

Supplementary Materials

Ecophysiological Features Shape the Distribution of Prophages and CRISPR in Sulfate Reducing Prokaryotes

Roberto Orellana¹, Alejandra Arancibia¹, Leonardo Badilla¹, Jonathan Acosta³, Gabriela Arancibia², Rodrigo Escar², Gustavo Ferrada², Michael Seeger².

¹Laboratorio de Biología Celular y Ecofisiología Microbiana. Facultad de Ciencias Naturales y Exactas. Universidad de Playa Ancha, Leopoldo Carvallo 270, Valparaíso, Chile. ²Laboratorio de Microbiología Molecular y Biotecnología Ambiental, Departamento de Química & Centro de Biotecnología Daniel Alkalay-Lowitt, Universidad Técnica Federico Santa María, Avenida España 1680, Valparaíso, Chile. ³ Departamento de Estadística, Pontificia Universidad Católica de Chile, Chile.

Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1.

Figures S1, S1.1 – S1.83, Phylogenetic trees of 16S rRNA gene sequences of SBR strains and microbial strains belonging to the training set of PhiSpy.

Figure S2: Effect of Mitomycin C on the growth of (a) *D. vulgaris* str. Hildenborough, (b) *D. africanus* 2603 and (c) *D. acrylicus* DSM 10141. White circles indicate cultures grown in the absence of Mitomycin C; orange circles, cultures grown in the presence of 1 µg ml⁻¹ of Mitomycin C; red circles, cultures grown in the presence of 3.5 µg ml⁻¹ of Mitomycin C. In (a), black triangles indicate cultures grown in the presence of 10 µg ml⁻¹ of Mitomycin C. Data represent the mean±sd from three independent replicate cultures. Bars designate one standard deviation of the mean. The table in the upper right section indicate presence (+) or absence (-) of prophages and CRISPR. (d) TEM micrographs of viral-like particles with typical morphotype of *Podoviridae* were obtained from *D. vulgaris* str. Hildenborough batch cultures after induction with Mitomycin C. (e-f) TEM micrographs presents structures that resembles outer membrane vesicles previously observed in *D. alaskensis* DSM16109. Most of the micrographs obtained in this study contained low-resolution viral particles and structures, cell debris, and a noisy background as a result of the interactions of the compounds of the growth medium of SRP.

Figure S3A: Effect of filtrates from mitomycin induced SRB cultures added at early exponential phase on the growth of *Desulfovibrio acrylicus* DSM 10141 (A-C), *Desulfovibrio vulgaris* str. Hildenborough (D-F), and *Desulfovibrio africanus* DSM 2603 (G-I).

Figure S3B: Effect of filtrates from mitomycin induced SRB cultures added at early stationary phase on the growth of *Desulfovibrio acrylicus* DSM 10141 (A-C), *Desulfovibrio vulgaris* str. Hildenborough (D-F), and *Desulfovibrio africanus* DSM 2603 (G-I).

Figure S4: Frequencies of integrated prophages (light red) and CRISPR arrays (light blue) in the genomes of SRP strains.

Figure S5: Box-plots of (A) DNA prophage per cell (volume) and (B) prophage density of lysogens belonging to five families of SRP; (C) red bars indicate the median of the length of prophages and (D) represents the median cellular volume and median genome size found in each family. Box-plots of (E) CRISPR DNA per cell and (F) CRISPR density of CRISPR-carrying strains belonging to five families of SRP; (G) light blue bars indicate the median of number of spacers belonging to strains of each family.

Figure S6: Distribution of prophages (red) and CRISPR (blue) according to different ecophysiological traits. In the left top (A), it is shown the distribution of prophages and CRISPR arrays according to the type of growth (doubling time ≤ 12 hours or > 12 hours, as fast-growing or slow-growing strains, respectively). In the left bottom (B), it is shown the distribution of prophages and CRISPR arrays according to the presence of flagellum, classified as strains with flagellum (Y), strains for which flagellum has not been observed (N) and strains with no information (nd). In the right (C), it is shown the distribution of prophages and CRISPR arrays according to type of environment in which strains were isolated or the source of material that allowed the reconstruction of the genomes.

