

Figure S1. Intergenic sequences between *flhC* and *motA* for 99 proteobacterial species.

Species where Asp178 of FlhC is conserved

>D319_RS0112640|Arsenophonus_endosymbiont_of_Nilaparvata_lugens_GCF_000757905.1_ASM75790v1|D319_RS0112640 D319_RS0112640; downstream from 1 to 124; size: 124; feature type:gene; location: Arsenophonus_endosymbiont_of_Nilaparvata_lugens_GCF_000757905.1_ASM75790v1:NZ_JRLH01000021.1:5968:6091:R; downstream neighbour: D319_RS0112635 (distance: 124)
TGGAGCAACTGAGCTTATAAAATAGAGAATTATGGTTTAGGTTTACCATAGCTCTCTTAT
AGGTCGGTATGTTAGCTTTGAATACGGATCTCTAGTTCATCATTATCAATAAAGGGAATA
TCAG

>EH105704_RS01935|Atlantibacter_hermannii_GCF_000248015.1_ASM24801v2|EH105704_RS01935 EH105704_RS01935; downstream from 1 to 124; size: 124; feature type:gene; location: Atlantibacter_hermannii_GCF_000248015.1_ASM24801v2:NZ_BAFF01000001.1:350450:350573:R; downstream neighbour: EH105704_RS01930 (distance: 124)
GCTTCAGATGTGGTGAAACACTCCAGCAGCGCCAGGTTTCCTGTCGCTGCTTTTTTTTCG
CCCTCCGTCGCTGAGCCCTTCGCTTGCCAATCCTTGTCCCAGCCAACAGCGGAAGGAAGA
TGTC

>BWI17_RS17980|Betaproteobacteria_bacterium_GR16-43_GCF_001953215.1_ASM195321v1|BWI17_RS17980 BWI17_RS17980; downstream from 1 to 308; size: 308; feature type:gene; location: Betaproteobacteria_bacterium_GR16-43_GCF_001953215.1_ASM195321v1:NZ_CP019169.1:3859807:3860114:R; downstream neighbour: BWI17_RS17975 (distance: 308)
GGGTTTGTCAAAAAGCATTGAACCGCAGAGGCCCGGAGGCCCGGAGAAAAGCCTGTTT
GGCTGGATGCTCTTCTTGGCGGTGATGACAGCAGAACGGGAATGCCACTGACCAGATCGG
CTCTTGACGGGTTTGGCTTTTCTCCGGGCTCAGGGGCTCTGCGGTTCAATGCCTTTT
GCATGCCCTTCCCGATCCCTAAAGAAACCCCGTTCCAAGCCGTAATTCCTTCGGGAACG
GGCGTCATGGGACGCTCGACGGTTCGCGCCTCACCGGCAACGGCGGGGATGACGAGAGGG
AAGATTTCG

>BN1221_RS21630|Brenneria_goodwinii_GCF_001049335.1_B_goodwinii_PB|BN1221_RS21630 BN1221_RS21630; downstream from 1 to 135; size: 135; feature type:gene; location: Brenneria_goodwinii_GCF_001049335.1_B_goodwinii_PB:NZ_CGIG01000001.1:4973401:4973535:R; downstream neighbour: BN1221_RS21625 (distance: 135)
GCTTGGTAGCGATTTGTGAATCTATCACTGTTTGTATTGAGGGCAGTGATAGATTTCTC
CTCAAGTAATTCCTGGCTTTATAACCGCTGCGTTTTTATCTAATCTTCCGCTACCTTTTT
TTATAAGGAATTCTT

>GBAG_RS11615|Buttiauxella_agrestis_GCF_000735355.1_GBAG_DRAFTv1|GBAG_RS11615 GBAG_RS11615; downstream from 1 to 127; size: 127; feature type:gene; location: Buttiauxella_agrestis_GCF_000735355.1_GBAG_DRAFTv1:NZ_JMPI01000030.1:288406:288532:R; downstream neighbour: GBAG_RS11610 (distance: 127)
CAGTTCGGTGTGGTAAACACTCCAGCAGCGATAAGCCATTATCGCTGCTTTTTTTTGCCC
CGCATCTGACTGTTTTTCCCTTTGATTTGTGATTCTCGTCACATTTAACAGCAGAAGGA
TGTACTION

>HMPREF0201_RS12215|Cedecea_davisae_GCF_000412335.2_ASM41233v2|HMPREF0201_RS12215 HMPREF0201_RS12215; downstream from 1 to 126; size: 126; feature type:gene;

location:

Cedecea_davisae_GCF_000412335.2_ASM41233v2:NZ_KE161030.1:2687632:2687757:R;
downstream neighbour: HMPREF0201_RS12210 (distance: 126)
CAGATTCTGTGTTTGGAGCATTCCAGCAGCGGTGAGTGATTGCCGCTGCTTTTTTTATGCC
CGCACATAACGCTGCTTCTGCCTTCTGGGCATCCTCGCTACACTCAACGGCGTAAGGAT
GATCTC

>Z042_RS18555|Chania_multitudinisentens_GCF_000520015.2_ASM52001v2|Z042_RS18555
Z042_RS18555; downstream from 1 to 156; size: 156; feature type:gene;

location:

Chania_multitudinisentens_GCF_000520015.2_ASM52001v2:NZ_CP007044.2:4182972:418312
7:R; downstream neighbour: Z042_RS18550 (distance: 156)
GTCTGCAATAAGGCCGATTCACTACAGCTAAACCAGATAAGTGAAACGCAGAGGCTCAAC
TTATCGAGTCTAGGGCGTGGCTTGAGCTGTGTATCTGTCATTTCATCCGAACCGATGATCC
CACGTCCACCTCACCTTGTGCATTTAAGGAACACGC

>DQ02_RS06235|Citrobacter_amalonaticus_GCF_000731055.1_ASM73105v1|DQ02_RS06235
DQ02_RS06235; downstream from 1 to 125; size: 125; feature type:gene;

location:

Citrobacter_amalonaticus_GCF_000731055.1_ASM73105v1:NZ_JMQQ01000013.1:102527:1026
51:R; downstream neighbour: DQ02_RS06230 (distance: 125)
CCGATACGGTGTGGACGAAACACTCCAGCAGCGGTAAGTCATTACCGCTGCTTTTTTTTGG
CCTCGCCAACGCGTTAACGCCCCGACTGCACATCCTGTCATAGTCAACAGCAGAAGGATG
ATGTC

>M983_RS02530|Cosenzaea_myxofaciens_GCF_001654855.1_Cmy19692_DRAFTv1|M983_RS02530
M983_RS02530; downstream from 1 to 133; size: 133; feature type:gene;

location:

Cosenzaea_myxofaciens_GCF_001654855.1_Cmy19692_DRAFTv1:NZ_LXEN01000019.1:53346:53
478:R; downstream neighbour: M983_RS02525 (distance: 133)
TTCGAGATTGAAAGTTAACTATCAGGTTATAGAAATCAGTTATCTATAACCTGAGTCACT
CCTCTTACCCTCCTATCCTTTGCTGCTATGTTAGCCATTCTATCTATAACGAAATTAGCT
AAAGGGATATCGC

>BN137_RS04585|Cronobacter_condimenti_GCF_000319285.1_ASM31928v1|BN137_RS04585
BN137_RS04585; downstream from 1 to 130; size: 130; feature type:gene;

location:

Cronobacter_condimenti_GCF_000319285.1_ASM31928v1:NZ_CAKW01000118.1:57549:57678:R
; downstream neighbour: BN137_RS04590 (distance: 130)
CCGGATAGGTGTGGAAAACCACTCCAGCAGCGGCCAAAAGGCCGCTGCTTTTTTTTCTCCT
AACTTAAACCGCAACGTTTTCTGCTTACCTGAACGTCCTCGCCATAGCCAACAGCGGAA
GGATGATGTC

>DCH516_RS07695|Dickeya_chrysanthemi_GCF_000406065.1_DCH516_1.0|DCH516_RS07695
DCH516_RS07695; downstream from 1 to 133; size: 133; feature type:gene;

location:

Dickeya_chrysanthemi_GCF_000406065.1_DCH516_1.0:NZ_CM001904.1:1648499:1648631:D;
downstream neighbour: DCH516_RS07700 (distance: 133)
GCCTGATGGCGATTTTGTGGTTCTGTCATCGCGGTTTCATTGCTCGATGGCAGTATTCCC
TCCAAATAAGTCGTTGGTAAGACTGCATTTATAACCCTCTCCGCTACCCTTTTACTATCT
ATAAGGAATTCTT

>ETEE_RS15000|Edwardsiella_anguillarum_GCF_000264765.2_ASM26476v2|ETEE_RS15000
ETEE_RS15000; downstream from 1 to 153; size: 153; feature type:gene;

location:

Edwardsiella_anguillarum_GCF_000264765.2_ASM26476v2:NZ_CP006664.1:3331772:3331924
:D; downstream neighbour: ETEE_RS15005 (distance: 153)

CTGATTGAGGCAATCAGTCCAATAGCGTGCGGTGCAGCGGTAGTGCTGCCGCACGCTGTC
TTCGGGCAGCATTCTGTCATCGACCTTCTTCCGGCTTTGCGCCGGCAGATTACATC
CGACTGTTCACTCCGATCATGTAAGGAATTCAC

