene transfer protein	Exodeoxyribonuclease VII	0.29
DEFDS_1091	transcription elongation factor GreA		0.33
DEFDS_1092	*pilR*		0.29
7 genes			
DEFDS_1100	putative horizontal gene transfer protein	NusB antitermination factor	0.3
6 genes			
DEFDS_1108	*aroE*		0.25
DEFDS_1109	*pilB*		0.35
DEFDS_1110	*pilT*		0.35
DEFDS_1111	*pilC*		0.34
DEFDS_1112	*pilS*		0.23
DEFDS_1252	***pilN***		**0.21**
DEFDS_1253	hypothetical protein		0.25
DEFDS_1254	hypothetical protein		0.24
DEFDS_1255	*pilQ*		0.3

DEFDS_1256	*pilB*	0.33
DEFDS_1258	Biotin transporter BioY	0.3
DEFDS_1259	patatin-like phospholipase family protein	0.32
DEFDS_1260	NAD-dependent formate dehydrogenase catalytic subunit	0.33
DEFDS_1261	NADH dehydrogenase I, F subunit	0.31
DEFDS_1262	S-adenosyl-L-methionine-dependent methyltransferases	0.33
DEFDS_1263	hypothetical protein	0.27
DEFDS_1264	biopolymer transport protein, ExbB/TolQ family	0.35
DEFDS_1265	Tetratricopeptide-like helical	0.24
DEFDS_1266	Survival protein SurE-like phosphatase/nucleotidase	0.36
DEFDS_1267	stationary-phase survival protein	0.36
DEFDS_1268	**ATP-binding protein, CobQ/CobB/MinD/ParA family**	**0.38**
DEFDS_1269	AAA-ATPase_like	0.29
DEFDS_1270	e-pilin	0.33
DEFDS_1271	*pilA*-C	0.33
DEFDS_1272	*xapD*, ABC transporter ATP-binding protein	0.31
DEFDS_1273	*xapA*, Tetratricopeptide-like helical	0.28
DEFDS_1274	*xapB*, ATP-binding Cassette (ABC) Superfamily	0.25
DEFDS_1275	pyruvate carboxylase	0.33
DEFDS_1276	mechanosensitive ion channel, MscS family	0.34
DEFDS_1277	Stringent starvation protein B	0.28
DEFDS_1278	mechanosensitive ion channel, MscS family	0.28
DEFDS_1279	chorismate dehydratase	0.25
DEFDS_1724	*pilQ*	0.29
DEFDS_1725	*pilP*	0.28
DEFDS_1726	*pilO*	0.26
DEFDS_1727	*pilN*	0.26
DEFDS_1728	*pilM*	0.32

AF. Pilin gene clusters found in the *Desulfobacula toluolica* genome. Seven pilin gene clusters were identified in this genome. Seventy-five genes coding for horizontal gene transfer proteins were present in these pilin clusters. Gene from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of *D. toluolica* is 41.45%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty-four out of 187 genes (13%) in these clusters have GC content that is > 7% from the overall average, including *xapG, xapH*, *pilN* and *pilO*.

Locus ID	Gene	Horizontal transfer gene	GC content
TOL2_05690	*pilT*		0.46
TOL2_05700	*pilT*		0.43
TOL2_05710	CheY-like receiver domain		0.37
TOL2_05720	conserved uncharacterized protein		0.41
TOL2_05730	PbpA: penicillin-binding protein 1A		0.45
TOL2_05740	Sporulation related domain-containing protein		0.36
TOL2_05750	selenium metabolism protein YedF		0.4
TOL2_05760	Fe-S-cluster containining protein		0.38
TOL2_05770	tRNA-dihydrouridine synthase		0.43
TOL2_05780	Fur: ferric uptake regulator		0.39
TOL2_05790	FeoB: ferrous iron transport protein B		0.41
TOL2_05800	SH3-like domain-containing protein		0.39
TOL2_05810	Tetratricopeptide repeat-containing protein		0.35
TOL2_05820	*pilR*		0.44
TOL2_05830	*pilS*		0.38
TOL2_05840	*pilM*		0.37
TOL2_05850	***pilN***		**0.32**
TOL2_05860	***pilO***		**0.33**
TOL2_05870	*pilP*		0.37
TOL2_05880	*pilQ*		0.37
TOL2_05890	pilF		0.38
TOL2_05900	putative horizontal	LysM domain protein	0.35

	gene transfer protein		
TOL2_13280	putative horizontal gene transfer protein	integration host factor subunit beta	0.36
TOL2_13290	putative horizontal gene transfer protein	Transcription antitermination factor NusG	0.39
TOL2_13300	LPS-assembly protein		0.41
TOL2_13310	cysteinyl-tRNA synthetase		0.42
TOL2_13320	conserved uncharacterized protein, precursor		0.39
TOL2_13330	*pilB*		0.42
TOL2_13340	putative horizontal gene transfer protein	LysM domain-containing protein	0.38
TOL2_13640	putative horizontal gene transfer protein	Integration host factor (IHF)-like DNA-binding domain	0.38
TOL2_13650	chemotaxis protein CheX		0.39
TOL2_13660	*pilD*		0.39
TOL2_13670	ATP-dependent Lon protease		0.42
TOL2_13680	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB		0.45
TOL2_13690	phosphatidylserine decarboxylase		0.41
TOL2_13700	CDP-diacylglycerol---serine O-phosphatidyltransferase		0.38
TOL2_13710	transcription elongation factor GreA		0.44
TOL2_16880	putative horizontal gene transfer protein	Transposase	0.47

TOL2_16900	conserved uncharacterized protein		0.4
TOL2_16910	Cytidylate kinase		0.33
TOL2_16920	Glycine cleavage system H protein (lipoate-binding)		0.47
TOL2_16930	archaemetzincin		0.48
TOL2_16940	*pilR*		0.46
TOL2_16950	*pilS*		0.46
TOL2_16960	**uncharacterized protein**		**0.32**
TOL2_16970	predicted pyridoxamine-phosphate oxidase		0.44
TOL2_16980	Rhomboid family protein		0.39
TOL2_16990	DUF3820		0.38
TOL2_17000	voltage-gated potassium channel		0.42
TOL2_17010	Heme-degrading monooxygenase HmoA		0.37
TOL2_17020	protein of unknown function (DUF3786)		0.43
TOL2_17030	Flavin-binding protein dodecin		0.38
TOL2_17040	HD-like signal output (HDOD) domain, no enzymatic activity		0.41
TOL2_17050	conserved uncharacterized protein		0.45
TOL2_17060	*pilT*		0.48
TOL2_17070	hypothetical protein		0.41
TOL2_17080	**putative horizontal gene transfer protein**	**Predicted endonuclease, GIY-YIG superfamily**	**0.33**
TOL2_17090	putative horizontal gene transfer protein	exodeoxyribonuclease	0.43
TOL2_20060	*pilS*		0.35
TOL2_20070	*pilC*		0.4
TOL2_20080	tRNA nucleotidyltransferase (CCA-adding enzyme)		0.38
TOL2_20090	tryptophanyl-tRNA synthetase		0.42
TOL2_20100	23S rRNA pseudouridine2605 synthase		0.38