Figure S7: Comparison of genome annotations among SRP prophages. Pie charts indicate the annotation of prophages from *Desulfocurvibacter africanus* 2603, *Desulfovibrio vulgaris* str. Miyazaki, *Desulfovibrio vulgaris* str. Hildenborough and *Desulfovibrio vulgaris* DP4. The inner circle indicates functional classification (see color bar) and outer circle indicates the classification in the following categories; genes with bacterial origin (light green), genes with viral origin (light orange) and genes with unknown function (light gray).

Figure S8: (A) Network shows the degree of homology among SRP prophages. Circles indicate each SRP, colored by the taxonomy of the host. Edges show the presence of homologous genes among prophages. (B) Network shows the degree of homology among SRP prophages that share more than 10 homologs. The width of edges indicates the number of homologous genes between two prophages.

Figure S9: Whole-genome dot plot comparison of prophage nucleotides sequences of *Desulfovibrio* strains, prophages 1R1, 1R5 and 1R6 of *D. vulgaris* Hildenborough, 2R3 of *Desulfovibrio africanus* DSM 260, 5R2 of *Desulfovibrio aespoensis* Aspo-2, 14R1 of *Desulfovibrio vulgaris* str. Miyazaki, 18R1 of *Desulfovibrio fructosivorans* JJ, 28R1 of *Desulfovibrio* sp. X2, 44R1 of *Desulfovibrio alaskensis* G20, and 90R2 and 90R3 of *Desulfovibrio vulgaris* DP4. Lack of grouping in dot plots are both reflection of the overall high degree of diversity and low level of synteny of the SRP prophages. The symbols indicate the classification of each prophage according to VIRFAM. The numbers in the right and bottom indicate the length of each prophage (in bp).

Table S1: CRISPR and putative CRISPR arrays identified in plasmids of SRP analysed in this study.

Table S2. List of prophages predicted by Phaster and PhiSpy. Columns indicate the following; total number of predicted prophages per host, prophage ID, prophage sequence ID, the start and end of the prophage in the genome, the length of the prophage (bp), the number of ORF, total prophage length (bp), average of the length, genome size of the host, prophage density, total prophage density, and taxonomic classification according to Virfam. Prophage density represents the portion of the host genome that contain each prophage ($\text{bp prophage} * \text{bp}^{-1} \text{host} * 100$).

Table S3: Ecophysiological traits of SRP. The columns show the different SRP in this study, pH range, temperature range, classification with respect to temperature, cell wall type (gram), motility (denoted with Y for those for which the flagellum has been observed and N for which it has not been observed), habitat type, growth type under optimal conditions, oxidation (complete or incomplete), size (μm^2), cell volume (μm^3) and cell surface area.

Table S4: List of CRISPR elements found by CRISPRCas-Finder. The columns indicate the following: The number assigned to each strain in this study, strain name, CRISPR sequence ID, CRISPR ID (named by CRISPRCas-Finder), beginning and end of each CRISPR array, consensus repeat, repeat length, number of spacers, level of evidence and the total size of each CRISPR found.

Table S5: List of CRISPR elements found inside prophages. The columns indicate the strain name, the prophage sequence ID, the beginning and end of the prophage in the genome, CRISPR sequence ID and the beginning and end of CRISPR in the nucleotide sequence.

Table S6: Classification of prophages according to Virfam. Columns indicate the following: Prophage ID, classification assigned by Virfam using head-neck-tail module genes, the length of the prophage (bp) and the name of the host.

Table S7: Pairwise amino acid comparison of all predicted open reading frames (ORFs) from the SRP prophages. The abbreviation used is the following: pident, percentage of identical matches, length, alignment length, mismatch, number of mismatches, gaopen, number of gap openings, qstart, start of alignment in query, qend, end of alignment in query, sstart, start of alignment in subject, send, end of alignment in subject, and evalue, expected value.