>ENTAS_RS13140|Enterobacter_asburiae_GCF_000224675.1_ASM22467v1|ENTAS_RS13140
ENTAS_RS13140; downstream from 1 to 123; size: 123; feature type:gene;
location:
Enterobacter_asburiae_GCF_000224675.1_ASM22467v1:NC_015968.1:2802771:2802893:R;
downstream neighbour: ENTAS_RS13135 (distance: 123)
CCCGAACGTGTGGCAAGATTCCAGCAGCGGTAAGAAATTACCGCTGCTTTTTTTTACCC
CGCATTCCGGTCACACACTCGAAATGAACGTCTCCTGCCTTAGTCACTAGCGGAAGGATGAT
GTC

>HMPREF0864_RS15025|Enterobacteriaceae_bacterium_9_2_54FAA_GCF_000185685.2_Entebact_9_2_54FAA_V2|HMPREF0864_RS15025 HMPREF0864_RS15025; downstream from 1 to 184; size: 184; feature type:gene; location:
Enterobacteriaceae_bacterium_9_2_54FAA_GCF_000185685.2_Entebact_9_2_54FAA_V2:NZ_ADCU02000001.1:3344735:3344918:R; downstream neighbour: HMPREF0864_RS15020 (distance: 184)
CCTGATTGAGGCAATCAGTCTTATAGGTTGGCGATCGGTGGTGTGGCTTTAAACGATGTT
ATCAGGTCAACCCACCGGTTATCTTCTTTTCGAGCCGTCATCCGACGGCCTCTGAATTCT
CCTTCTCCGTCTCCCGGACAGCGGTTACACCCAATTTCCATTTTGAGCATTAAAGGAAT
TCGC

>EAM_RS09805|Erwinia_amylovora_GCF_000027205.1_ASM2720v1|EAM_RS09805
EAM_RS09805; downstream from 1 to 134; size: 134; feature type:gene;
location:
Erwinia_amylovora_GCF_000027205.1_ASM2720v1:NC_013971.1:2181823:2181956:R;
downstream neighbour: EAM_RS09800 (distance: 134)
TCGCGTCTGCCACACGGAGTGAATCCAGCAGCGGTCTTTGACCGCTGCTTTTTTTTGCCC
CGTGACTGGCGCACAGATCTGCCTGACTTCTGGCTCTCCTCTCACCCACACGTTTTGCGAG
CGTAAGGATTTATC

>ESCAB7627_RS21600|Escherichia_albertii_GCF_000155105.1_ASM15510v1|ESCAB7627_RS21600 ESCAB7627_RS21600; downstream from 1 to 125; size: 125; feature type:gene;
location:
Escherichia_albertii_GCF_000155105.1_ASM15510v1:NZ_CH991859.1:4351003:4351127:R;
downstream neighbour: ESCAB7627_RS21595 (distance: 125)
CGGAAATGGTGTGGCTAAATATCCCAGCAGCGGTAAGCCATTATCGCTGCTTTTTTTTGCCC
CTGACCGTGGGTAAACAACCTGGCAACTGAACATCCTGTTCATGGTCAACAGTGAAGGATG
ATGTC

>GEAM_RS07005|Ewingella_americana_GCF_000735345.1_GEAM_DRAFTv1|GEAM_RS07005
GEAM_RS07005; downstream from 1 to 194; size: 194; feature type:gene;
location:
Ewingella_americana_GCF_000735345.1_GEAM_DRAFTv1:NZ_JMPJ01000039.1:40187:40380:D;
downstream neighbour: GEAM_RS07010 (distance: 194)
GATGATGTGGGCAGCATAGTGCAGAAAGGTCACGTGATGCTAAAGAGTGGTGAAATGCCAC
TCTTTACAATCCCTCCCAACATCCCAATAGTTTTGGTTGTCGGCTGACAAGACAAAAC
CTCAATTCTCTCTTCAAGCGGCTTCTTCTGGTCTGGCCTATACCCAAAAGCCACATCGA
ATTAAGGAATCATC

>DW56_RS01685|Franconibacter_helveticus_GCF_000463115.2_CroHelLMG23732_1.0|DW56_RS01685 DW56_RS01685; downstream from 1 to 126; size: 126; feature type:gene;
location:
Franconibacter_helveticus_GCF_000463115.2_CroHelLMG23732_1.0:NZ_AWFX01000005.1:103313:103438:R; downstream neighbour: DW56_RS01680 (distance: 126)

CCGGTTCGGTGTGGAACTCACTCCAGCAGCGGCGATTTTCGCCGCTGCTTTTTTTATTCCC
TCCGTTCCGCTAAACGTCTCTCCATCTGCGCATCCTCACTTTTCGTCAACAGCAGAAGGAT
GATGTC

>HMPREF0454_RS07080|Hafnia_alvei_GCF_000239255.1_ASM23925v1|HMPREF0454_RS07080
HMPREF0454_RS07080; downstream from 1 to 184; size: 184; feature type:gene;
location: Hafnia_alvei_GCF_000239255.1_ASM23925v1:NZ_JH417506.1:42161:42344:D;
downstream neighbour: HMPREF0454_RS07085 (distance: 184)
CCTGATTGAGGCAATCAGTCTTATAGGTTGGCGATCGGTGGTGTGGCTTTAAACGATGTT
ATCAGGTCAACCCACCGGTTATCTTCCTTTTCGAGCCGTCATCCGACGGCCTCTGAATTCT
CCTTCTCCGTCTCCCGGACAGCGGTTACACCCAATTTCCATTCTGAGCATTAAAGGAAT
TCGC

>EAE_15510|Klebsiella_aerogenes_GCF_000215745.1_ASM21574v1|EAE_15510 EAE_15510;
downstream from 1 to 141; size: 141; feature type:gene; location:
Klebsiella_aerogenes_GCF_000215745.1_ASM21574v1:NC_015663.1:3353723:3353863:D;
downstream neighbour: EAE_15515 (distance: 141)
GTCGCCGTTCCGACGACTTACGGCAATCCATTTTCGACGTGTAATACGCAGGGGGCGGTATG
CCGCCCCCATTCCCCGCCTGGTTTACGCCAGGGCGCGTTTGCTCGCCCGCCATCCACA
TTGTTAATTTGAGGTATGCGT

>GKAS_RS21160|Kluyvera_ascorbata_GCF_000735365.1_GKAS_DRAFTv1|GKAS_RS21160
GKAS_RS21160; downstream from 1 to 122; size: 122; feature type:gene;
location:
Kluyvera_ascorbata_GCF_000735365.1_GKAS_DRAFTv1:NZ_JMPL01000147.1:973:1094:R;
downstream neighbour: GKAS_RS21155 (distance: 122)
CCCACACGGTGTGGATAAAACACTCCAGCAGCGGTCTTGATGATCGCTGCTTTTTTTTAC
CCGTCGGTTAGTGATTTTGCTCATCTGTCTCCACTCATGGTCAACGGTGGAAGGATGATT
AC

>BWI95_RS19280|Kosakonia_cowanii_GCF_001975225.1_ASM197522v1|BWI95_RS19280
BWI95_RS19280; downstream from 1 to 127; size: 127; feature type:gene;
location:
Kosakonia_cowanii_GCF_001975225.1_ASM197522v1:NZ_CP019445.1:4063376:4063502:R;
downstream neighbour: BWI95_RS19275 (distance: 127)
CCGAATCAGGTGGAATCAAACCTCCAGCAGCGGTGCTTTAATGCCGCTGCTTTTTTTTGC
CCGCCATTTCGTGAAAACCCTCCGAAATGTTTCTCTTAAGCCTTAGTCATTAGCAGAAGGA
TGATGTC

>GLAD_RS19555|Leclercia_adecarboxylata_GCF_000735515.1_GLAD_DRAFTv1|GLAD_RS19555
GLAD_RS19555; downstream from 1 to 123; size: 123; feature type:gene;
location:
Leclercia_adecarboxylata_GCF_000735515.1_GLAD_DRAFTv1:NZ_JMPM01000048.1:86442:865
64:R; downstream neighbour: GLAD_RS19560 (distance: 123)
CCCGAACGTACGGGCAAGACTCCAGCAGCGGTAAAGCAATTACCGCTGCTTTTTTTTGCCC
CGCGGTCAGGTAAACCCTCGACCTGTGTCTCCTGGCTAAAGTCACTAGCGGAAGGATGAT
GTC

>AF34_RS03465|Lelliottia_amnigena_GCF_000694955.1_Lell_amni_CHS_78_V1|AF34_RS0346
5 AF34_RS03465; downstream from 1 to 123; size: 123; feature type:gene;
location:
Lelliottia_amnigena_GCF_000694955.1_Lell_amni_CHS_78_V1:NZ_KK737781.1:100257:1003
79:D; downstream neighbour: AF34_RS03460 (distance: 123)
CCCGAACCTGTGGCAAGATTCCAGCAGCGGTAAAGCGATTACCGCTGCTTTTTTTTACCC
TGCGTTCAGGTCACGCGCTCGAAATGAACGTCTGCCATAGTCACTAGCGGAAGGATGAT
GTC

>RZ35_RS09155|Lonsdalea_quercina_GCF_000688655.1_LonsB104|RZ35_RS09155
RZ35_RS09155; downstream from 1 to 133; size: 133; feature type:gene;
location:
Lonsdalea_quercina_GCF_000688655.1_LonsB104:NZ_JIBO01000008.1:49956:50088:R;
downstream neighbour: RZ35_RS09150 (distance: 133)
GCTTGGTAGCGCTAGTGAACCTGCCATTGAGCATTGTAGGCATAATGGCAGGGCTCTTTC
CTTCTGAAGTCGTACGCGATAAGACTGCGTTTTAACCTCACTCCACTACCCCTTGTTACT
ATAAGGAATGCTT