TOL2_20110	glutamate N-acetyltransferase		0.44
TOL2_20120	putative horizontal gene transfer protein	integron integrase	0.43
TOL2_20130	putative horizontal gene transfer protein	Predicted nuclease of the RNAse H fold, HicB family	0.36
TOL2_20140	putative horizontal gene transfer protein	Putative abortive phage resistance protein AbiGi, antitoxin	0.36
TOL2_20150	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20160	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20170	**uncharacterized protein**		**0.54**
TOL2_20180	Protein of unknown function (DUF3800)		0.45
TOL2_20190	uncharacterized protein		0.38
TOL2_20200	putative horizontal gene transfer protein	Predicted nuclease of the RNAse H fold, HicB family	0.39
TOL2_20210	putative horizontal gene transfer protein	Transposase zinc-binding domain-containing protein	0.43
TOL2_20220	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.44
TOL2_20230	**uncharacterized protein**		**0.31**

TOL2_20240	**orotate phosphoribosyltransferase**		**0.3**
TOL2_20250	conserved uncharacterized integral membrane protein, DUF165		0.35
TOL2_20260	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20270	uncharacterized protein		0.33
TOL2_20280	conserved uncharacterized protein		0.37
TOL2_20290	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20300	putative horizontal gene transfer protein	transposase, IS801/IS1294 family	0.43
TOL2_20310	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.44
TOL2_20320	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20330	uncharacterized protein		0.32
TOL2_20340	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20350	putative horizontal gene transfer protein	Transposase zinc-binding domain-containing protein	0.43
TOL2_20360	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.43
TOL2_20370	putative horizontal	Transposase zinc-binding domain-containing	0.43

	gene transfer protein	protein	
TOL2_20380	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.43
TOL2_20390	putative horizontal gene transfer protein	HicA toxin of toxin-antitoxin	0.41
TOL2_20400	putative horizontal gene transfer protein	Predicted nuclease of the RNAse H fold, HicB family	0.46
TOL2_20410	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20420	uncharacterized protein		0.45
TOL2_20430	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20440	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20450	**uncharacterized protein**		**0.6**
TOL2_20460	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20470	**uncharacterized protein**		**0.54**
TOL2_20480	putative horizontal gene transfer protein	antitoxin StbD	0.44

TOL2_20490	putative horizontal gene transfer protein	mRNA interferase RelE/StbE	0.41
TOL2_20500	putative horizontal gene transfer protein	Transposase zinc-binding domain-containing protein	0.43
TOL2_20510	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.43
TOL2_20520	putative horizontal gene transfer protein	HicA toxin of toxin-antitoxin	0.35
TOL2_20530	putative horizontal gene transfer protein	Predicted nuclease of the RNAse H fold, HicB family	0.36
TOL2_20540	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20550	putative horizontal gene transfer protein	Helix-turn-helix domain-containing protein	0.37
TOL2_20560	putative horizontal gene transfer protein	mRNA interferase RelE/StbE	0.34
TOL2_20570	putative horizontal gene transfer protein	prevent-host-death family protein	0.4
TOL2_20580	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20590	**uncharacterized protein**		**0.6**

TOL2_20600	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45
TOL2_20610	**putative horizontal gene transfer protein**	**prevent-host-death family protein**	**0.31**
TOL2_20620	putative horizontal gene transfer protein	Predicted nucleic acid-binding protein, contains PIN domain	0.34
TOL2_20630	putative horizontal gene transfer protein	Transposase and inactivated derivatives	0.4
TOL2_20640	putative horizontal gene transfer protein	putative transposase	0.41
TOL2_20650	putative horizontal gene transfer protein	Transposase	0.45
TOL2_20660	conserved uncharacterized protein		0.45
TOL2_20670	putative horizontal gene transfer protein	transposase, IS66 family Orf2	0.42
TOL2_20680	putative horizontal gene transfer protein	Transposase	0.44
TOL2_20690	**uncharacterized protein**		**0.27**
TOL2_20700	conserved uncharacterized protein		0.39
TOL2_20710	protein of unknown function (DUF4160)		0.39
TOL2_20720	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.45

TOL2_20730	uncharacterized protein		0.47
TOL2_20740	conserved uncharacterized protein		0.43
TOL2_20750	putative horizontal gene transfer protein	transposase, IS66 family Orf2	0.47
TOL2_20760	putative horizontal gene transfer protein	Transposase IS66 family protein	0.45
TOL2_20770	putative horizontal gene transfer protein	Phage-related protein	0.39
TOL2_20780	putative horizontal gene transfer protein	Lambda repressor-like, DNA-binding domain	0.41
TOL2_20790	putative horizontal gene transfer protein	group II intron reverse transcriptase/maturase	0.46
TOL2_20800	conserved uncharacterized protein		0.45
TOL2_20810	putative horizontal gene transfer protein	transposase, IS66 family Orf2	0.4
TOL2_20820	putative horizontal gene transfer protein	Transposase	0.45
TOL2_20830	putative horizontal gene transfer protein	mRNA interferase MazF	0.34
TOL2_20840	putative horizontal gene transfer protein	antitoxin MazE	0.41
TOL2_20850	putative horizontal	group II intron reverse transcriptase/maturase	0.45

	gene transfer protein		
TOL2_20860	**uncharacterized protein**		**0.51**
TOL2_20870	putative horizontal gene transfer protein	Transposase zinc-binding domain-containing protein	0.43
TOL2_20880	putative horizontal gene transfer protein	Site-specific recombinase XerD	0.44
TOL2_20890	putative horizontal gene transfer protein	phage Homeodomain-like	0.38
TOL2_20900	putative horizontal gene transfer protein	phage Homeodomain-like	0.42
TOL2_20910	putative horizontal gene transfer protein	Transposase DDE domain-containing protein	0.41
TOL2_20920	putative horizontal gene transfer protein	Transposase IS116/IS110/IS902 family protein	0.4
TOL2_20930	putative horizontal gene transfer protein	Transposase	0.39
13 genes			
TOL2_21080	putative horizontal gene transfer protein	Transposase IS116/IS110/IS902 family protein	0.4
TOL2_21300	putative lipoprotein		0.4
TOL2_21310	***xapA*, TPR-like membrane protein**		**0.32**

TOL2_21320	pili subunit family		0.35
TOL2_21330	*xapB*, ABC-2 family transporter protein		0.34
TOL2_21340	*xapD*, ABC-2 type transport system ATP-binding protein		0.39
TOL2_21350	e-pilin		0.41
TOL2_21360	*xapE*, 4-hydroxybenzoate polyprenyltransferase		0.4
TOL2_21370	ADP-heptose:LPS heptosyltransferase		0.38
TOL2_21380	*xapF*, Glycosyltransferase, GT2 family		0.36
TOL2_21390	UDP-galactopyranose mutase		0.38
TOL2_21400	**predicted glycosyl transferase, family 2**		**0.32**
TOL2_21410	**Glycosyltransferase, GT2 family**		**0.31**
TOL2_21420	**Iron-sulfur cluster-binding domain-containing protein**		**0.29**
TOL2_21430	**Protein of unknown function DUF115**		**0.32**
TOL2_21440	**N-acylneuraminate cytidylyltransferase**		**0.3**
TOL2_21450	***xapG***		**0.3**
TOL2_21460	***xapH*, lipopolysaccharide transport system ATP-binding protein**		**0.31**
TOL2_21470	ABC-type polysaccharide/polyol phosphate export permease		0.35
TOL2_21480	Kynurenine formamidase		0.41
TOL2_21490	UDP-glucose 4-epimerase		0.38
TOL2_21500	2-dehydro-3-deoxyglucarate aldolase		0.39
TOL2_21510	**HAD-superfamily hydrolase, subfamily IA, variant 1**		**0.3**
TOL2_21520	**D-3-phosphoglycerate dehydrogenase**		**0.33**
TOL2_21530	*xapG*, predicted O-antigen export system, permease protein		0.35
TOL2_21540	putative horizontal gene transfer protein	Fic/DOC family protein	0.4
TOL2_21550	**putative horizontal gene transfer protein**	**nucleoside triphosphate hydrolase**	**0.31**
TOL2_21560	*fimT*		0.43