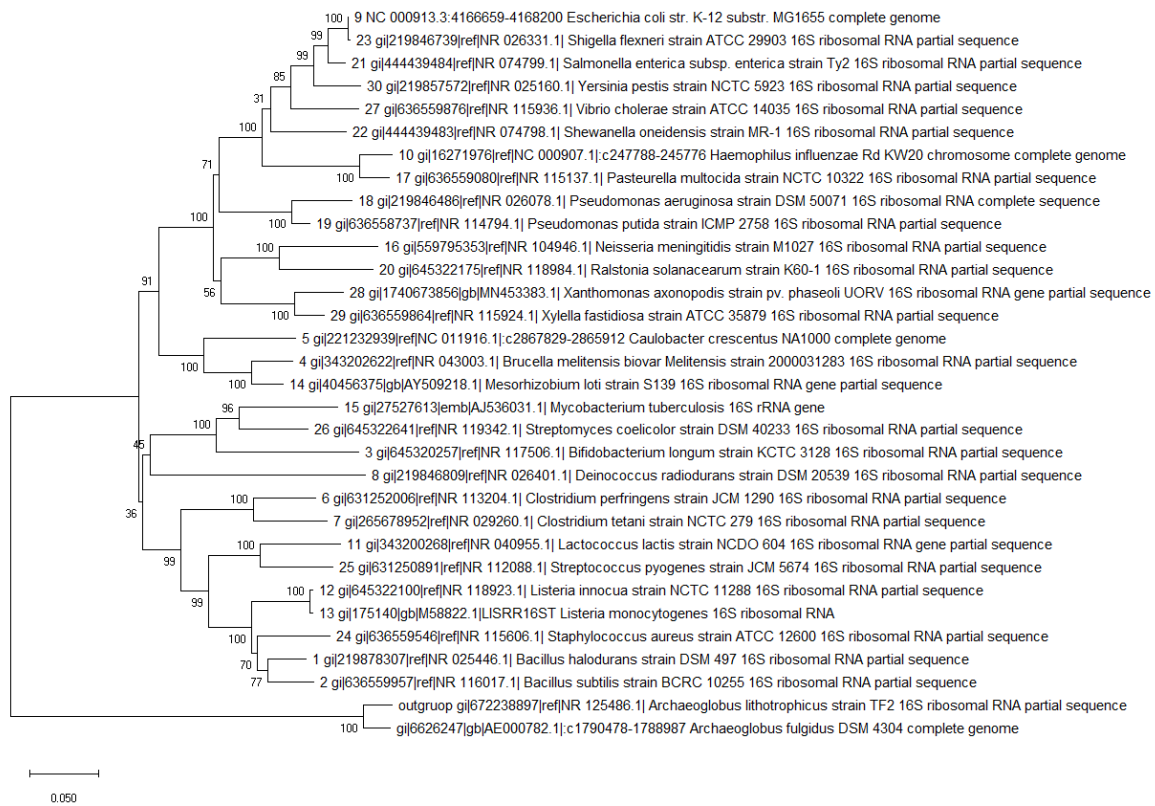


Figure S1.1: Phylogenetic tree of 16S rRNA gene sequences of *Archaeoglobus fulgidus* DSM 4304 and microbial strains belonging to the training set of PhiSpy.