>A9B99_RS02380|Mangrovibacter_phragmitis_GCF_001655675.1_ASM165567v1|A9B99_RS02380
A9B99_RS02380; downstream from 1 to 116; size: 116; feature type:gene;
location:
Mangrovibacter_phragmitis_GCF_001655675.1_ASM165567v1:NZ_LYRP01000001.1:530272:53
0387:R; downstream neighbour: A9B99_RS02375 (distance: 116)
CGTAACAGGCTCGTAAATCCAGCAGCGGACACGAAAGTGCCGCTGCTTTTTTTTACCCTG
AATGCAACGTAACCTACTGTTATCCTTGACTTTTAACACAGCGGAAAGGTGATGTC

>VK86_RS10545|Moellerella_wisconsensis_GCF_001020485.1_ASM102048v1|VK86_RS10545
VK86_RS10545; downstream from 1 to 79; size: 79; feature type:gene;
location:
Moellerella_wisconsensis_GCF_001020485.1_ASM102048v1:NZ_LDOF01000056.1:954:1032:D
; downstream neighbour: VK86_RS10550 (distance: 79)
AAAGACAATGTACAGGAATGATGAGCATTCCCGATAATTCAGGCCTATCCCGTCATTTAT
GTTTTATAAGGAATGTCAT

>MU9_RS09095|Morganella_morganii_GCF_000286435.2_ASM28643v2|MU9_RS09095
MU9_RS09095; downstream from 1 to 99; size: 99; feature type:gene; location:
Morganella_morganii_GCF_000286435.2_ASM28643v2:NC_020418.1:1988559:1988657:D;
downstream neighbour: MU9_RS09100 (distance: 99)
CTGGATTGATTTGGTAAACAGGCAAATCCGTTTTGCCTGTCCTTCCTGAAAATTCCTTT
GACTGCCATCCGATACCTAACTGAGTTAAAGGGAATAGT

>BQ7994_RS09700|Nissabacter_archeti_GCF_900130115.1_PRJEB18266|BQ7994_RS09700
BQ7994_RS09700; downstream from 1 to 156; size: 156; feature type:gene;
location:
Nissabacter_archeti_GCF_900130115.1_PRJEB18266:NZ_FQXW01000005.1:165987:166142:D;
downstream neighbour: BQ7994_RS09705 (distance: 156)
GCGGAATAACGGCAACCTACTGAATTGGGGCCGGCAACAGGCCGCCCCGTTTCAGCAAGC
ACCACCCCCCGATGTTCCGTGTCCGTGGCGTACGCCCGGCCTCTCCCGCTGTGCGCAAC
ACCCCGCCTTTCCAACCACTTTATTAAGGAATCATC

>DSM2777_RS09155|Obesumbacterium_proteus_GCF_001586165.1_ASM158616v1|DSM2777_RS09155
DSM2777_RS09155; downstream from 1 to 186; size: 186; feature type:gene;
location:
Obesumbacterium_proteus_GCF_001586165.1_ASM158616v1:NZ_CP014608.1:1964591:1964776
:D; downstream neighbour: DSM2777_RS09160 (distance: 186)
CTTGATTGAGGCAATCAGTCTTATAGGTGCGGATCGGTGGAGTAGCAAGAGCAACGATG
TTGTTTAGCTAAACCACCGGTTAACTTCCTTTTCGAGCCGTCATCTGACGGCTTCTGAATT
CTCCTTCTCCGTCTCCTGGACAGCGGTTACACCAATTTCCATTCTAAGCATTAAAGGA
ATTGCG

>XM39_RS08495|Pandoraea_apista_GCF_001010785.1_ASM101078v1|XM39_RS08495
XM39_RS08495; downstream from 1 to 116; size: 116; feature type:gene;
location:
Pandoraea_apista_GCF_001010785.1_ASM101078v1:NZ_CP011279.1:1890053:1890168:R;
downstream neighbour: XM39_RS08490 (distance: 116)
ACGAGCCCACTTACGAGGTCGCACCCCTACAGTTTCCCTGCGTGTCTGCCGTTAAGCC

CTCTGAACAGGAAGGACATTTTTCCGTAGACGTATTTTTGCGAGAGGTATCCGGCA

>PAGG_RS08965|*Pantoea agglomerans*_GCF_000241285.1_ASM24128v2|PAGG_RS08965
PAGG_RS08965; downstream from 1 to 133; size: 133; feature type:gene;
location:

*Pantoea agglomerans*_GCF_000241285.1_ASM24128v2:NZ_BAEF01000003.1:125112:125244:R;
downstream neighbour: PAGG_RS08960 (distance: 133)
GTTTGTTCGCACTGTGGAAGCCATCCAGCAGCGGTTAATACCGCTGCTTTTTTTTTGCTT
GCGGTTTCAGGAATAACATCTGCGGCTCTCTGGCTTAACTTCCACCAACACGTTACGGACG
TAAGGATTTTTTT

>ECA_RS08345|*Pectobacterium atrosepticum*_GCF_000011605.1_ASM1160v1|ECA_RS08345
ECA_RS08345; downstream from 1 to 134; size: 134; feature type:gene;
location:

*Pectobacterium atrosepticum*_GCF_000011605.1_ASM1160v1:NC_004547.2:1935303:1935436
:D; downstream neighbour: ECA_RS08350 (distance: 134)
GCCTGTAGCGATTTGTGAATCTATCACTGTTGGTTGTGACGGCGGTGATAGATTTCTTCC
TCAAGAACGTCTGGCTACGGCTCCGCAGTTTTATCTCGCTTCCCGCCCACCTTTTTTAT
TATAAGGATTTCTT

>PAU_RS13035|*Photorhabdus asymbiotica*_GCF_000196475.1_ASM19647v1|PAU_RS13035
PAU_RS13035; downstream from 1 to 137; size: 137; feature type:gene;
location:

*Photorhabdus asymbiotica*_GCF_000196475.1_ASM19647v1:NC_012962.1:3095506:3095642:R
; downstream neighbour: PAU_RS13030 (distance: 137)
ATTTAAATGGGAATTTGTTCTACAGGTTACGGACTTATATTTTTCTTCCTGTAACCTGT
ATTGAAATTGCCGCATTCTGAATTCTCAAACCTGTTCAACTTCCCATCCGCTCACCACT
TAGCTAAAGGATATCGC

>EO5_RS04655|*Plautia stali*_symbiont_GCF_000180175.2_ASM18017v2|EO5_RS04655
EO5_RS04655; downstream from 1 to 131; size: 131; feature type:gene;
location:

*Plautia stali*_symbiont_GCF_000180175.2_ASM18017v2:NC_022546.1:963125:963255:D;
downstream neighbour: EO5_RS04660 (distance: 131)
GTTTGTTCGCATCGTGAAACATCCAGCAGCGGTTAATACCGCTGCTTTTTTTTTTGCCC
ACACCCTGCGAATAACACCTACGGCTCTCTGGCTTAACTTCCACCAAACGTTACGGACGT
AAGATGTTTTT

>LG71_RS14010|*Pluralibacter gergoviae*_GCF_000757785.1_ASM75778v1|LG71_RS14010
LG71_RS14010; downstream from 1 to 116; size: 116; feature type:gene;
location:

*Pluralibacter gergoviae*_GCF_000757785.1_ASM75778v1:NZ_CP009450.1:3027309:3027424:
D; downstream neighbour: LG71_RS14015 (distance: 116)
CCTCCTCTCAGGTGCGGCAAACACCCGGCAGCGGACTTCGGTCCGCTGTTTTTTTTGCCCC
CTAAACCGCGCGCCGCTGCTTCATCCCTGGCTTTTTAACAGCGGAAGGATGATGTC

>K151_RS05905|*Proteus hauseri*_GCF_000497855.1_version_3_of_Proteus_hauseri_genome
|K151_RS05905 K151_RS05905; downstream from 1 to 134; size: 134; feature
type:gene; location:

*Proteus hauseri*_GCF_000497855.1_version_3_of_Proteus_hauseri_genome:NZ_AWXP010000
08.1:488320:488453:D; downstream neighbour: K151_RS05910 (distance: 134)
TTCGAGATTGAAAGTTAAATATCAGGTTATAGAGCTGAGTTATCTATAACCTGAACCGTT
TCCTCTCCCCCTCCTATCTCTTGCTGCTATGTTCCGCAATTCTCTCCATAACGAAATTAGC
TAAAGGGATATCGC

>PROVALCAL_RS02420|*Providencia alcalifaciens*_GCF_000173415.1_ASM17341v1|PROVALCAL
_RS02420 PROVALCAL_RS02420; downstream from 1 to 96; size: 96; feature

type:gene; location:

Providencia_alcalifaciens_GCF_000173415.1_ASM17341v1:NZ_ABXW01000007.1:19444:19539:D; downstream neighbour: PROVALCAL_RS02425 (distance: 96)
TTGGATTAATTTGGTTAACAGGCAAGTAGATTGCCCTGTCCTTCCTCATATTCCCTTTGAC
TGCCATCTGTAACTAACGGAGTGAAAGGGAATACT

>H597_RS0122850|Pseudoduganella_violaceinigra_GCF_000425385.1_ASM42538v1|H597_RS0122850 H597_RS0122850; downstream from 1 to 0; size: 0; feature type:gene; location:

Pseudoduganella_violaceinigra_GCF_000425385.1_ASM42538v1:NZ_KE384358.1:95444:95443:R; downstream neighbour: H597_RS0122845 (distance: 0)

