Figure S1

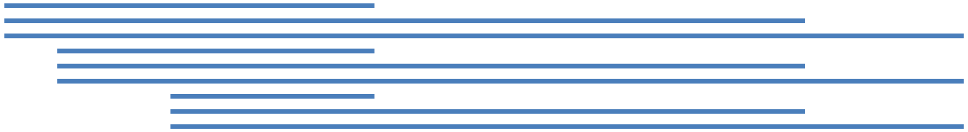
```
    >gi|110680168:2846062-2846169 Roseobacter denitrificans OCh 114, complete genome
    ATGACCGAGCATGCACCCGTGAACAAAGAAGCCGCC------ACC---------AAAGTC---CCCACCCTGCCCGACGCGCAAACCGTGACCGCCGTGCAGCACTATACTGACCGTCTGTTTTCG
1    M  T  E  H  A  P  V  N  K  E  A  A  -  -  T  -  -  -  K  V  -  P  T  L  P  D  A  Q  T  V  T  A  V  Q  H  Y  T  D  R  L  F  S
```

```
    >gi|254476318:403134-403012 Ruegeria sp. R11, complete genome
    ATGAATGAGATGACCTCCGTGACCGACACAGCAACCGACCAGAAG---CCCGCCAAAGCCACCCCCGCGCTGCCCGACGCACAGACCGTGACCGAGGTGAAGCACTGGACCGACCGCCTGTTTTCG
1    M  N  E  M  T  S  V  T  D  T  A  T  D  Q  K  -  P  A  K  A  T  P  A  L  P  D  A  Q  T  V  T  E  V  K  H  W  T  D  R  L  F  S

    >gi|159043699:1177432-1177313 Dinoroseobacter shibae DFL12, complete genome
    ATGAACAAACCGACCGACGTGATGAGCACCGTGACAGACGCAACA---CCGATCAAAGTC---CCCACCCTTCCGGATGCCCAGACCGTGCTGTCGGTCAAGCACTGGACAGACCGCCTGTTTTCC
1    M  N  K  P  T  D  V  M  S  T  V  T  D  A  T  -  P  I  K  V  -  P  T  L  P  D  A  Q  T  V  L  S  V  K  H  W  T  D  R  L  F  S

    >gi|84515523:295726-295601 Loktanella vestfoldensis SKA53, complete genome
    ATGGGTCACGATGAACATATGACAGAGCAAAGCCCCGTGAATCACGCCAGCGCCAAAATCGTCCCGCAATTGCCCGACATGCAGACCGTGACAGAGGTGAAACATTACACCGACCGGCTGTTTTCG
1    M  G  H  D  E  H  M  T  E  Q  S  P  V  N  H  A  S  A  K  I  V  P  Q  L  P  D  M  Q  T  V  T  E  V  K  H  Y  T  D  R  L  F  S

    >gi|99079841:1851729-1851854 Ruegeria sp. TM1040, complete genome
    ATGAACGAGATTACGCCCGTGAGTGAGCCTGTGACCGAAGCCGCCGCGCCTGCAAAGGCCAAACCCGCCCTGCCCGACGCCCAGACCGTGACGCAAGTGAAACACTGGACTGACCGGCTGTTTTCC
1    M  N  E  I  T  P  V  S  E  P  V  T  E  A  A  A  P  A  K  A  K  P  A  L  P  D  A  Q  T  V  T  Q  V  K  H  W  T  D  R  L  F  S

    >gi|149913791:70458-70571 Roseobacter sp. AzwK-3b, complete genome
    ATGAACGAGATCAGCACAGTGACCGAAGCACCCGCCAAGGCCGTC---------AAGACC---CCCACCCTGCCCGACGCGCAGAAAGTCACCCAAGTCACGCATTGGACGGATCGCCTGTTTTCC
1    M  N  E  I  S  T  V  T  E  A  P  A  K  A  V  -  -  -  K  T  -  P  T  L  P  D  A  Q  K  V  T  Q  V  T  H  W  T  D  R  L  F  S
```

Figure S1. Multiple translation start sites of the ferredoxin-NADP reductase (YP_683175.1). For this protein, two alternative initiation start sites were detected, the first one as an ATG codon and the second one as an GTG codon, 18 nucleotides downstream. A multiple sequence alignment with closely-related homologues demonstrates that both initiation sites are shown conserved in all the strains listed here. Current annotated codons are shown in red and the alternative codons are in blue. The correct initiation codons are underlined and in bold red. Blue lines represent the peptide sequence identified.

Figure S2

```
    >gi|1106678558:1197756-1197845 Roseobacter denitrificans OCh 114, complete genome
    ATGACCAACATGGAAAACCTTGAGAATCACTTGAACGAGCATGAGCGCCAGCGACTGGTGAATGAGGCAGCGCTGAAGCAGCTGCAGCAG
1    M  T  N  M  E  N  L  E  N  H  L  N  E  H  E  R  Q  R  L  V  N  E  A  A  L  K  Q  L  Q  Q
```



```
    >gi|339501577:3601466-3601377 Roseobacter litoralis OCh 149, complete genome
    ATGACCAACATGGAAAATCTTGAGAATCACTTGGAAGAACATGAACGCCAACGGCAGGTCAATGAGGTTGCCCTGAAGGGATTGCAGCAC
1             M  E  N  L  E  N  H  L  E  E  H  E  R  Q  R  Q  V  N  E  V  A  L  K  G  L  Q  H

2    M  T  N  M  E  N  L  E  N  H  L  E  E  H  E  R  Q  R  Q  V  N  E  V  A  L  K  G  L  Q  H


    >gi|159045286:2908728-2908642 Dinoroseobacter shibae DFL12, complete genome
    ATGTCCAATCTTGAAGATCGTAAGCTGGCGTTGTCGGAAAACCCTTACGCCGAGAAATAC---GCTGCGGCGCGGGCCTCGATCGAGGCG
1    M  S  N  L  E  D  R  K  L  A  L  S  E  N  P  Y  A  E  K  Y  -  A  A  A  R  A  S  I  E  A
```

Figure S2. Multiple translation start sites found in the hypothetical protein RD1_1231 (YP_681565.1). For this protein, two alternative initiation start sites were recorded, both ATG codons. A multiple sequence alignment with closely-related homologues demonstrated that the first initiation site is conserved in all three strains listed while the second one, 9 nucleotides downstream, is only confirmed in *R. litoralis* Och 149. Previously annotated codons are shown in red and their counterparts in other sequences are in blue. The correct initiation codons are underlined and in bold red. This protein should be re-annotated in *R. litoralis*. The translated polypeptide from the previous annotation and the new corrected annotation are labeled 1 and 2, respectively. Blue lines represent the peptide sequence identified. Peptide sequences differing from the modifications identified are not represented.