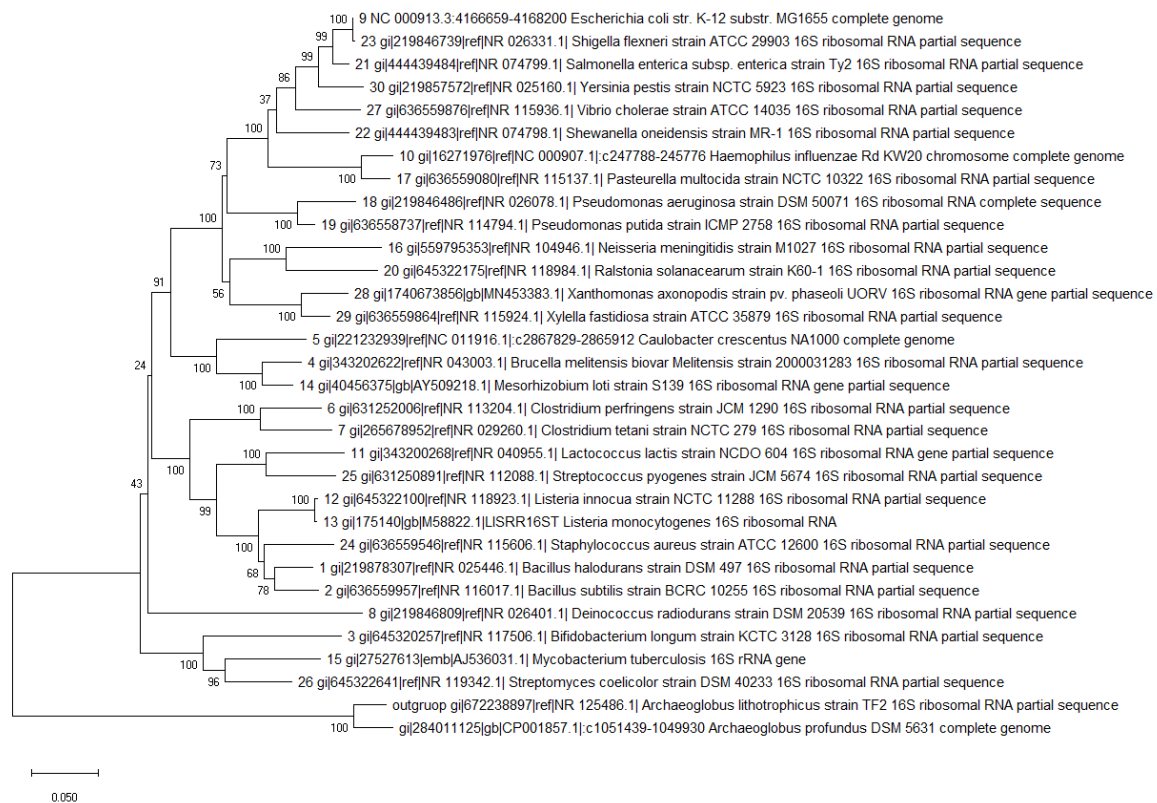


Figure S1.2: Phylogenetic tree of 16S rRNA gene sequences of *Archaeoglobus profundus* DSM 5631 and microbial strains belonging to the training set of PhiSpy.