>RAHAQ2_RS08910|Rahnella_aquatilis_GCF_000241955.1_ASM24195v1|RAHAQ2_RS08910 RAHAQ2_RS08910; downstream from 1 to 176; size: 176; feature type:gene; location:

Rahnella_aquatilis_GCF_000241955.1_ASM24195v1:NC_016818.1:1950707:1950882:D; downstream neighbour: RAHAQ2_RS08915 (distance: 176)
GATAGTTGGGTTGCAGTAAGTCGTTCTGAGCGGTGGTGACCACCGCTCATCAATTTCCCC
CCAGACATCTCAGTCATTCTCTGACACTTTCTATGCCGTTTCTGCGGCAAAAATGGGTCA
GGTACATGGCGCGCTTTACCTCGCCCTAAAACCACATCGAATTAAGGATTCATC

>SBG_RS09065|Salmonella_bongori_GCF_000252995.1_ASM25299v1|SBG_RS09065 SBG_RS09065; downstream from 1 to 124; size: 124; feature type:gene; location:

Salmonella_bongori_GCF_000252995.1_ASM25299v1:NC_015761.1:1923244:1923367:R; downstream neighbour: SBG_RS09060 (distance: 124)
CCGAAACGGTGTGGACAAACACTCCAGCAGCGGTAAGTCATTACCGCTGCTTTTTTTTGC
CTTACCATCGCGTTAATTGCCCGACTGCGCATCCTGTCATAGTCAACAGCGGAAGGATGA
TGTC

>SFI01_RS01355|Serratia_ficaria_GCF_001590885.1_ASM159088v1|SFI01_RS01355 SFI01_RS01355; downstream from 1 to 159; size: 159; feature type:gene; location:

Serratia_ficaria_GCF_001590885.1_ASM159088v1:NZ_BCTS01000002.1:258593:258751:R; downstream neighbour: SFI01_RS01350 (distance: 159)
GCCCCGAACATTGCCGTTCTCGGCAGTGAAAACAGACGTGTGATACGCAAGTGGGCGGC
CATGCCGCCCGTCGACGCAGCCCAATTTGCTGCGCCCGCGGTGCCATGGCGCGTTTG
CCCCACCTCCATCCACATTGTTAATTTAAGGAATGCGT

>SBO_RS06185|Shigella_boydii_GCF_000012025.1_ASM1202v1|SBO_RS06185 SBO_RS06185; downstream from 1 to 137; size: 137; feature type:gene; location:

Shigella_boydii_GCF_000012025.1_ASM1202v1:NC_007613.1:1120416:1120552:D; downstream neighbour: SBO_RS06190 (distance: 137)
CTGATACGGTGTGGCGCAACATGCCAGCAGCGGTAACGACGTACCGCTGCTTTTTTTTGC
CCCAATCGCGCGTTAACGCCTGACGACTGAACATCCTGTCATGGTCAACAGTGAAGGAT
GATGTCGTGCTTATCTT

>ET34_RS0108445|Siccibacter_colletis_GCF_000696575.1_C_colletis_1383|ET34_RS0108445 ET34_RS0108445; downstream from 1 to 127; size: 127; feature type:gene; location:

Siccibacter_colletis_GCF_000696575.1_C_colletis_1383:NZ_JMSQ01000006.1:590593:590719:D; downstream neighbour: ET34_RS0108450 (distance: 127)
CAGTTCGGTGTGGTGAACACTCCAGCAGCGGTAAGCAATTACCGCTGCTTTTTTTTACCC
CAACGAACCCCATAAACGGGCGTCACCTGCAACTCCTCAATGTATTCAACAGCGTAAGGA
TGATGTC

>SGP1_RS19025|Sodalis_glossinidius_GCF_000010085.1_ASM1008v1|SGP1_RS19025
SGP1_RS19025; downstream from 1 to 114; size: 114; feature type:gene;
location:
Sodalis_glossinidius_GCF_000010085.1_ASM1008v1:NC_007712.1:3570991:3571104:R;
downstream neighbour: SGP1_RS19020 (distance: 114)
CCGCCTGCGGCAGCTGGGTGTCTGCCGCCACGCCGCCACGGAGAAGAAGGGGGTAGCTAA
GGGTGCCAGCCGGTTCGCTTTTGCCTGCCTGCTCTTCGCTGAAGGAGCGCTATC

>HA49_RS05315|Tatumella_morbirosei_GCF_000757425.2_Tmorbiroseiasssem5|HA49_RS05315
HA49_RS05315; downstream from 1 to 117; size: 117; feature type:gene;
location:
Tatumella_morbirosei_GCF_000757425.2_Tmorbiroseiasssem5:NZ_JPKR02000003.1:529742:5
29858:R; downstream neighbour: HA49_RS05310 (distance: 117)
GTAGTGTTAAATTTATCAAATGTCCGGTAGTAGTGATTTTCTTTGCTTTATTATTGACTT
TAAATAATTTTACGCATAAATAAATTTTCGTAAGATATCGGCGACGTAAGGGGCTCTCC

>GTGU_RS00575|Trabulsiella_guamensis_GCF_000734965.1_ASM73496v1|GTGU_RS00575
GTGU_RS00575; downstream from 1 to 126; size: 126; feature type:gene;
location:
Trabulsiella_guamensis_GCF_000734965.1_ASM73496v1:NZ_JMTB01000006.1:6422:6547:D;
downstream neighbour: GTGU_RS00580 (distance: 126)
CCGAATCGGTGTGGACAAACACTCCAGCAGCGGTAAGCGATTACCGCTGCTTTTTTTTTGTC
CCTAACGAAGACGGACAACGCTTATCTGCTCCTCCTCGCCTTAGTCAACAGTGGAAGGAT
GATGTC

>PSSC_RS08730|Type-C_symbiont_of_Plautia_stali_GCF_001485315.1_C_1.0|PSSC_RS08730
PSSC_RS08730; downstream from 1 to 133; size: 133; feature type:gene;
location: Type-
C_symbiont_of_Plautia_stali_GCF_001485315.1_C_1.0:NZ_BBOB01000014.1:77918:78050:D
; downstream neighbour: PSSC_RS08735 (distance: 133)
GTTTTGTTTCGCATCGTGGAAAGCATCCAGCAGCGGTTAATACCGCTGCTTTTTTTTTTGCCC
ACACCTGCGAATAACACCTGCGGCTCTCTGGCTTAACTTCCACCAACACGTTACGGACG
TAAGGATGTTTTT

>PSSD_RS11760|Type-D_symbiont_of_Plautia_stali_GCF_001485335.1_D_1.0|PSSD_RS11760
PSSD_RS11760; downstream from 1 to 131; size: 131; feature type:gene;
location: Type-
D_symbiont_of_Plautia_stali_GCF_001485335.1_D_1.0:NZ_BBOC01000031.1:20468:20598:R
; downstream neighbour: PSSD_RS11755 (distance: 131)
ATTTGTTTCGCATCGTGGAAAGCATCCAGCAGCGGTTAATCCCGCTGCTTTTTTTTTGCCCCA
CGATCACCGAATAACACCTGCGGCTCTCTGGCTTAACTTCTACCAACACGTTACGGACGT
AAGGATTTTTT

>PSSE_RS05055|Type-E_symbiont_of_Plautia_stali_GCF_001485355.1_D_1.0|PSSE_RS05055
PSSE_RS05055; downstream from 1 to 131; size: 131; feature type:gene;
location: Type-
E_symbiont_of_Plautia_stali_GCF_001485355.1_D_1.0:NZ_BBOD01000006.1:46583:46713:D
; downstream neighbour: PSSE_RS05060 (distance: 131)
GTTTTGTTTCGCATCGTGGAAAACATCCAGCAGCGGTTAGTCCGCTGCTTTTTTTTTGCCCCA
CGATTTACGAATAACACCTGCGGCTCTCTGGCTTAACTTCTACCAACACGTTACGGACGT
AAGGATTTTTT

>PSSF_RS19745|Type-F_symbiont_of_Plautia_stali_GCF_001485375.1_F_1.0|PSSF_RS19745
PSSF_RS19745; downstream from 1 to 132; size: 132; feature type:gene;
location: Type-

F_symbiont_of_Plautia_stali_GCF_001485375.1_F_1.0:NZ_BBOE01000049.1:21027:21158:D
; downstream neighbour: PSSF_RS19750 (distance: 132)
GTTTGTTCGCACTGTGGAAGCCATCCAGCAGCGGTTAATACCGCTGCTTTTTTTTTTGCTT
CCGGTTTGAATAACGCCTGCGGCTCTCTGGCTTAACTTCCACCAACACGTTACGGACG
TAAGGATTTTTT

>WGL_RS00190|Wigglesworthia_glossinidia_GCF_000008885.1_ASM888v1|WGL_RS00190
WGL_RS00190; downstream from 1 to 112; size: 112; feature type:gene;
location:
Wigglesworthia_glossinidia_GCF_000008885.1_ASM888v1:NC_004344.2:38885:38996:D;
downstream neighbour: WGL_RS00195 (distance: 112)
TTAAAATATAATTTTTTAAATTTAAAAATATAATTTTTTAAAATAAAAATACATAATAAATTG
ATCTTTTTATTAAAAGACATATTTTAAATATTAATTTCTAAGGGATTATT

>XBJ1_RS08155|Xenorhabdus_bovienii_GCF_000027225.1_ASM2722v1|XBJ1_RS08155
XBJ1_RS08155; downstream from 1 to 138; size: 138; feature type:gene;
location:
Xenorhabdus_bovienii_GCF_000027225.1_ASM2722v1:NC_013892.1:1852992:1853129:D;
downstream neighbour: XBJ1_RS08160 (distance: 138)
ATTTAAATGGGAAACTTAAAAGCAGGTTACAGGTTTTTTATGTGCAGACCTGTAACCTTGC
TCTGTCATACCGTTCTTCGTTTACTAATTCGCCCTGTTCAAATCCCATCTGCTCACCAAC
TTAGCTAAAGGATATCGC