TOL2_21570	*pilW*		0.42
TOL2_21580	*pilV*		0.4
TOL2_21590	*pilX*		0.41
TOL2_21600	*pilY1*		0.42
29 genes			
TOL2_21900	*pilR*		0.41
TOL2_21910	PyrC: dihydroorotase		0.43
TOL2_21920	PyrB: aspartate carbamoyltransferase		0.42
TOL2_21930	signal peptidase I		0.36
TOL2_21940	Uncharacterized conserved protein, DUF39 family		0.41
TOL2_21950	putative horizontal gene transfer protein	Murein DD-endopeptidase MepM and murein hydrolase activator NlpD, contain LysM domain	0.37
TOL2_24450	*pilB*		0.42
15 genes			
TOL2_24610	putative horizontal gene transfer protein	integrase/recombinase XerC	0.4
TOL2_24620	putative horizontal gene transfer protein	dpo DNA polymerase bacteriophage-type	0.37

AG. Pilin gene clusters found in the *Desulfobacula phenolica* genome. Seven pilin gene clusters were identified in this genome. 10 genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of *D. phenolica* is 41.33%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Five out of 72 genes (7%) in these clusters have GC content that is > 7% from the overall average, including *xapA, pilN* and *pilO*.

Locus ID	Gene	horizontal transfer gene	GC content
Ga0066824_102262	pilF		0.38
Ga0066824_102263	*pilQ*		0.37

Ga0066824_102264	*pilP*		0.37
Ga0066824_102265	***pilO***		**0.33**
Ga0066824_102266	***pilN***		**0.32**
Ga0066824_102267	*pilM*		0.37
Ga0066824_102268	*pilS*		0.4
Ga0066824_102269	*pilR*		0.46
Ga0066824_102270	Putative negative regulator of RcsB-dependent stress response		0.36
Ga0066824_102271	SH3-like domain-containing protein		0.41
Ga0066824_102272	ferrous iron transport protein B		0.41
Ga0066824_102273	Fur family transcriptional regulator		0.41
Ga0066824_102274	tRNA-dihydrouridine synthase		0.45
Ga0066824_102275	Fe-S-cluster containining protein		0.39
Ga0066824_102276	hypothetical protein		0.42
Ga0066824_102277	selenium metabolism protein YedF		0.4
Ga0066824_102278	Sporulation related domain-containing protein		0.37
Ga0066824_102279	penicillin-binding protein 1A		0.44
Ga0066824_102280	hypothetical protein		0.41
Ga0066824_102281	CheY-like superfamily		0.38
Ga0066824_102282	*pilT*		0.42
Ga0066824_102283	*pilT*		0.45
Ga0066824_101248	putative horizontal gene transfer protein	integration host factor subunit beta	0.36
Ga0066824_101249	putative horizontal gene transfer protein	Transcription antitermination factor NusG	0.41
Ga0066824_101250	LPS-assembly protein		0.4
Ga0066824_101251	cysteinyl-tRNA synthetase		0.42
Ga0066824_101252	hypothetical protein		0.38
Ga0066824_101253	4Fe-4S dicluster domain-containing protein		0.41
Ga0066824_101254	*pilB*		0.42
Ga0066824_101296	*pilZ*		0.36
Ga0066824_101297	putative horizontal gene transfer protein	Integration host factor (IHF)-like DNA-binding domain	0.38
Ga0066824_101298	chemotaxis protein CheX		0.39

Ga0066824_101299	*pilD*		0.39
Ga0066824_1194	hypothetical protein		0.34
Ga0066824_1195	putative horizontal gene transfer protein	Predicted nuclease of the RNAse H fold, HicB family	0.41
Ga0066824_1196	putative horizontal gene transfer protein	YcfA-like protein	0.4
Ga0066824_1197	hypothetical protein		0.35
Ga0066824_1198	putative horizontal gene transfer protein	integron integrase	0.45
Ga0066824_1199	glutamate N-acetyltransferase		0.44
Ga0066824_11910	23S rRNA pseudouridine(2605) synthase		0.4
Ga0066824_11911	tryptophanyl-tRNA synthetase		0.42
Ga0066824_11912	tRNA nucleotidyltransferase (CCA-adding enzyme)		0.38
Ga0066824_11913	*pilC*		0.4
Ga0066824_11914	*pilS*		0.36
Ga0066824_11639	4-oxalocrotonate tautomerase		0.36
Ga0066824_11640	Thioesterase/thiol ester dehydrase-isomerase		0.38
Ga0066824_11641	phosphopantothenoylcysteine decarboxylase		0.42
Ga0066824_11642	PS51257 Prokaryotic membrane lipoprotein lipid attachment		0.4
Ga0066824_11643	***xapA*, TPR-like membrane protein**		**0.32**
Ga0066824_11644	**Pili subunit family**		**0.33**
Ga0066824_11645	*xapB*, ABC-2 family transporter protein		0.34
Ga0066824_11646	*xapD*, ABC-2 type transport system ATP-binding protein		0.43
Ga0066824_11647	*pilA*-C		0.47
Ga0066824_11648	epilin		0.38
Ga0066824_11649	*xapE*, 4-hydroxybenzoate polyprenyltransferase		0.39
Ga0066824_11650	*xapJ*, ADP-heptose:LPS heptosyltransferase		0.38
Ga0066824_11651	*xapF*, Glycosyltransferase, GT2 family		0.37
Ga0066824_11652	UDP-galactopyranose mutase		0.37
Ga0066824_11653	putative horizontal transfer gene protein	DDE superfamily endonuclease	0.38
Ga0066824_103400	*pilR*		0.4
23 genes			
Ga0066824_103424	*pilY1*		0.42

Ga0066824_103425	*pilX*		0.4
Ga0066824_103426	*pilV*		0.4
Ga0066824_103427	*pilW*		0.42
Ga0066824_103428	*fimT*		0.43
Ga0066824_103429	**Predicted ATPase, AAA+ superfamily**		**0.31**
Ga0066824_103430	putative horizontal gene transfer protein	Fido domain	0.38
Ga0066824_103431	hypothetical protein		0.41
Ga0066824_103432	*xapG*, lipopolysaccharide transport system permease		0.35
Ga0066824_103433	putative horizontal gene transfer protein	Integrase core domain-containing protein	0.4
Ga0066824_103136	*pilB*		0.41
8 genes			
Ga0066824_103145	putative horizontal gene transfer protein	Phage integrase family protein	0.37

AH. Pilin gene clusters found in the *Geobacter soli* genome. Three pilin gene clusters were identified in this genome. Three genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of *G. soli* is 61.76%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty out of 72 genes (28%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin, xapA, xapE, pilV, pilW* and *pilX*.