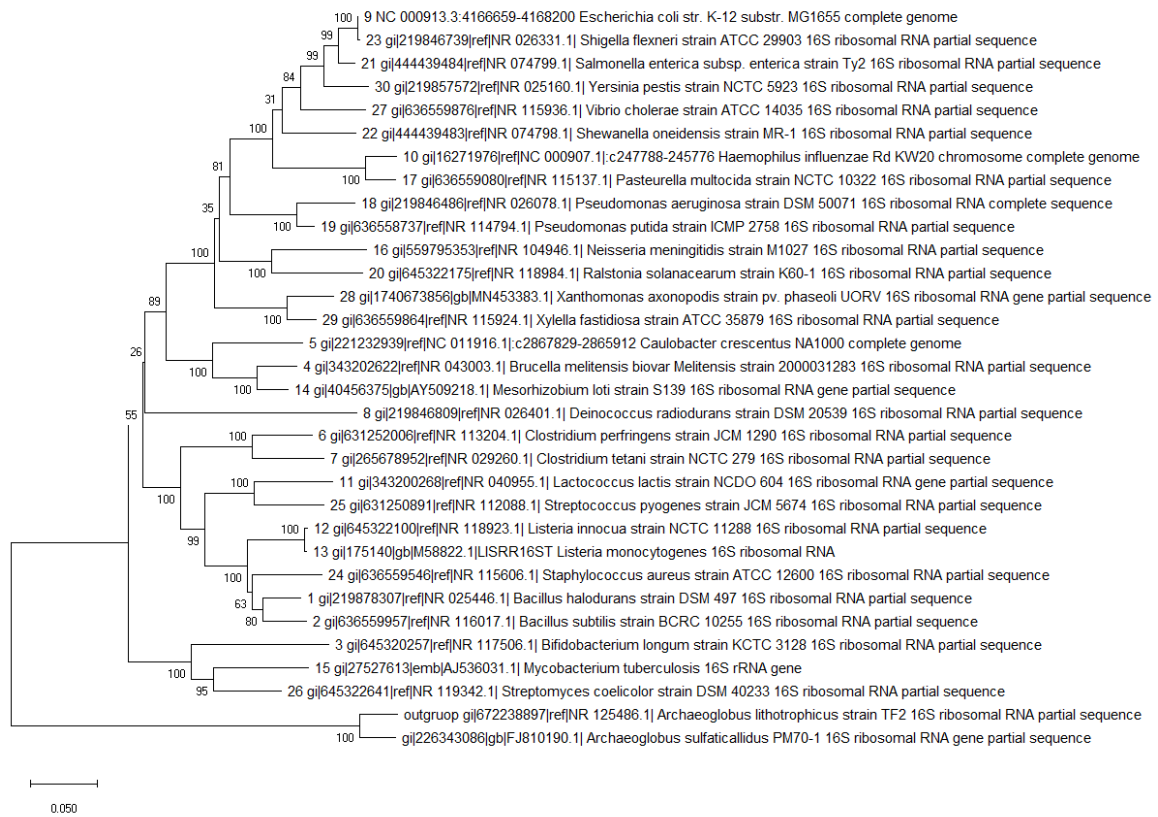


Figure S1.3: Phylogenetic tree of 16S rRNA gene sequences of *Archaeoglobus sulfaticallidus* PM70-1 and microbial strains belonging to the training set of PhiSpy.

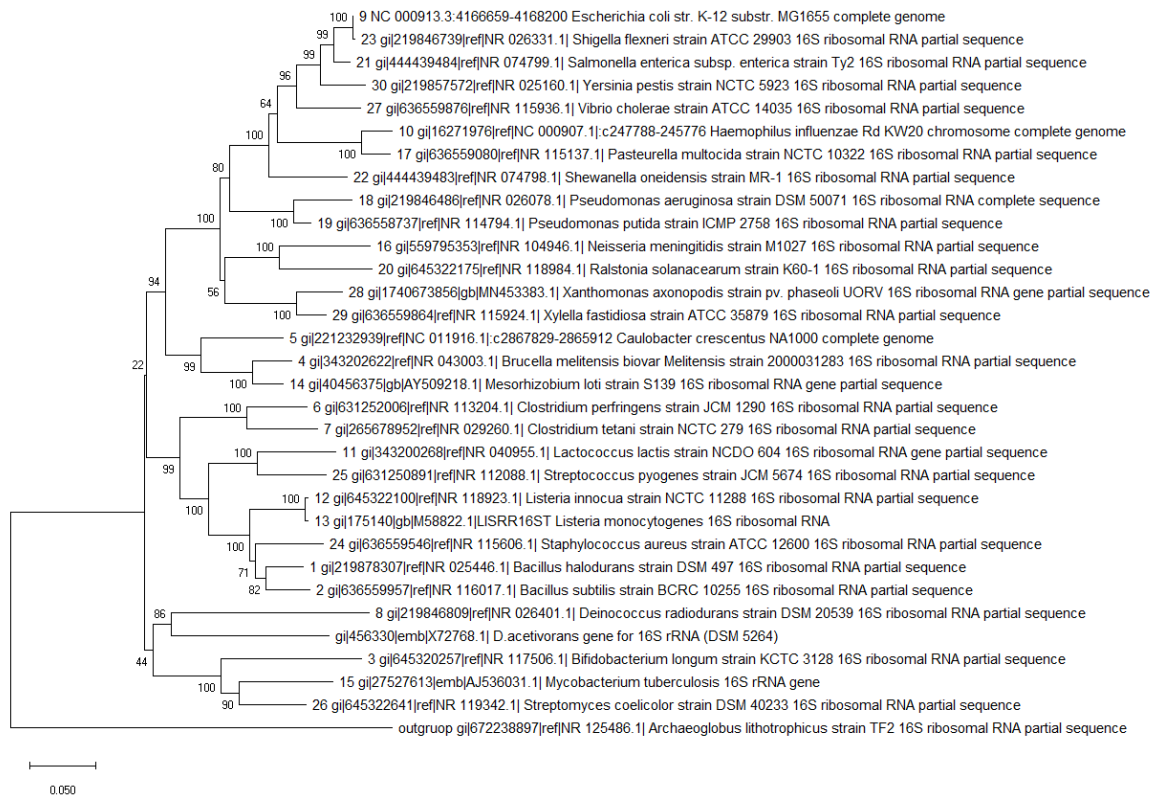


Figure S1.4: Phylogenetic tree of 16S rRNA gene sequences of *D. acetivorans* and microbial strains belonging to the training set of PhiSpy.