>YALDO0001_RS06210|Yersinia_aldovae_GCF_000173735.1_ASM17373v1|YALDO0001_RS06210
YALDO0001_RS06210; downstream from 1 to 136; size: 136; feature type:gene;
location:
Yersinia_aldovae_GCF_000173735.1_ASM17373v1:NZ_ACCB01000009.1:67555:67690:R;
downstream neighbour: YALDO0001_RS06205 (distance: 136)
GTTTATTTGAGTTATCAGAATTTTTGGCTACAGCATCGGTATGGATACCGTTGCTGTAAT
GTTCTAAGACAACCTCATTGCCCTCAAAGGGTGCTAACGCCTCACCTTCCACCCACACACT
TTGCTAAGGATGTCGC

>HMPREF0880_RS18420|Yokenella_regensburgei_GCF_000239335.1_ASM23933v1|HMPREF0880_
RS18420 HMPREF0880_RS18420; downstream from 1 to 124; size: 124; feature
type:gene; location:
Yokenella_regensburgei_GCF_000239335.1_ASM23933v1:NZ_JH417874.1:1824138:1824261:R
; downstream neighbour: HMPREF0880_RS18415 (distance: 124)
CCTTGACGGCGTGGACAACACTCCAGCAGCGGTAAGCAATTACCGCTGCTTTTTTTTGCC
CCTCTGTCAGGTTTTCTCTGACGCTGTTTATTCTTGCCTTAGTCAACACTGGAAGGATGA
TGTC

Species where Asp178 of FlhC is not conserved (putative FlhA promoters identified by MEME are highlighted in yellow)

>KYC_RS19640|Achromobacter_arsenitoxydans_GCF_000236785.1_ASM23678v2|KYC_RS19640
KYC_RS19640; downstream from 1 to 118; size: 118; feature type:gene;
location:
Achromobacter_arsenitoxydans_GCF_000236785.1_ASM23678v2:NZ_AGUF01000062.1:2798:29
15:R; downstream neighbour: KYC_RS19635 (distance: 118)
CCGGGCGTCCAAATACATCAAAAGCCCTGGAAAACCCCCCTAACCCGCCTTTTTGGGTC
GGGGGGACAGGGGATCATTGACGCCAGTTTTTCAGACTTCGTTGGCAGGGGCCGGAT

>QWA_RS14775|Alcaligenes_faecalis_GCF_000275465.1_Gretchen3|QWA_RS14775
QWA_RS14775; downstream from 1 to 191; size: 191; feature type:gene;
location:
Alcaligenes_faecalis_GCF_000275465.1_Gretchen3:NZ_AKMR01000014.1:97318:97508:R;
downstream neighbour: QWA_RS14770 (distance: 191)
CAATAGCTTTTTGTCTCAGTATGCAGCAAAGCCGGATGGATGCTGGTTTTTGATGTGGAT
CTGATACCAATCTGAATGTGTCAAGGCAACCGGAAGCGTTGATCTAGGCTGGAAAAAGGC
CGTTAACGTGTCTGTTTTAGCCCGGTTGCTTGCCGCCATCATTAGCAGCGTGTATTTGAAG
AAGCGTATCC

>ABG80_RS16110|Aquabacterium_parvum_GCF_001447195.1_ASM144719v1|ABG80_RS16110
ABG80_RS16110; downstream from 1 to 297; size: 297; feature type:gene;
location:
Aquabacterium_parvum_GCF_001447195.1_ASM144719v1:NZ_LFRI01000386.1:439108:439404:
R; downstream neighbour: ABG80_RS16105 (distance: 297)
TTTCACGCGCCTTCAAAAAAGGGCTCAAGTTGCGGGCAGCTCGCCGATACAACA
GAGCGTCTTTTTGGAAGGAAGGCGTTCTTGCTTGTCTCCTCCTGGCACGAATCCGTGCTT
TCCTGCGGACCCTGATCGGGTCCGCCTTTTTTTTGGGGCGCCCGCTTGCCTGGGGATTCCA
TGTGCTGGAAGTTGATCCGAAATAGCGGCTTGC GCGGCGTTGTTACGGGTTC CCGGC
GGGGCAAGTGGGAACAAGATCACGCCATGACCCGAAACAGCACCTGAGCGAGACCCC

>dqs_RS07715|Azoarcus_olearius_GCF_001682385.1_ASM168238v1|dqs_RS07715
dqs_RS07715; downstream from 1 to 139; size: 139; feature type:gene;
location:
Azoarcus_olearius_GCF_001682385.1_ASM168238v1:NZ_CP016210.1:1663170:1663308:D;
downstream neighbour: dqs_RS07720 (distance: 139)
TTTCCGCCCCATCTCACGGGCCGCTGCGTTAGCAGCGGCCCGTGTCTTTTTCCACG
GCCGGC GTTCAAGTTGGCGGATGCGGGACGATA CAATTCCGGCGGTCCAAATCTTCGT
CCGGCTTCTGGAGTAAGCG

>A7W11_RS15040|Bordetella_ansorpii_GCF_900078315.1_7642_7_30|A7W11_RS15040
A7W11_RS15040; downstream from 1 to 126; size: 126; feature type:gene;
location:
Bordetella_ansorpii_GCF_900078315.1_7642_7_30:NZ_FKBS01000017.1:6080:6205:R;
downstream neighbour: A7W11_RS15035 (distance: 126)
ATTCTTAAGGGTGC GCAAACACGCCAAGAAGCCCGAAAAACCCCGTAACCCCTCGCTT
TTGCCGAGGGCGGGGCGGGCGATCATTACGGCGGGATTGTTCCGACTACATTGGCAGGGG
CCTAAT

>AWB78_RS27405|Burkholderia_calidae_GCF_900044055.2_Burkholderia_sp._LMG_29321|AW
B78_RS27405 AWB78_RS27405; downstream from 1 to 129; size: 129; feature
type:gene; location:
Burkholderia_calidae_GCF_900044055.2_Burkholderia_sp._LMG_29321:NZ_FCOX02000036.1
:57284:57412:R; downstream neighbour: AWB78_RS27400 (distance: 129)
CGCCGCACCCAGTCGCCACGCGGGGTTTACCGTTTGCCTCCCGCGGAATCAACCTCAA
AGTTTTTCAGCCGAGTGCCGTAAACCACTTAACGGCGGTCTTACCGCATCAAAACGTGAG

GACTCGACT

>UB46_RS02275|Burkholderiaceae_bacterium_16_GCF_000955785.1_ASM95578v1|UB46_RS02275
UB46_RS02275; downstream from 1 to 457; size: 457; feature type:gene;
location:

Burkholderiaceae_bacterium_16_GCF_000955785.1_ASM95578v1:NZ_JYOD01000006.1:139657
:140113:R; downstream neighbour: UB46_RS02270 (distance: 457)
CTGAAGCGATTTCGGCTGAGACGCTACCAAGCGGATAGTCCGGGCACATGCCCGGGCTGCC
GTTGGGAATCCTGCCCGCGTGCCTGGATGCCGGAAGTACCCGGCATCCACGCGTATT
CCCGTGGCAGCCTGCTAAGCGTACCAACGCTCAGGCAGGGCCATCGCGGGAACCTCGGAAG
GAAACCAAGCTTATTCGCCGGATCGCCGGTCCCCGCGTTGGAAGATCATCGATGCCGGG
TCAATAAGTCTTCAAGTCTTGCCGTCTTGCGTCGTTAAGTCATAAGACTGCAAGGCTTCA
GAACTCCAGATCACTGGGCCTTCAGGTCCTGGGTCTCGGGTCCGAGGGCGGTTTGCCTG
GTTGGTGAGTCTTGCCAGGGCAGGCGGTAAATCCGCTTCTCCCGGAGGGCGACCTTGTG
CGTGCTGACGCGTGTCTTCTGACGGGGAATCAATC

>ACU09_RS02155|Caballeronia_cordobensis_GCF_001278535.1_ASM127853v1|ACU09_RS02155
ACU09_RS02155; downstream from 1 to 93; size: 93; feature type:gene;
location:

Caballeronia_cordobensis_GCF_001278535.1_ASM127853v1:NZ_LGRC01000001.1:458849:458
941:D; downstream neighbour: ACU09_RS02160 (distance: 93)
CGCGGCGAGAACGCCATATCTCAAAGTTTTTCAGTCGAGTGCCGTAAACCACTTAACGGC
GGTCTTACCGCATCGAAACGTGAGGACTCGACT

>F615_RS0100125|Caldimonas_manganoxidans_GCF_000381125.1_ASM38112v1|F615_RS0100125
F615_RS0100125; downstream from 1 to 202; size: 202; feature type:gene;
location:

Caldimonas_manganoxidans_GCF_000381125.1_ASM38112v1:NZ_KB905929.1:20880:21081:R;
downstream neighbour: F615_RS0100120 (distance: 202)
TTGCCGCCGCGGCGAAGTTTCATCCGTCGTCTCCTCCTGAGCGCCTCGCTGGCGCCTTGA
CCACGGGCTCCCCGCGAGCCCGTGCTTTTTGGTTCCCCCAAGACGGGCTCAAAGTCAGAGG
CAAAGCGGTCGATA TCCCCTGGGACCCCGTCAAAGCGCGCACTGCCCGTGGTGCGTCAA
CCCACCTGGAAAGACCCGCAAC