Geobacter soli	GC content is 61.76%	horizontal transfer gene	GC content
Ga0077628_111560	**Haloacid dehalogenase-like hydrolase**		**0.54**
Ga0077628_111561	Glycosyltransferase involved in cell wall bisynthesis		0.56
Ga0077628_111562	Glycosyltransferase involved in cell wall bisynthesis		0.56
Ga0077628_111563	Methyltransferase domain-containing protein		0.57
Ga0077628_111564	perosamine synthetase		0.57
Ga0077628_111565	**RmlC-like cupin domain**		**0.53**
Ga0077628_111566	**Glycosyl transferase family 2**		**0.53**
Ga0077628_111567	**Glycosyltransferase involved in cell wall bisynthesis**		**0.49**
Ga0077628_111568	**Glycosyltransferase involved in cell wall bisynthesis**		**0.5**
Ga0077628_111569	**UDP-glucose 4-epimerase**		**0.49**
Ga0077628_111570	**Glycosyl transferases group 1**		**0.39**

Ga0077628_111571	***xapI*, Methyltransferase domain-containing protein**	**0.41**
Ga0077628_111572	**ABC-type polysaccharide/polyol phosphate transport system, ATPase component**	**0.47**
Ga0077628_111573	*xapG*, lipopolysaccharide transport system permease protein	0.56
Ga0077628_111574	*xapF*, Glycosyl transferase family 2	0.57
Ga0077628_111575	***xapE*, 4-hydroxybenzoate polyprenyltransferase**	**0.54**
Ga0077628_111576	***xapD*, ABC-2 type transport system ATP-binding protein**	**0.47**
Ga0077628_111577	**hypothetical protein**	**0.45**
Ga0077628_111578	***xapB*, ABC-2 family transporter protein**	**0.41**
Ga0077628_111579	***xapA*, Tetratricopeptide repeat-containing protein**	**0.45**
Ga0077628_111580	**e-pilin**	**0.49**
Ga0077628_111581	*pilR*	0.59
Ga0077628_111582	*pilS*	0.59
Ga0077628_111583	*pilC*	0.58
Ga0077628_111584	*pilT*	0.61
Ga0077628_111585	*pilB*	0.6
Ga0077628_111586	*aroE*	0.63
Ga0077628_111587	DUF2723	0.6
Ga0077628_111588	Lysylphosphatidylglycerol synthase TM region	0.64
Ga0077628_111589	flavokinase	0.61
Ga0077628_111590	*tatC*	0.56
Ga0077628_111591	RNAse R	0.63
Ga0077628_111592	soluble lytic murein transglycosylase	0.63
Ga0077628_111593	DNA-binding transcriptional regulator, MarR family	0.59
Ga0077628_111977	Putative nucleotidyltransferase substrate binding domain-containing protein	0.62
Ga0077628_111978	*pilY1*	0.62
Ga0077628_111979	*pilX*	0.62
Ga0077628_111980	*pilW*	0.62
Ga0077628_111981	*pilV*	0.59
Ga0077628_111982	hypothetical protein	0.64
Ga0077628_111983	aspartate aminotransferase	0.65

Ga0077628_111984	hypothetical protein	0.61
Ga0077628_11906	diguanylate cyclase (GGDEF) domain	0.62
Ga0077628_11907	*pilD*	0.6
Ga0077628_11908	*pilS*	0.65
Ga0077628_11909	*pilR*	0.62
Ga0077628_11910	prepilin-type N-terminal cleavage/methylation domain-containing protein	0.6
Ga0077628_11911	*pilY1*	0.55
Ga0077628_11912	Pili subunits	0.52
Ga0077628_11913	***pilV***	**0.53**
Ga0077628_11914	***pilW***	**0.54**
Ga0077628_11915	***pilX***	**0.53**
Ga0077628_11916	GEMM cis-regulatory element	0.52
Ga0077628_11917	**putative horizontal transfer gene protein Lambda repressor-like, DNA-binding domain**	**0.53**
Ga0077628_11918	*pilM*	0.56
Ga0077628_11919	*pilN*	0.57
Ga0077628_11920	*pilO*	0.55
Ga0077628_11921	*pilP*	0.59
Ga0077628_11922	*pilQ*	0.6
Ga0077628_11923	**PS51257 Prokaryotic membrane lipoprotein lipid attachment**	**0.48**
Ga0077628_11924	*aroC*	0.63
Ga0077628_11925	*aroK*	0.61
Ga0077628_11926	*aroB*	0.64
Ga0077628_11927	Tetratricopeptide repeat-containing protein	0.62
Ga0077628_11928	Roadblock/LC7 domain	0.61
Ga0077628_11929	*aroQ*	0.6
Ga0077628_11930	Xaa-Pro aminopeptidase	0.61
Ga0077628_11931	biotin carboxyl carrier protein	0.62
Ga0077628_11932	biotin carboxylase	0.6
Ga0077628_11933	glycine cleavage system H protein	0.59
Ga0077628_11934	chorismate dehydratase	0.61

Ga0077628_11935	diguanylate cyclase (GGDEF) domain	0.58

AI. Pilin gene clusters found in the *Geobacter sp. OR-1* genome. Three pilin gene clusters were identified in this genome. Four genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of strain OR-1 is 54.18%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty out of 84 genes (24%) in these clusters have GC content that is > 7% from the overall average, including *pilO, pilN,* and *pilM.*

Geobacter OR-1	GC content is 54.18%	Horizontal transfer gene	GC content
Ga0098289_12615	BioD-like N-terminal domain of phosphotransacetylase		0.57
Ga0098289_12616	soluble lytic murein transglycosylase		0.57
Ga0098289_12617	RNAse R		0.61
Ga0098289_12618	sec-independent protein translocase protein *TatC*		0.53
Ga0098289_12619	Flavokinase		0.56
Ga0098289_12620	Lysylphosphatidylglycerol synthase TM region		0.57
Ga0098289_12621	DUF2723		0.54
Ga0098289_12622	*pilB*		0.55
Ga0098289_12623	*pilT*		0.56
Ga0098289_12624	*pilC*		0.53
Ga0098289_12625	*pilS*		0.54
Ga0098289_12626	*pilR*		0.55
Ga0098289_12627	e-pilin		0.52
Ga0098289_12628	*pilA*-C		0.49
Ga0098289_12629	hypothetical protein		0.51
Ga0098289_12630	*xapA*, TPR-like		0.49
Ga0098289_12631	*xapB*, ABC-2 family transporter protein		0.53
Ga0098289_12632	TPR-like		0.48
Ga0098289_12633	*xapD*, ABC-2 type transport system ATP-binding protein		0.52
Ga0098289_12634	*xapE*, 4-hydroxybenzoate polyprenyltransferase		0.5
Ga0098289_12635	*xapF*, Glycosyltransferase, GT2 family		0.53
Ga0098289_12636	*xapG*, lipopolysaccharide transport system permease protein		0.53

Ga0098289_12637	*xapH*, lipopolysaccharide transport system ATP-binding protein	0.48
Ga0098289_12638	**Radical SAM superfamily enzyme, MoaA/NifB/PqqE/SkfB family**	**0.46**
Ga0098289_12639	Glycosyl transferases group 1	0.49
Ga0098289_12640	**S-adenosyl-L-methionine-dependent methyltransferases**	**0.46**
Ga0098289_12641	**hypothetical protein**	**0.45**
Ga0098289_12642	**hypothetical protein**	**0.46**
Ga0098289_12643	***xapI*, Methyltransferase small domain-containing protein**	**0.43**
Ga0098289_12644	**Polysaccharide pyruvyl transferase family protein WcaK**	**0.46**
Ga0098289_12645	Glycosyltransferase involved in cell wall bisynthesis	0.48
Ga0098289_12646	Glycosyltransferase involved in cell wall bisynthesis	0.47
Ga0098289_12647	**Glycosyltransferase involved in cell wall bisynthesis**	**0.38**
Ga0098289_12648	**Glycosyltransferase, GT2 family**	**0.41**
Ga0098289_12649	CDP-alcohol phosphatidyltransferase	0.48
Ga0098289_12650	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	0.49
Ga0098289_10198	chorismate dehydratase	0.5
Ga0098289_10199	glycine cleavage system H protein	0.51
Ga0098289_10200	biotin carboxylase	0.53
Ga0098289_10201	biotin carboxyl carrier protein	0.52
Ga0098289_10202	Xaa-Pro aminopeptidase	0.55
Ga0098289_10203	*aroQ*	0.49
Ga0098289_10204	Roadblock/LC7 domain	0.47
Ga0098289_10205	Tetratricopeptide repeat-containing protein	0.52
Ga0098289_10206	*aroB*	0.55
Ga0098289_10207	*aroC*	0.55
Ga0098289_10208	PS51257 Prokaryotic membrane lipoprotein lipid attachment	0.5
Ga0098289_10209	PS51257 Prokaryotic membrane lipoprotein lipid attachment	0.49
Ga0098289_10210	*pilQ*	0.5
Ga0098289_10211	*pilP*	0.44
Ga0098289_10212	***pilO***	**0.46**
Ga0098289_10213	***pilN***	**0.43**