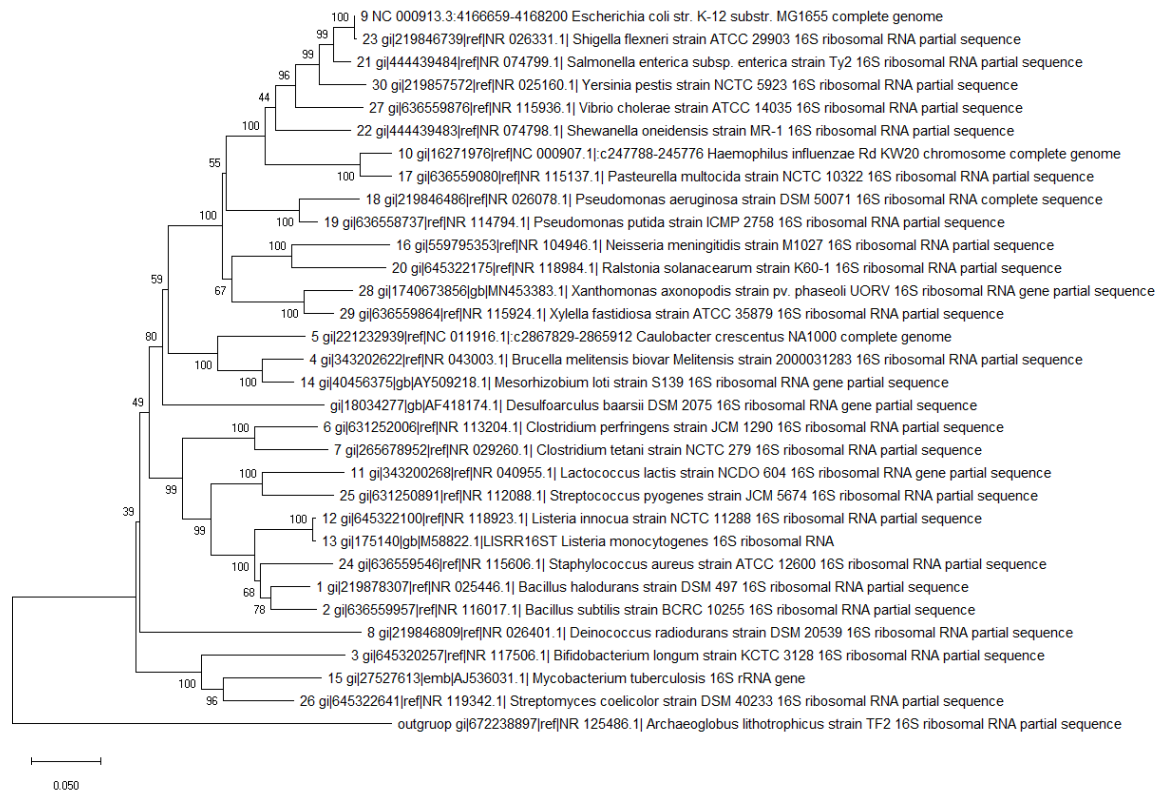


Figure S1.5: Phylogenetic tree of 16S rRNA gene sequences of *Desulfarculus baarsii* DSM 2075 and microbial strains belonging to the training set of PhiSpy.