>CCA01S_RS03825|Castellaniella_caeni_GCF_001592225.1_ASM159222v1|CCA01S_RS03825
CCA01S_RS03825; downstream from 1 to 109; size: 109; feature type:gene;
location:

Castellaniella_caeni_GCF_001592225.1_ASM159222v1:NZ_BCWN01000004.1:92030:92138:R;
downstream neighbour: CCA01S_RS03820 (distance: 109)
TTACAGTCAGATACGGGATTTACGTACA AAAAGTCTGTTGAACCATGCTTTTGAAAGCC
TGAAAACGGGCGAACATTGACATCATTCTGACTATCGAGGCGTGCGCAC

>LT85_RS05845|Collimonas_arenae_GCF_000786695.1_ASM78669v1|LT85_RS05845
LT85_RS05845; downstream from 1 to 60; size: 60; feature type:gene;
location:

Collimonas_arenae_GCF_000786695.1_ASM78669v1:NZ_CP009962.1:1290451:1290510:D;
downstream neighbour: LT85_RS05850 (distance: 60)
ATCAGGTGAGCAGTTCCGGTTAGCGTGCCGTTCAAGGTTTATTTCAAGGGGAATCAATA

>OR16_RS31100|Cupriavidus_basilensis_GCF_000243095.1_ASM24309v2|OR16_RS31100
OR16_RS31100; downstream from 1 to 241; size: 241; feature type:gene;
location:

Cupriavidus_basilensis_GCF_000243095.1_ASM24309v2:NZ_AHJE01000102.1:4772:5012:D;
downstream neighbour: OR16_RS31105 (distance: 241)
CTGAAATCCTTGGGTCGATAGGTCATAAGTCTTCAAGTCTTGCCGTCTTGAGTCGTTAA
GTCATAAGACGGACCAGACTTCAGGACCCACGGCTTTAAGGTCCGAACGTCCCAAGGTCT
CAGATTCGATGGCAGCCTGCGTGACAGGTGAGCCCAGCCAAGGCAGGCGTTAATCCGTC

TGCCTTGAGGGGTGACCCTTGTGCATGCCTGACGTGTGTTTTCTGACGGGAATCAAT
C

>CDE01S_RS08735|Curvibacter_delicatus_GCF_001592265.1_ASM159226v1|CDE01S_RS08735
CDE01S_RS08735; downstream from 1 to 157; size: 157; feature type:gene;
location:
Curvibacter_delicatus_GCF_001592265.1_ASM159226v1:NZ_BCWP01000015.1:2495:2651:D;
downstream neighbour: CDE01S_RS08740 (distance: 157)
AGTGCTCAAAGACGCCAATTAAATGCCGATAAAGGGTCCTTAGGGCCCTTTTTCACGTT
TGGCGCACGGGCTGAATCCCCTAGAAATGGTTTGATCTGATTCATCAGTTTGGTTACTTTT
CCCCAGCTGCAACCCTCAACTCTGACACCGCACCAAC

>OYT1_RS00615|Ferriphaselus_amicola_GCF_000974685.1_ASM97468v1|OYT1_RS00615
OYT1_RS00615; downstream from 1 to 207; size: 207; feature type:gene;
location:
Ferriphaselus_amicola_GCF_000974685.1_ASM97468v1:NZ_BBTH01000001.1:125620:125826
:R; downstream neighbour: OYT1_RS00610 (distance: 207)
TGCAGGCTAGGAGAAATCCCTAAAGTTTTACCCCCATTGGCCGTTACCACCGATATAAGT
TTTGAGTGGTAACGGCTTTCTTCTTGGCGGGCTTGGGGCAACGGAAGAACAAGTAAGAA
TAAATCCGGTTAATTGGGTGATTGAGTTTAGCGGGCTGGTGATAATTTGCTAGCCAGTGA
GACAGAAACGATAAGCAGGGGGCGGTT

>IV91_RS0102865|Ferrovum_myxofaciens_GCF_000735045.1_Fv_myxofaciens_P3G_1.0|IV91_
RS0102865 IV91_RS0102865; downstream from 1 to 113; size: 113; feature
type:gene; location:
Ferrovum_myxofaciens_GCF_000735045.1_Fv_myxofaciens_P3G_1.0:NZ_JPOQ01000011.1:392
71:39383:D; downstream neighbour: IV91_RS0102870 (distance: 113)
AGTTCAAAAAATTAGTGAAAATCCCGCAGACAGGATGCGCTCGCGCTCAATTCATGGT
TGAATGGCGCCTTGTAACCCTCCAAGAATTTATAACGTATCTGGAGCCTTTCC

>FPB0191_RS01295|Frischella_perrara_GCF_000807275.1_ASM80727v1|FPB0191_RS01295
FPB0191_RS01295; downstream from 1 to 65; size: 65; feature type:gene;
location:
Frischella_perrara_GCF_000807275.1_ASM80727v1:NZ_CP009056.1:266264:266328:R;
downstream neighbour: FPB0191_RS01290 (distance: 65)
ACGAAAAGTAAATTGATTGTGTTAAATAGCATTAAATAGTAATTAATTAAGATAGGGAA
AATCA

>GALF_RS05015|Gallionella_capsiferriiformans_GCF_000145255.1_ASM14525v1|GALF_RS050
15 GALF_RS05015; downstream from 1 to 154; size: 154; feature type:gene;
location:
Gallionella_capsiferriiformans_GCF_000145255.1_ASM14525v1:NC_014394.1:1061241:1061
394:D; downstream neighbour: GALF_RS05020 (distance: 154)
CAATTTCTTTGTTTTTTCAGGCCGACTAAGCATACTCTGGTCGCGCGCTACCCGTA
CTAAAAAATAAGCGCATAGTGCAATCTGCCATCACTCGTTTGGCGGATTTGTTTTAGA
ATGCAGAGGCAGAAATAATACTTAGGAGTGCTGC

>GAPWK_RS13040|Gilliamella_apicola_GCF_000599985.1_ASM59998v1|GAPWK_RS13040
GAPWK_RS13040; downstream from 1 to 43; size: 43; feature type:gene;
location:
Gilliamella_apicola_GCF_000599985.1_ASM59998v1:NZ_CP007445.1:2919131:2919173:D;
downstream neighbour: GAPWK_RS13045 (distance: 43)
AATAAATATTAATAATTAATTAATGATGATAAAAAGGAAAACCA

>CR46_RS0115550|Halomonas_alkaliantarctica_GCF_000712975.1_Version_1.2.07|CR46_RS
0115550 CR46_RS0115550; downstream from 1 to 225; size: 225; feature
type:gene; location:

Halomonas_alkaliantarctica_GCF_000712975.1_Version_1.2.07:NZ_JHQL01000005.1:22673
9:226963:R; downstream neighbour: CR46_RS0115545 (distance: 225)
ACTACAAAATTATCTTGCCCGGTGCGGTGAGGTATATAGCCAATAAAATGCGTCTTTAA
CGTATAGATAGCACCAAAGGGGTGGTACTTTTTTCATTAACACCGCCAGCGCCTGAGTA
AGCTATGGCTAAGAAACGCGTGGAAACCAACGCTCTGTGTTCTCTTTTTGAAACACAGGAA
TAGCGCTCCACTGATACAAAACACTGATATCGCAAGGATACTGCTT

>HFL01S_RS18300|Hydrogenophaga_flava_GCF_001571145.1_ASM157114v1|HFL01S_RS18300
HFL01S_RS18300; downstream from 1 to 152; size: 152; feature type:gene;
location:
Hydrogenophaga_flava_GCF_001571145.1_ASM157114v1:NZ_BCTF01000022.1:51511:51662:R;
downstream neighbour: HFL01S_RS18295 (distance: 152)
ACGCCTGCTCCGTTCAAACCCCTGAAAAGGACCCTTGCAGGGTCTTTTTTTCGTTTCTGG
CGGACCTCAATCACCCCTAGAGTTGGACCGATAGGAAAGACAGTCGTTGGGGCATTTGCGC
TCCGGGTTCCGTTTCAACTCAAGGTTCACTTC

>ISF6_RS19785|Ideonella_sakaiensis_GCF_001293525.1_ASM129352v1|ISF6_RS19785
ISF6_RS19785; downstream from 1 to 385; size: 385; feature type:gene;
location:
Ideonella_sakaiensis_GCF_001293525.1_ASM129352v1:NZ_BBYR01000050.1:7240:7624:D;
downstream neighbour: ISF6_RS19790 (distance: 385)
GTTCCACCGGGGCGAGCCCCCGCCTTTCAGTTCCGCGCCGCGCGCCGATAGAAGGAAG
GCGAACGGCTCTCCCTGCGGGGAGCCGACGTTGGCTCGAAGTTTGCTTGGGTCTTTTGC
TTTTGTTTCGTTTCGTGTCTCCTCCTGGCACATCCCCGCATGTGCTTTCGACCACGGGCC
TTCGGGCCCGTTTTTTTTTGGTCCGGCGCATCCCCCGGGCCGAGGTGGTGCCGGCGGTT
TGGCCCGCTTTCCCGCCTCATCGGCCGATGGCCCCCGCGCTCGCCGCCGACACTCAA
GACCTGGGCTCCCCGTCCGATA TAGGACGCGACCGGCGCCCGGTTTCTGGATGGATCCCG
CCCCCACCACGGATTTCCCGACC