Ga0098289_10214	***pilM***		**0.45**
Ga0098289_10215	**putative horizontal transfer gene protein**	**Lambda repressor-like, DNA-binding domain**	**0.38**
Ga0098289_10216	**putative horizontal transfer gene protein**	**DNA polymerase lambda, fingers domain**	**0.42**
Ga0098289_10217	*pilX*		0.49
Ga0098289_10218	*pilW*		0.5
Ga0098289_10219	*pilV*		0.51
Ga0098289_10220	pilE		0.48
Ga0098289_10221	*pilY1*		0.52
Ga0098289_10222	**hypothetical protein**		**0.41**
Ga0098289_10223	thiol:disulfide interchange protein DsbC		0.49
Ga0098289_10224	*pilR*		0.51
Ga0098289_10225	*pilS*		0.51
Ga0098289_10226	*pilD*		0.51
Ga0098289_101108	S51257 Prokaryotic membrane lipoprotein lipid attachment		0.5
Ga0098289_101109	S51257 Prokaryotic membrane lipoprotein lipid attachment		0.49
Ga0098289_101110	*pilQ*		0.5
Ga0098289_101111	*pilP*		0.44
Ga0098289_101112	*pilO*		0.46
Ga0098289_101113	*pilN*		0.43
Ga0098289_101114	*pilM*		0.45
Ga0098289_101115	putative horizontal transfer gene	Lambda repressor-like, DNA-binding domain	0.38
Ga0098289_101116	putative horizontal transfer gene	DNA polymerase lambda, fingers domain	0.42
Ga0098289_101117	hypothetical protein		0.49
Ga0098289_101118	*pilW*		0.5
Ga0098289_101119	*pilV*		0.51
Ga0098289_101120	*pile*		0.48
Ga0098289_101121	*pilY1*		0.52
Ga0098289_101122	**hypothetical protein**		**0.41**
Ga0098289_101123	*pilR*		0.49
Ga0098289_101124	*pilS*		0.51

Ga0098289_101125	*pilD*	0.51
Ga0098289_101126		0.51

Supplementary Table S2. Comparison of amino acid sequences from pilin accessory proteins found in the genomes of e-pilin harboring organisms to accessory proteins from such well-characterized species as *Neisseria gonorrhoeae*, *Escherichia coli, Pseudomonas aeruginosa*, and *Myxococcus fulvus*. Percent identity and percent similarity values were generated with the BLASTp algorithm. If query coverage was lower than 65%, similarity values were not included in the table and these cells were given a grey background. NA indicates that a homologous gene was not detected in the specified genome.

Geobacter sulfurreducens	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	GSU1063				NA
pilW	GSU1064		NA		NA
pilX	GSU1065				NA
pilY1	GSU1066		NA		
pilB	GSU1491	44/64	46/66	45/66	65/83
pilT	GSU1492	48/67		51/67	50/69
pilC	GSU1493		30/53	41/62	60/76
pilS	GSU1494			27/43	35/53
pilR	GSU1495			43/62	48/65
pilQ	GSU2028	33/49			35/52
pilP	GSU2029				
pilO	GSU2030	26/48			33/56
pilN	GSU2031	22/43			
pilM	GSU2032	26/46			52/72
pilD	GSU2043	36/55	34/53	41/58	41/62

Pelobacter carbinolicus	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Pcar_2158				NA
pilW	Pcar_2157		NA	37/66	NA
pilX	Pcar_2156	25/39			NA
pilY1	Pcar_2155		NA		
pilB	Pcar_2149	42/64	43/64	45/66	65/83
pilT	Pcar_2148	46/63		51/67	49/67
pilC	Pcar_2147		28/48	44/63	61/75

pilS	Pcar_2146	▨	▨	27/45	34/53
pilR	Pcar_2145	▨	▨	42/61	46/62
pilQ	Pcar_2134	32/48	▨	▨	30/46
pilP	Pcar_2135	▨	▨	▨	37/52
pilO	Pcar_2136	24/51	▨	▨	32/55
pilN	Pcar_2137	26/48	▨	▨	▨
pilM	Pcar_2138	25/44	▨	▨	47/68
pilD	Pcar_2139	37/54	33/52	35/55	38/62

Geobacter metallireducens	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Gmet_0734	▨	▨	▨	NA
pilW	Gmet_0735	▨	NA	▨	NA
pilX	Gmet_0736	▨	▨	▨	NA
pilY1	Gmet_0737	▨	NA	▨	▨
pilB	Gmet_1393	44/65	46/65	45/66	65/83
pilT	Gmet_1394	48/67	▨	51/68	49/68
pilC	Gmet_1395	▨	30/52	41/62	62/77
pilS	Gmet_1396	▨	▨	27/45	36/53
pilR	Gmet_1397	▨	▨	44/62	49/66
pilQ	Gmet_0975	31/49	▨	▨	35/52
pilP	Gmet_0974	▨	▨	▨	▨
pilO	Gmet_0973	30/50	▨	▨	31/52
pilN	Gmet_0972	25/45	▨	▨	▨
pilM	Gmet_0971	25/44	▨	▨	51/70
pilD	Gmet_0959	37/54	33/51	40/55	39/61

Desulfobacterium autotrophicum	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	HRM2_27670	▨	▨	31/69	NA

pilW	HRM2_27680	28/62	NA	▨	NA
pilX	HRM2_27660	▨	▨	17/34	NA
pilY1	HRM2_27650	▨	NA	23/34	23/35
pilB	HRM2_23080	40/61	42/60	40/60	46/64
pilC	HRM2_22330	▨	28/49	40/61	55/70
pilT	HRM2_04990	52/72	▨	58/74	46/65
pilS	HRM2_10980	▨	▨	▨	▨
pilR	HRM2_10970	▨	▨	39/58	42/58
pilQ	HRM2_11030	▨	▨	▨	32/51
pilP	HRM2_11020	28/41	▨	▨	▨
pilO	HRM2_11010	30/50	▨	▨	30/52
pilN	HRM2_11000	27/50	▨	▨	28/53
PilM	HRM2_10990	22/41	▨	▨	33/57
pilD	HRM2_30410	34/50	33/49	34/49	36/57

Desulfobotulus sapovorans	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	BR04DRAFT_02178	▨	▨	▨	NA
pilW	BR04DRAFT_02177	▨	NA	▨	NA
pilX	BR04DRAFT_02176	▨	▨	▨	NA
pilY1	BR04DRAFT_02174	▨	NA	▨	▨
pilB	BR04DRAFT_02193	37/57	34/52	38/55	NA
pilT	BR04DRAFT_00210	53/72	▨	52/75	48/64
pilC	BR04DRAFT_02614	▨	▨	▨	▨
pilS	BR04DRAFT_01794	▨	▨	▨	▨
pilR	BR04DRAFT_01795	▨	▨	43/60	42/59
pilQ	BR04DRAFT_01789	▨	▨	▨	33/49
pilP	BR04DRAFT_01790	▨	▨	▨	▨
pilO	BR04DRAFT_01791	19/39	▨	▨	29/48
pilN	BR04DRAFT_01792	23/42	▨	▨	▨
pilM	BR04DRAFT_01793	21/43	▨	▨	40/60