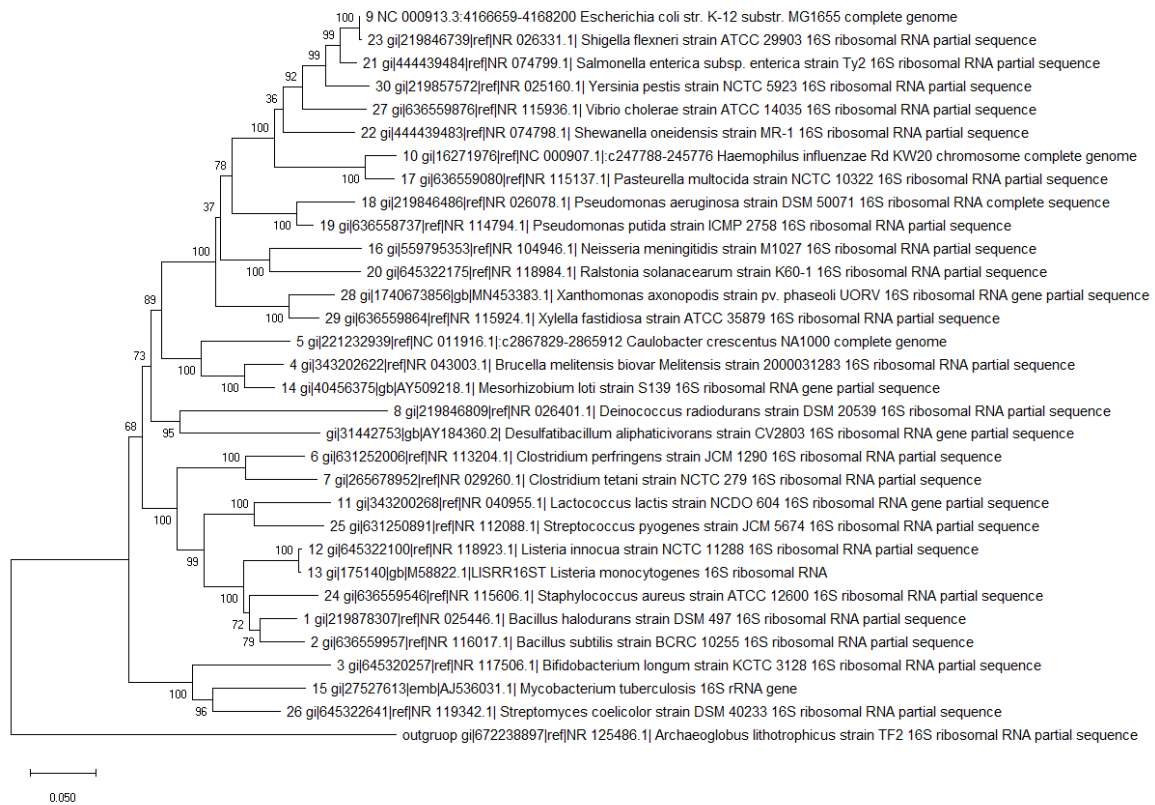


Figure S1.6: Phylogenetic tree of 16S rRNA gene sequences of *Desulfatibacillum aliphaticivorans* DSM 15576 and microbial strains belonging to the training set of PhiSpy.