>AAV32_RS11395|Kerstersia_gyiorum_GCF_000988095.1_ASM98809v1|AAV32_RS11395
AAV32_RS11395; downstream from 1 to 150; size: 150; feature type:gene;
location:
Kerstersia_gyiorum_GCF_000988095.1_ASM98809v1:NZ_LBNE01000007.1:126728:126877:D;
downstream neighbour: AAV32_RS11400 (distance: 150)
CGCCGCGGTAGGGACGGCAGTCTAGCCGTCCCGCTCTCTCAAAGCGGCAAGGAATGCCGC
AAAAATCGTTCTGACTCACGCTTCCCGGATGCTTTCCGGTTGAAGATTAGGCTTTCTT
GCGGCTTTTTTCGAGCTAAGGGCTTTTTATT

>H146_RS0112390|Kushneria_aurantia_GCF_000382245.1_ASM38224v1|H146_RS0112390
H146_RS0112390; downstream from 1 to 326; size: 326; feature type:gene;
location:
Kushneria_aurantia_GCF_000382245.1_ASM38224v1:NZ_KB907878.1:47005:47330:R;
downstream neighbour: H146_RS0112385 (distance: 326)
GCTATCACTCCCGCTTCTAATGCGGTGACACGAATCGTAACCTTTTTCAAGCCCCTGGCAC
TCAGTGTCAAGGGCTTTCTATCTCCTCCCCAAAGCCGCGGTGCGCTTGTCTTTCAGA
ATATTTAAAGCGTGAATTGAGAGCTTTTTTGGCGGTACGTCCAGCGCTGAAGCGCTCCTG
TCCTGTTCCATAATCGTTACCGATCCGCTTGGTTGGCAGGTATTTTCGCGCTGCCATATGA
AATCGCCATGTGAAACAGGCTTCATACTCAAGTCCAGGCGTTTTCTGCCGATGTTACAGG
CAGGTCACGAACGCCGAGGAAATGCA

>HMPREF0551_RS06190|Lautropia_mirabilis_GCF_000186425.1_ASM18642v1|HMPREF0551_RS0
6190 HMPREF0551_RS06190; downstream from 1 to 399; size: 399; feature
type:gene; location:
Lautropia_mirabilis_GCF_000186425.1_ASM18642v1:NZ_GL636062.1:1478200:1478598:R;
downstream neighbour: HMPREF0551_RS06185 (distance: 399)
CAGGTCGACTGAACTCCGGCTGGCTGGCCACCTCCATTCCGTCTGCAGCGATCCGAGGG
TTCGGATCGCTGCAGGAAGGGCAAGGCGCGCCAGCCCGAACATGCGAAGCATTTTTTGGG

CATTCGGACGGATCTTTCGGGATCCTGATGAATGCCTTTTTTTCATGGGCGTTTCCTTGGC
CTTGGGGAGTTTGACCATGGATCGAGCCTGAAAGTGTTCCTGGATATATCCACTGTCC
CTGACAGGTGCCCCGACCTGACGCCGTTCCCGCTGGGTGTCCGTCTGACCGTCATGGGTG
CCGCAGGGCAGGGCGATGCTCAAGAATGCCGGGTATCGACCGATAAGGAGGGGAGCCCCG
GGCCCATGCCCGGTGTGAACCAGTCAAGGGATACACAAC

>H663_RS15295|Limnohabitans_planktonicus_GCF_001270065.1_ASM127006v1|H663_RS15295
H663_RS15295; downstream from 1 to 148; size: 148; feature type:gene;
location:
Limnohabitans_planktonicus_GCF_001270065.1_ASM127006v1:NZ_LFYT01000007.1:610169:6
10316:R; downstream neighbour: H663_RS15290 (distance: 148)
ATCCAAGCACTTGAATAGCCTTGCAAACGGTCATCTATTGAAACGATCGGCTGGTGACTC
ACCAAATACCATCAGTGTTTCATTGGCGTCATGCGCACCCAGCCTTGACTCTTTTTTCTA
TGGTCACCTGAATTGAACGCTTTACAAC

>YWC_RS0101370|Massilia_alkalitolerans_GCF_000427785.1_ASM42778v1|YWC_RS0101370
YWC_RS0101370; downstream from 1 to 17; size: 17; feature type:gene;
location:
Massilia_alkalitolerans_GCF_000427785.1_ASM42778v1:NZ_ATYR01000001.1:294709:29472
5:R; downstream neighbour: YWC_RS0101365 (distance: 17)
AACCCGCCGTTGCGGCG

>B594_RS0108715|Methyloversatilis_discipulorum_GCF_000374245.1_ASM37424v1|B594_RS
0108715 B594_RS0108715; downstream from 1 to 205; size: 205; feature
type:gene; location:
Methyloversatilis_discipulorum_GCF_000374245.1_ASM37424v1:NZ_KB910520.1:1870551:1
870755:D; downstream neighbour: B594_RS0108720 (distance: 205)
TCCGTTTTCTCTCTCCTGTCTGACCTCCTCCTTGCGCGAGCAAGGAGCTCGCCGCTGCGG
GGCAACCCGAGCGGCATTTTTTTGTGCGTGGGTGCTGTCCACCTGCGCAGCAGACTTG
GTCAAGTTTCTCTGAGGTGGTGCCGTTAAGACCAACAGGCACGCAGTGATTGATGCCCGAA
CATCCGTCATACACAGGGAAATTCC

>F822_RS01105|Nitrosospira_briensis_GCF_000619905.2_ASM61990v2|F822_RS01105
F822_RS01105; downstream from 1 to 382; size: 382; feature type:gene;
location:
Nitrosospira_briensis_GCF_000619905.2_ASM61990v2:NZ_CP012371.1:237740:238121:D;
downstream neighbour: F822_RS01110 (distance: 382)
CATTCTGCCGGGCTTGAAGAATCGCAGCAAAAAATGAACTGGCCAGCCGATTTCTGTAA
GTTTCGACAGGCTGCTGGCAACCAACCTCCCGGCGTCATCGATCCGGGAGGTTTCTTTCT
CCTCTGGTTGAAATCTTTTCTTTCCCGCGCTTCTCTCTCACTTCTTCCGGTTTTTCG
CTATTTCTCTCTCTAAAGTTTACCGGGTTCCGGCCGTTACAAAGGTGGAGTATTTCAAGT
TGACTGCCTTTGCTCCAATGCCGGTGAATCAGGCCACGTAAGTGCACGCAATAACCGGCAA
TGGCTGGGCAATGGCTGCCGACACCGGCAGCGCTGATTATGCAATCAGCACAACAATTCC
AACTGGAGAAGTGTAGGGGAAT

>ODI_RS05230|Orrella_dioscoreae_GCF_900089455.1_OrrDiv1|ODI_RS05230 ODI_RS05230;
downstream from 1 to 129; size: 129; feature type:gene; location:
Orrella_dioscoreae_GCF_900089455.1_OrrDiv1:NZ_FLRC01000010.1:52881:53009:R;
downstream neighbour: ODI_RS05225 (distance: 129)
GCGTCATCCCTCTCCGTGGCCGATAAGGCCAAAAAGCCACGAAAAAGCCCTTTGAACCC
GGTTTTCAAACCGGGCTTAGAGGAGATCATTCTGGGCGATTGCGTGTTAATTCTAGGCA
GAGGGTCGT

>D827_RS11310|Pseudacidovorax_intermedius_GCF_000333675.2_Pseudacidovorax_interme
dius_NH-1|D827_RS11310 D827_RS11310; downstream from 1 to 121; size: 121;
feature type:gene; location:
Pseudacidovorax_intermedius_GCF_000333675.2_Pseudacidovorax_intermedius_NH-

1:NZ_ANOY02000603.1:2105:2225:D; downstream neighbour: D827_RS11315 (distance: 121)

ATTGAACCCAGGCACGCCGCTCCGAAGTGTGATATGGGCCCGCGATCGGGCCCTTTT
TGCGGGACCGGCTCAGCCGTCGTCAGGCCAATAGCACCTGATCTTCGCCCTCCAC
C

>ON18_RS13280|Pusillimonas_noertemannii_GCF_000308195.1_PusiNoerBS8|ON18_RS13280
ON18_RS13280; downstream from 1 to 196; size: 196; feature type:gene;
location:

Pusillimonas_noertemannii_GCF_000308195.1_PusiNoerBS8:NZ_AMZF01000045.1:4854:5049
:D; downstream neighbour: ON18_RS13285 (distance: 196)
GGCCTGCAGGCGAACCCACGGCCCGGGCGGCGCGCAAAGGGCGGCCACTTGCAAAGTGT
GTCTTGGGCGCAAAGCCTGCATTCCGCGGTTTGCCAGAACGCTGATCTAGCTTCTAAAA
ACCCATTGACGGACGCTTTTGCCGCGCCGATCGGGGTGATCATAGAGCCCCATGCATT
TATCGAGGATACGCTC

>ACS15_RS27355|Ralstonia_insidiosa_GCF_001653935.1_ASM165393v1|ACS15_RS27355
ACS15_RS27355; downstream from 1 to 271; size: 271; feature type:gene;
location:

Ralstonia_insidiosa_GCF_001653935.1_ASM165393v1:NZ_CP012606.1:1954956:1955226:D;
downstream neighbour: ACS15_RS27360 (distance: 271)
GCGGTACCACCGGGATTACGGGACGTACGGGAACGAACGCCGGGAATGACGGGAAATAC
GGGAACACAACAACAATAGCCGGCAAGTTCGGCACATAACAAGACAGCACAGAACACAGA
GCAGCAACAGCACAGGGGCTCAGACAGCACAAAAGGGGAAGGGGGTAGGCCGGTTCGTCGC
AGGAAACTGCGGACCGGCATTTTTTTGCGCCGCGCATGAAGGAAGGGACGGAAAGCAAT
TTCCGTCCTTTTTTCTTTCGTTTCGGCTTGG