Desulfobotulus alkaliphilus	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	LZ24DRAFT_01832	▨	▨	▨	NA
pilW	LZ24DRAFT_01831	▨	NA	▨	NA
pilX	LZ24DRAFT_01830	▨	▨	▨	NA
pilY1	LZ24DRAFT_01833	▨	NA	27/40	▨
pilB	LZ24DRAFT_00346	37/55	41/58	38/57	NA
pilT	LZ24DRAFT_01987	46/67	▨	49/69	44/63
pilC	LZ24DRAFT_00347	▨	27/48	25/53	28/53
pilS	LZ24DRAFT_01063	▨	▨	▨	▨
pilR	LZ24DRAFT_01064	▨	▨	41/61	41/58
pilQ	LZ24DRAFT_01057	35/54	▨	▨	34/51
pilP	LZ24DRAFT_01058	▨	▨	▨	▨
pilO	LZ24DRAFT_01059	19/38	▨	▨	26/46
pilN	LZ24DRAFT_01060	24/44	▨	▨	▨
pilM	LZ24DRAFT_01061	22/43	▨	▨	39/58
pilD	LZ24DRAFT_01979	38/55	33/52	37/56	40/60

Thauera linaloolentis	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	C666_05435	▨	▨	▨	NA
pilW	C666_05440	▨	NA	▨	NA
pilX	C666_05445	▨	▨	▨	NA
pilY1	C666_05450	▨	NA	34/48	▨
pilB	C666_04895	52/68	38/57	54/71	NA
pilT	C666_06340	72/84	▨	78/89	52/68
pilC	C666_04900	▨	29/51	54/74	40/62
pilS	C666_00260	▨	▨	34/49	28/46
pilR	C666_00255	▨	▨	58/71	39/56
pilQ	C666_15955	▨	▨	▨	▨
pilP	C666_08645	34/51	▨	▨	▨

pilO	C666_08640	32/54			31/53
pilN	C666_08635	31/53			
pilM	C666_08630	27/48			33/57
pilD	C666_04905				

Thauera terpenica	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	M622_01610			25/46	NA
pilW	M622_01605		NA		NA
pilX	M622_01600				NA
pilY1	M622_01595		NA		
pilB	M622_11740	54/71	44/62	54/71	45/65
pilT	M622_11340				
pilC	M622_11745		29/49	52/72	38/61
pilS	M622_13930			34/51	27/45
pilR	M622_13925			59/73	39/57
pilQ	M622_00030				
pilP	M622_00040	35/51			
pilO	M622_00045	29/51			31/56
pilN	M622_00050	32/51			
pilM	M622_00055	24/47			32/57
pilD	M622_11750	47/61	52/67	61/71	35/50

Thauera humireducens	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	WP_048709381.1				NA
pilW	WP_048709383.1		NA	23/37	NA
pilX	WP_048710599.1				NA
pilY1	WP_048709385.1		NA	31/43	
pilB	WP_048705994	52/69	39/57	54/71	47/67

pilT	WP_048706607.1	38/57	▨	42/60	44/65
pilC	WP_038011757.1	▨	29/51	54/73	41/62
pilS	WP_048706145.1	▨	▨	33/50	27/45
pilR	WP_048706143.1	▨	▨	▨	▨
pilQ	WP_048710322.1	36/54	▨	▨	33/51
pilP	WP_004253787.1	34/52	▨	▨	28/50
pilO	WP_038010918.1	32/52	▨	▨	29/53
pilN	WP_004253781.1	33/51	▨	▨	32/56
pilM	WP_004253778	25/47	▨	▨	34/55
pilD	WP_048705996.1	51/66	49/65	60/70	36/50

Flexistipes sinusarabici	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Flexsi_0849	▨	▨	▨	NA
pilW	Flexsi_0850	▨	NA	▨	NA
pilX	Flexsi_0851	▨	▨	▨	NA
pilY1	Flexsi_0847	▨	NA	▨	▨
pilB	Flexsi_1222	42/63	45/63	45/64	59/75
pilT	Flexsi_1221	51/68	▨	48/66	50/68
pilC	Flexsi_1220	▨	▨	40/63	46/65
pilS	Flexsi_1214	▨	▨	▨	▨
pilR	Flexsi_1215	▨	▨	36/57	31/54
pilQ	Flexsi_0514	▨	▨	▨	28/47
pilP	Flexsi_0513	▨	▨	▨	0
pilO	Flexsi_0512	21/46	▨	▨	22/50
pilN	Flexsi_0511	27/52	▨	▨	23/48
pilM	Flexsi_0510	22/43	▨	▨	33/55
no pilD					

Hippea maritima	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Hipma_1087	21/45	▨	▨	NA

pilW	Hipma_1086	▨	NA	▨	NA
no pilX					
pilY1	Hipma_1089	▨	NA	▨	▨
pilB	Hipma_0476	44/65	45/65	44/66	52/73
pilT	Hipma_0475	51/69	0	50/66	48/67
pilC	Hipma_0474	▨	29/51	36/62	41/64
no pilS					
no pilR					
pilQ	Hipma_1185	▨	▨	▨	28/47
pilP	Hipma_1186	▨	▨	▨	▨
pilO	Hipma_1187	23/41	▨	▨	▨
pilN	Hipma_1188	0	▨	▨	▨
pilM	Hipma_1189	20/40	▨	▨	29/50
pilD	Hipma_0610	33/52	31/49	30/50	42/61

Hippea alviniae	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	G415DRAFT_0791	24/43	▨	▨	NA
pilW	G415DRAFT_0790	▨	NA	▨	NA
no pilX					
pilY1	G415DRAFT_0793	▨	NA	▨	▨
pilB	G415DRAFT_0938	44/65	41/61	45/66	50/73
pilT	G415DRAFT_0937	51/67	▨	51/66	47/67
pilC	G415DRAFT_0936	▨	31/51	37/63	41/64
no pilS					
no pilR					
pilQ	G415DRAFT_0173	▨	▨	▨	33/52
pilP	G415DRAFT_0172	▨	▨	▨	▨
pilO	G415DRAFT_0171	25/40	▨	▨	▨
pilN	G415DRAFT_0170	▨	▨	▨	▨
pilM	G415DRAFT_0169	22/48	▨	▨	25/48
pilD	G415DRAFT_0998	33/52	31/52	38/55	36/58

Deferribacter desulfuricans	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	DEFDS_0860				NA
pilW	DEFDS_0859		NA		NA
pilX	DEFDS_0858				NA
pilY1	DEFDS_0862		NA		
pilB	DEFDS_1109	43/64	46/64	44/67	58/77
pilT	DEFDS_1110	51/68		52/68	52/69
pilC	DEFDS_1111		31/52	41/61	46/64
pilS	DEFDS_1112			24/48	23/46
pilR	DEFDS_1092			42/64	42/61
pilQ	DEFDS_1724	29/54			
pilP	DEFDS_1725				26/42
pilO	DEFDS_1726				
pilN	DEFDS_1727	24/45			
pilM	DEFDS_1728	25/46			32/55
pilD	DEFDS_0112	33/52	31/53	36/57	39/58