>BLL52_RS08285|Rhodoferrax_antarcticus_GCF_001938565.1_ASM193856v1|BLL52_RS08285
BLL52_RS08285; downstream from 1 to 176; size: 176; feature type:gene;
location:

Rhodoferrax_antarcticus_GCF_001938565.1_ASM193856v1:NZ_MSYM01000011.1:274507:27468
2:R; downstream neighbour: BLL52_RS08280 (distance: 176)
GCGGCCTACTCCAAAAATATATTTTTATAGCTACTAACGCTTTGTTTATAAGGGCTAGAA
GCTTATTTCACTCATAACTCAAGTGACTGGGAAAGCGGTCGATA TGATAGAGAGCAGAGT
GGCACCTAGCACTGCTCGTCTTTTGAAACACAAGCCCTTCTAAAGTAGACCGTCT

>BTW07_RS14530|Salinicola_socius_GCF_001937195.1_ASM193719v1|BTW07_RS14530
BTW07_RS14530; downstream from 1 to 207; size: 207; feature type:gene;
location:

Salinicola_socius_GCF_001937195.1_ASM193719v1:NZ_MSDO01000022.1:19182:19388:D;
downstream neighbour: BTW07_RS14535 (distance: 207)
TTCGGCGATATCTTTCGAAGCGGGCTCCATGGCCGCTTTTTTCATGTCTGCGTTATTTT
TTCTTTCCCATCCGTGTCGCCGCATCAAGTCGGCTGTGTCGTTGTCGACGAATCACGCT
TTTCTGATATTTCTACCCTCAAGGGTGATGGTCCCGCTGCCGATA CAGTCATCAGGTTCCG
CCACGCACTGTCATCGGGAGCATTTAC

>C41B8_RS07165|Salinisphaera_hydrothermalis_GCF_000732535.1_ASM73253v1|C41B8_RS07
165 C41B8_RS07165; downstream from 1 to 206; size: 206; feature type:gene;
location:

Salinisphaera_hydrothermalis_GCF_000732535.1_ASM73253v1:NZ_APNK01000007.1:119488:
119693:R; downstream neighbour: C41B8_RS07160 (distance: 206)
CGAACGTATGACGCTGCGCCCGGGCTTGCCCTGGGGCGGGCGTCTTACGCATGCGTC
TCGCCGTCCGGTGTCTGAGTGCACCGCATCGACGAATCAAAAATCGATGGGCATCCAGC
GTTCAAGTTCCCATGTGCGCCGGCGTTA TGTGCTGTACGCCTAAACCGTCGTCAAATGCG
GTCGTGTCTGATCGCCAGGGGTTCCA

>SLIT_RS02695|Sideroxydans_lithotrophicus_GCF_000025705.1_ASM2570v1|SLIT_RS02695
SLIT_RS02695; downstream from 1 to 188; size: 188; feature type:gene;
location:
Sideroxydans_lithotrophicus_GCF_000025705.1_ASM2570v1:NC_013959.1:549846:550033:D
; downstream neighbour: SLIT_RS02700 (distance: 188)
AGTTTACTTTCGAGCGCCGCTACTACTGACGAGATGTATCATCAGCAGTGGCGGCGTTG
TTGCGTCTGAGGCCCGAACAGCGAAAATGCCGGTGGATATTCGTTTTGATCCATGCAT
GGCCGGGATGCCTGGCTGTTACGATGCAACAGTAGACTTGAAGAGTGTGACTCAGGGA
GCGTGATT

>BG74_RS04485|Sodalis-
like_endosymbiont_of_Proechinophthirus_fluctus_GCF_001602625.1_ASM160262v1|BG74_R
S04485 BG74_RS04485; downstream from 1 to 98; size: 98; feature type:gene;
location: Sodalis-
like_endosymbiont_of_Proechinophthirus_fluctus_GCF_001602625.1_ASM160262v1:NZ_LEC
R0100040.1:24121:24218:R; downstream neighbour: BG74_RS04480 (distance: 98)
GAAGAGTGATGCATTGAATGCCATTTTCACAAACGGATTATTCATCACTGGCAAAAACG
TTCATTTTCTGGATGCCACTGTCTTGTAAGGAATCACT

>SUTH_RS04425|Sulfuritalea_hydrogenivorans_GCF_000828635.1_ASM82863v1|SUTH_RS0442
5 SUTH_RS04425; downstream from 1 to 299; size: 299; feature type:gene;
location:
Sulfuritalea_hydrogenivorans_GCF_000828635.1_ASM82863v1:NZ_AP012547.1:902267:9025
65:D; downstream neighbour: SUTH_RS04430 (distance: 299)
GGTCGGCAGCAGAACCCGCTCTCCACTAGTTCGTTAGTTATATCCGACGCGCTCCTCCGG
CAAGCCGGCAGGGGCGGTTCCATTTAGCATAGTCTCGACGGGAATTTTTTCGGCGTGGT
TTCAGCGCCGACTTTCGATTCATGTTTCGCCCGGCATCCTCTGCCAAGGGCCTCGACCT
GTGTTGAAACTTGGCTTTGATTGCCGCGAGCCCTCTGTTTGCCGTTATGATTGCATTTCA
GGCAGGCTCCGAGATAGCATCGTTTCGCAAAAGAACAACAGTTCAGGGTAGGGTCCAAG

>H607_RS0104250|Tepidiphilus_margaritifer_GCF_000425565.1_ASM42556v1|H607_RS01042
50 H607_RS0104250; downstream from 1 to 148; size: 148; feature type:gene;
location:
Tepidiphilus_margaritifer_GCF_000425565.1_ASM42556v1:NZ_AUDR01000015.1:20307:2045
4:R; downstream neighbour: H607_RS0104245 (distance: 148)
CCGCACCGTCATGGCTCCCGCCTGACGCAAATTTCTTCATTCCGTCCTTCGCCAAGGGCG
CTCTGCTCATGCTACCATTGCATGCCAGGCGTAGGGCCGTGATTCTTGGCCCTTGCTGCG
GCACTAGCGGCATCGAACGGAGGGCTCT

>C665_RS11025|Thauera_aminoaromatica_GCF_000310185.1_ASM31018v1|C665_RS11025
C665_RS11025; downstream from 1 to 192; size: 192; feature type:gene;
location:
Thauera_aminoaromatica_GCF_000310185.1_ASM31018v1:NZ_AMXD01000063.1:15893:16084:D
; downstream neighbour: C665_RS11030 (distance: 192)
CCCCGGCGGGCCCTCCGGCCCGCATGCAGGTTCCCTACATGGGCCGCGCTGGAAACAGGCG
GCCCATGTCACGTCCGCGCACGGCGTGGCGTCGCGCCCCGGCGCG **GTTCAAGTTCCCTCCC**
CCGCCGCGGTTATCCCCTGCGAGAGCCGTGCCGGTCCGTGCGCGGCGCAGCGAAACGCTT
CGGAGTTTCCCC

>B145_RS0106465|Uliginosibacterium_gangwonense_GCF_000373965.1_ASM37396v1|B145_RS
0106465 B145_RS0106465; downstream from 1 to 252; size: 252; feature
type:gene; location:
Uliginosibacterium_gangwonense_GCF_000373965.1_ASM37396v1:NZ_KB892836.1:193927:19
4178:R; downstream neighbour: B145_RS0106460 (distance: 252)
TGGACTATTGTTGATTTGCCGCAACCCTCCTCAGAACCCTGTGGTGTGTAATCATTGAG
CCGCCAAGCTTTTGGCGGCTTTTGTATTAAAGTGA **CTTCAAGTTTCCGATTGCGGTGC**
CGATAGCCAGCATGGATGGTGGATAATCCTGTCTTGGGTTTCAAACAAAAGGGCGCGGA

CGCTGAACAAGCGTGTTTATGGCCCTGGCGACACCCGGTTTTTCGCATTCTGCGGCACACA
AGGGTCTTGAAG

>VBO01S_RS01450|Variovorax_boronicumulans_GCF_001591345.1_ASM159134v1|VBO01S_RS01
450 VBO01S_RS01450; downstream from 1 to 62; size: 62; feature type:gene;
location:
Variovorax_boronicumulans_GCF_001591345.1_ASM159134v1:NZ_BCUS01000002.1:127845:12
7906:D; downstream neighbour: VBO01S_RS01455 (distance: 62)
AAGTGCCCCGGCGCCCGGCGGGTTTTTTGTTTTGGACGCCTCAGGGCATAGGGGAAGC
GC

>AX739_RS08130|Xylophilus_ampelinus_GCF_001556675.1_ASM155667v1|AX739_RS08130
AX739_RS08130; downstream from 1 to 152; size: 152; feature type:gene;
location:
Xylophilus_ampelinus_GCF_001556675.1_ASM155667v1:NZ_LSJH01000364.1:1806:1957:R;
downstream neighbour: AX739_RS08125 (distance: 152)
TTCTGTTCGGCGCACCCCGACCGGAAACCGCGAACAGGGGCCTCTGAGGGCCCCCTTTTTTC
ATGGACTGCCCGCCGGCAGATGCAGGCCCAATAGCGTCAACCGCCGAAGCGCCCCCGGCC
TGAAGCGCCCTCCCCGTTCTCCTCACACGCC