Desulfobacula toluolica	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	TOL2_21580				NA
pilW	TOL2_21570		NA		NA
pilX	TOL2_21590				NA
pilY1	TOL2_21600		NA		
pilB	TOL2_24450	39/61	42/60	40/60	44/63
pilT	TOL2_17060	46/64		39/58	47/68
pilC	TOL2_20070		29/50	40/62	56/71
pilS	TOL2_20060				35/57
pilR	TOL2_16940			37/61	37/57
pilQ	TOL2_05880	31/51			31/52
pilP	TOL2_05870				29/48
pilO	TOL2_05860	30/49			28/51

pilN	TOL2_05850	24/42			28/48
pilM	TOL2_05840	23/43			39/57
pilD	TOL2_13660	35/51	30/50	33/50	35/56

Desulfobacula phenolica	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Ga0066824_103426				NA
pilW	Ga0066824_103427		NA		NA
pilX	Ga0066824_103425				NA
pilY1	Ga0066824_103424		NA		
pilB	Ga0066824_103136	39/61	42/61	43/63	44/64
pilT	Ga0066824_102282	39/58	0	40/59	41/61
pilC	Ga0066824_11913		29/50	39/62	56/70
pilS	Ga0066824_102268				
pilR	Ga0066824_102269			39/58	43/62
pilQ	Ga0066824_102263				30/52
pilP	Ga0066824_102264				29/48
pilO	Ga0066824_102265	30/49			28/51
pilN	Ga0066824_102266	24/42			28/48
pilM	Ga0066824_102267	24/44			39/57
pilD	Ga0066824_101299	34/50	29/50	34/50	33/56

Geobacter uraniireducens	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Gura_1806				NA
pilW	Gura_1807		NA	27/39	NA
pilX	Gura_1808				NA
pilY1	Gura_1804		NA	23/34	
pilB	Gura_2682	43/64	44/64	45/64	65/83
pilT	Gura_2681	46/66		51/68	50/68
pilC	Gura_2680		29/50	41/63	60/75
pilS	Gura_1801				
pilR	Gura_1802			40/60	42/62

pilQ	Gura_1814	34/51			34/50
pilP	Gura_1813				25/48
pilO	Gura_1812	27/52			33/55
pilN	Gura_1811	28/41			
pilM	Gura_1810	25/45			49/70
pilD	Gura_1800	38/57	33/54	40/59	37/63

Geobacter lovleyi	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Glov_2153				NA
pilW	Glov_2152		NA		NA
pilX	Glov_2151			19/36	NA
pilY1	Glov_2155		NA	22/33	
pilB	Glov_1653	43/63	38/58	46/65	64/82
pilT	Glov_1654	48/66		52/69	48/68
pilC	Glov_1655		29/49	40/61	60/75
pilS	Glov_1656			27/43	34/52
pilR	Glov_1657			43/64	48/66
pilQ	Glov_1644	30/47			32/51
pilP	Glov_1643				
pilO	Glov_1642	22/47			35/56
pilN	Glov_1641				
pilM	Glov_1640	26/48			48/69
pilD	Glov_2160	40/53	32/52	38/53	41/60

Geobacter bemidjiensis	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Gbem_1542				NA
pilW	Gbem_1539		NA		NA
pilX	Gbem_1540				NA
pilY1	Gbem_1536		NA		
pilB	Gbem_2595	44/64	45/64	46/66	64/82

pilT	Gbem_2594	46/66		51/68	49/68
pilC	Gbem_2593		29/51	39/64	58/75
pilS	Gbem_2592			31/47	35/54
pilR	Gbem_2591			43/61	47/64
pilQ	Gbem_1550	33/51			36/52
pilP	Gbem_1549				
pilO	Gbem_1548	30/51			34/55
pilN	Gbem_1547	25/43			37/60
pilM	Gbem_1546	28/47			51/68
pilD	Gbem_1532	35/51	31/49	33/52	37/59

Geobacter daltonii	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Geob_3075				NA
pilW	Geob_3074		NA		NA
pilX	Geob_3073				NA
pilY1	Geob_3077		NA		
pilB	Geob_3374	43/65	38/58	46/65	65/83
pilT	Geob_3373	46/66		53/69	48/68
pilC	Geob_3372		29/51	40/64	59/75
pilS	Geob_3371			26/43	34/52
pilR	Geob_3370			43/61	49/67
pilQ	Geob_3066	33/50			32/51
pilP	Geob_3067	26/39			29/49
pilO	Geob_3068				33/56
pilN	Geob_3069	26/47			35/61
pilM	Geob_3070	25/46			51/70
pilD	Geob_3081	35/57	33/55	38/59	40/63

Geobacter sp. M21	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	GM21_2673				NA

pilW	GM21_2672		NA		NA
pilX	GM21_2671				NA
pilY1	GM21_2679		NA		
pilB	GM21_1631	43/63	45/64	46/65	64/82
pilT	GM21_1632	46/66	0	51/68	49/68
pilC	GM21_1633		29/51	39/64	59/75
pilS	GM21_1634			28/45	33/51
pilR	GM21_1635			42/61	47/65
pilQ	GM21_2665	33/51			33/49
pilP	GM21_2666				
pilO	GM21_2667	28/50			33/55
pilN	GM21_2668	27/45			35/58
pilM	GM21_2669	28/48			51/69
pilD	GM21_2684	36/52	32/50	34/52	37/58

Geobacter sp. M18	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	GM18_1373				NA
pilW	GM18_1374		NA		NA
pilX	GM18_1375				NA
pilY1	GM18_1371		NA		
pilB	GM18_2497	43/63	45/64	46/66	64/82
pilT	GM18_2496	46/67		51/68	49/68
pilC	GM18_2495		29/50	39/63	60/75
pilS	GM18_2494			28/45	34/53
pilR	GM18_2493			43/61	47/64
pilQ	GM18_1385	33/51			34/50
pilP	GM18_1384				
pilO	GM18_1383	30/50			31/51
pilN	GM18_1382	23/45			38/63
pilM	GM18_1381	26/46			50/71
pilD	GM18_1367	36/54	33/51	38/56	39/63

Geobacter bremensis	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	K419DRAFT_00175				NA
pilW	K419DRAFT_00174		NA		NA
pilX	K419DRAFT_00173			26/53	NA
pilY1	K419DRAFT_00177		NA		
pilB	K419DRAFT_00806	43/63	45/64	46/66	64/82
pilT	K419DRAFT_00805	46/66	0	51/68	49/68
pilC	K419DRAFT_00804		27/51	40/64	59/75
pilS	K419DRAFT_00803			28/46	32/50
pilR	K419DRAFT_00802			42/61	47/64
pilQ	K419DRAFT_00163	32/51			36/52
pilP	K419DRAFT_00164				
pilO	K419DRAFT_00165			28/49	33/54
pilN	K419DRAFT_00166	25/43			37/58
pilM	K419DRAFT_00167	28/48			51/69
pilD	K419DRAFT_00181	36/53	32/50	34/52	38/59

Desulfuromonas sp. TF	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	DTFDRAFT_03646				NA
pilW	DTFDRAFT_03645		NA		NA
pilX	DTFDRAFT_03644	23/33			NA
pilY1	DTFDRAFT_03643		NA	25/38	
pilB	DTFDRAFT_03635	41/63	43/62	46/66	65/83
pilT	DTFDRAFT_03634	46/63		53/69	49/67
pilC	DTFDRAFT_03633		30/52	43/65	62/77
pilS	DTFDRAFT_03632			28/46	34/55
pilR	DTFDRAFT_03631			44/64	49/66
pilQ	DTFDRAFT_03588	38/54			31/47
pilP	DTFDRAFT_03589	22/45			33/48

pilO	DTFDRAFT_03590	24/45	▨	▨	30/56
pilN	DTFDRAFT_03591	23/45	▨	▨	30/56
pilM	DTFDRAFT_03592	24/42	▨	▨	51/71
pilD	DTFDRAFT_03594	39/57	32/50	38/57	41/65

Pelobacter seleniigenes		% identity/sim to Neisseria gonnorhoae	% identity/sim toEscherichia coli	% identity/sim to Pseudomonas aeruginosa	% identity/sim to Myxococcus fulvus
pilV	N909DRAFT_0017	▨	▨	▨	NA
pilW	N909DRAFT_0018	▨	NA	▨	NA
pilX	N909DRAFT_0016	▨	▨	22/38	NA
pilY1	N909DRAFT_0014	▨	NA	▨	▨
pilB	N909DRAFT_0011	42/65	44/64	46/65	66/83
pilT	N909DRAFT_0010	47/65	▨	51/67	47/66
pilC	N909DRAFT_0009	▨	30/51	43/65	58/74
pilS	N909DRAFT_0008	▨	▨	28/46	33/51
pilR	N909DRAFT_0007	▨	▨	44/65	46/65
pilQ	N909DRAFT_4152	39/55	▨	▨	33/49
pilP	N909DRAFT_4151	24/42	▨	▨	29/46
pilO	N909DRAFT_4150	26/49	▨	▨	30/53
pilN	N909DRAFT_4149	28/45	▨	▨	34/56
pilM	N909DRAFT_4148	22/43	▨	▨	46/69
pilD	N909DRAFT_4146	38/54	36/55	37/54	41/63

Geobacter argillaceus	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Ga0052872_00762	▨	▨	▨	NA
pilW	Ga0052872_00761	▨	NA	▨	NA

no pilX					
pilY1	Ga0052872_00764		NA		
pilB	Ga0052872_02389	43/63	39/58	45/64	65/81
pilT	Ga0052872_02388	47/66		51/68	48/68
pilC	Ga0052872_02387		29/51	39/63	60/73
pilS	Ga0052872_02386			28/45	39/55
pilR	Ga0052872_02385			45/61	50/66
pilQ	Ga0052872_00754	35/53			35/54
pilP	Ga0052872_00755				27/48
pilO	Ga0052872_00756	26/50			33/54
pilN	Ga0052872_00757	27/44			38/58
pilM	Ga0052872_00758	25/43			51/70
pilD	Ga0052872_00767	37/55	34/53	39/56	41/59

Desulfuromusa kysingii	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Ga0056096_03279	21/43		29/51	NA
pilW	Ga0056096_03278	22/37	NA		NA
pilX	Ga0056096_03277				NA
pilY1	Ga0056096_03275		NA	31/46	
pilB	Ga0056096_03270	42/64	43/64	46/65	65/82
pilT	Ga0056096_03269	46/65		50/67	47/66
pilC	Ga0056096_03268		30/51	43/64	58/73
pilS	Ga0056096_03267			27/45	36/54
pilR	Ga0056096_03266			42/61	46/66
pilQ	Ga0056096_02727	32/48			33/49
pilP	Ga0056096_02726				29/48
pilO	Ga0056096_02725	23/47			35/55
pilN	Ga0056096_02724	28/47			32/57
pilM	Ga0056096_02723	22/43			47/68
pilD	Ga0056096_02721	40/57	33/52	39/58	42/65

Desulfuromonas thiophila	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Ga0056074_11723				NA
pilW	Ga0056074_11722		NA		NA
pilX	Ga0056074_11724	22/39			NA
pilY1	Ga0056074_11725		NA	32/46	
pilB	Ga0056074_104200	42/65	45/63	45/65	61/81
pilT	Ga0056074_104199	48/66		53/68	50/69
pilC	Ga0056074_104198		29/51	43/65	60/76
pilS	Ga0056074_104197			31/51	36/53
pilR	Ga0056074_104196			47/64	47/63
pilQ	Ga0056074_104188	31/48			33/47
pilP	Ga0056074_104189				29/44
pilO	Ga0056074_104190	23/48			34/59
pilN	Ga0056074_104191	23/47			31/61
pilM	Ga0056074_104192	22/45			43/66
pilD	Ga0056074_104193	35/56	34/56	40/58	41/63

Geobacter pickeringii	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Ga0069007_111121				NA
pilW	Ga0069007_111122	39/62	NA		NA
pilX	Ga0069007_111123				NA
pilY1	Ga0069007_111124		NA		
pilB	Ga0069007_111767	43/64	45/66	45/66	65/81
pilT	Ga0069007_111766	49/67		51/68	50/69
pilC	Ga0069007_111765		29/50	40/64	60/76
pilS	Ga0069007_111764			27/46	37/54
pilR	Ga0069007_111763			44/61	47/66
pilQ	Ga0069007_111133	34/51			34/51
pilP	Ga0069007_111132	23/39			
pilO	Ga0069007_111131	25/49			31/56

pilN	Ga0069007_111130	22/46	▨	▨	36/58
pilM	Ga0069007_111129	26/46	▨	▨	54/74
pilD	Ga0069007_111117	37/55	34/52	42/56	41/61

Geoalkalibacter ferrihydriticus	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	Ga0056053_00642	▨	▨	▨	NA
pilW	Ga0056053_00643	▨	NA	▨	NA
pilX	Ga0056053_00644	▨	▨	▨	NA
pilY1	Ga0056053_00645	▨	NA	▨	▨
pilB	Ga0056053_00652	42/64	43/62	44/64	64/82
pilT	Ga0056053_00653	48/65	▨	54/68	49/68
pilC	Ga0056053_00654	▨	30/50	42/64	62/76
pilS	Ga0056053_00655	▨	▨	27/46	36/54
pilR	Ga0056053_00656	▨	▨	44/64	48/64
pilQ	Ga0056053_00669	37/54	▨	▨	36/52
pilP	Ga0056053_00668	25/40	▨	▨	38/51
pilO	Ga0056053_00667	25/47	▨	▨	34/56
pilN	Ga0056053_00666	23/45	▨	▨	36/63
pilM	Ga0056053_00665	22/43	▨	▨	50/70
pilD	Ga0056053_00664	41/56	33/52	37/55	42/63

Geopsychrobacter electrodiphilus	Locus ID	% iden/sim N. gonorrhoeae	% iden/sim E. coli	% iden/sim P. aeruginosa	% iden/sim M. fulvus
pilV	D888DRAFT_0269	▨	▨	▨	NA
pilW	D888DRAFT_0270	▨	NA	▨	NA
pilX	D888DRAFT_0271	▨	▨	▨	NA
pilY1	D888DRAFT_0272	▨	NA	▨	▨
pilB	D888DRAFT_2047	41/63	43/64	43/65	67/84
pilT	D888DRAFT_2046	49/66	▨	50/67	47/66
pilC	D888DRAFT_2045	▨	29/49	42/64	58/74
pilS	D888DRAFT_2044	▨	▨	27/48	33/52

pilR	D888DRAFT_2043			44/63	48/65
pilQ	D888DRAFT_2018	36/51			33/48
pilP	D888DRAFT_2019				31/50
pilO	D888DRAFT_2020	26/50			32/56
pilN	D888DRAFT_2021	29/47			34/56
pilM	D888DRAFT_2022	23/43			46/67
pilD	D888DRAFT_2024	40/53	34/53	37/56	41/62