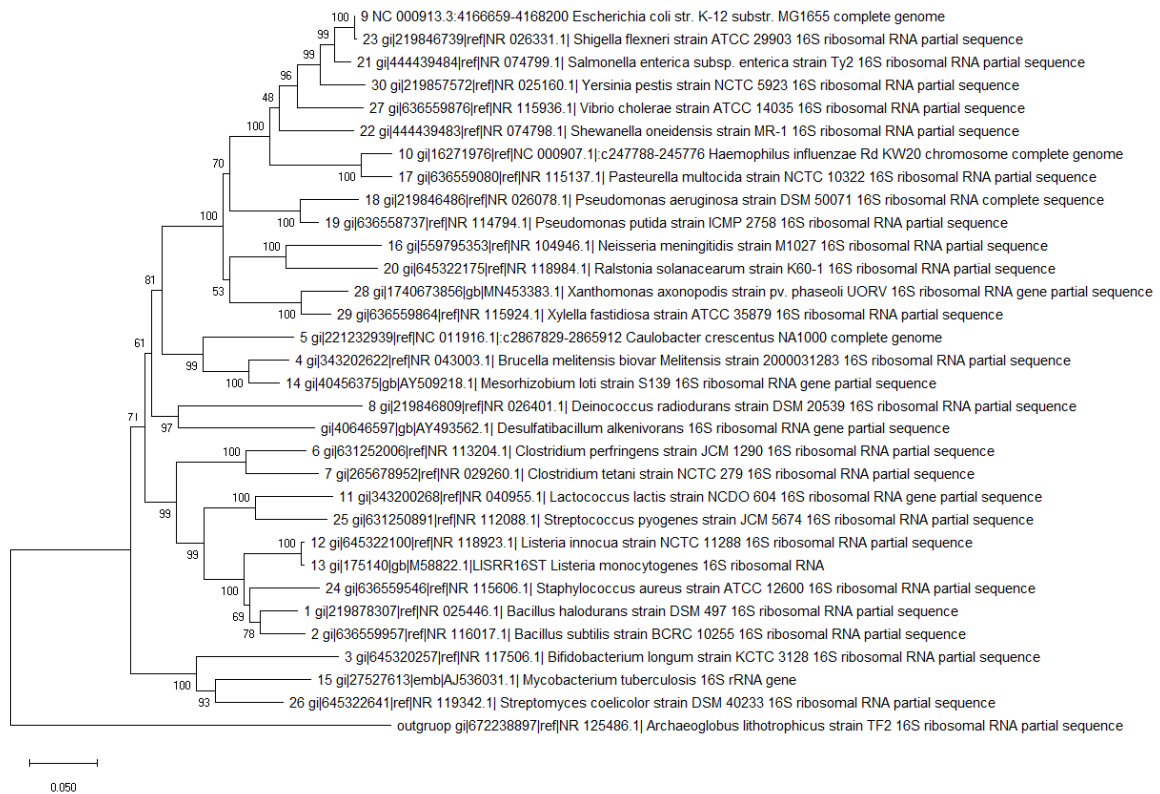


Figure S1.7: Phylogenetic tree of 16S rRNA gene sequences of *Desulfatibacillum alkenivorans* and microbial strains belonging to the training set of PhiSpy.

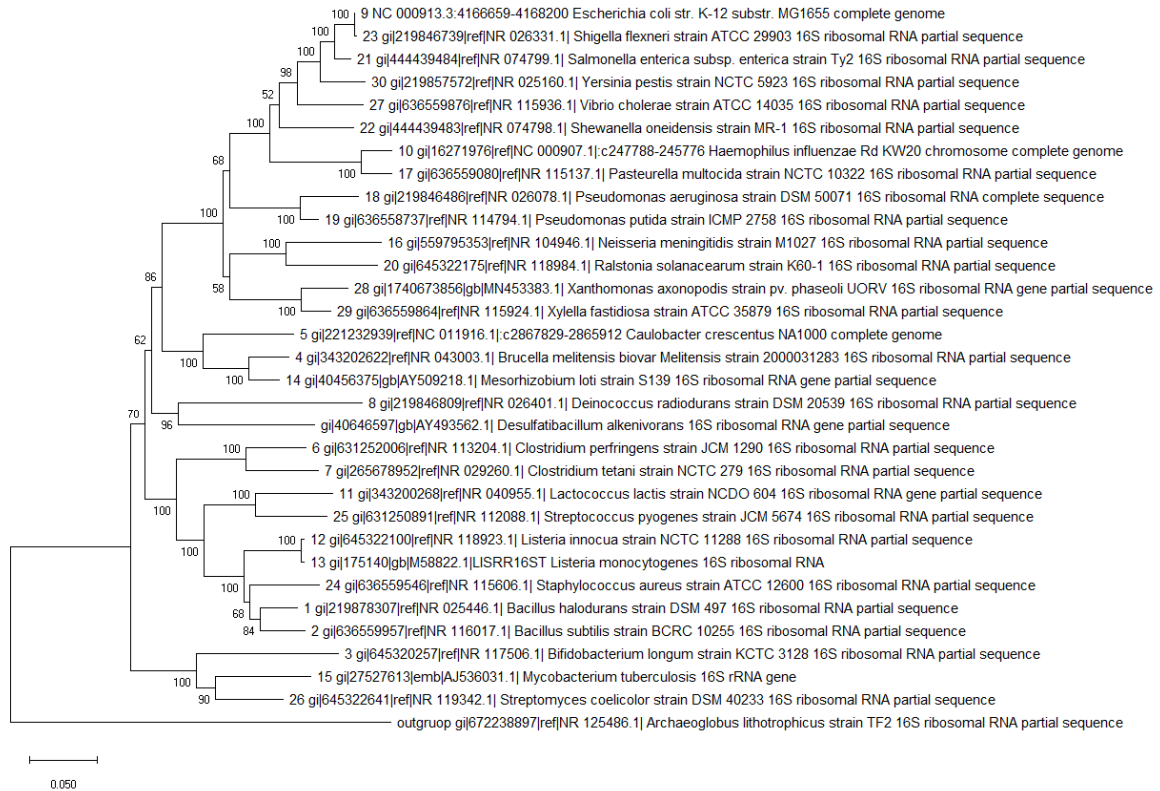


Figure S1.8: Phylogenetic tree of 16S rRNA gene sequences of *Desulfatibacillum alkenivorans* DSM 16219 and microbial strains belonging to the training set of PhiSpy.

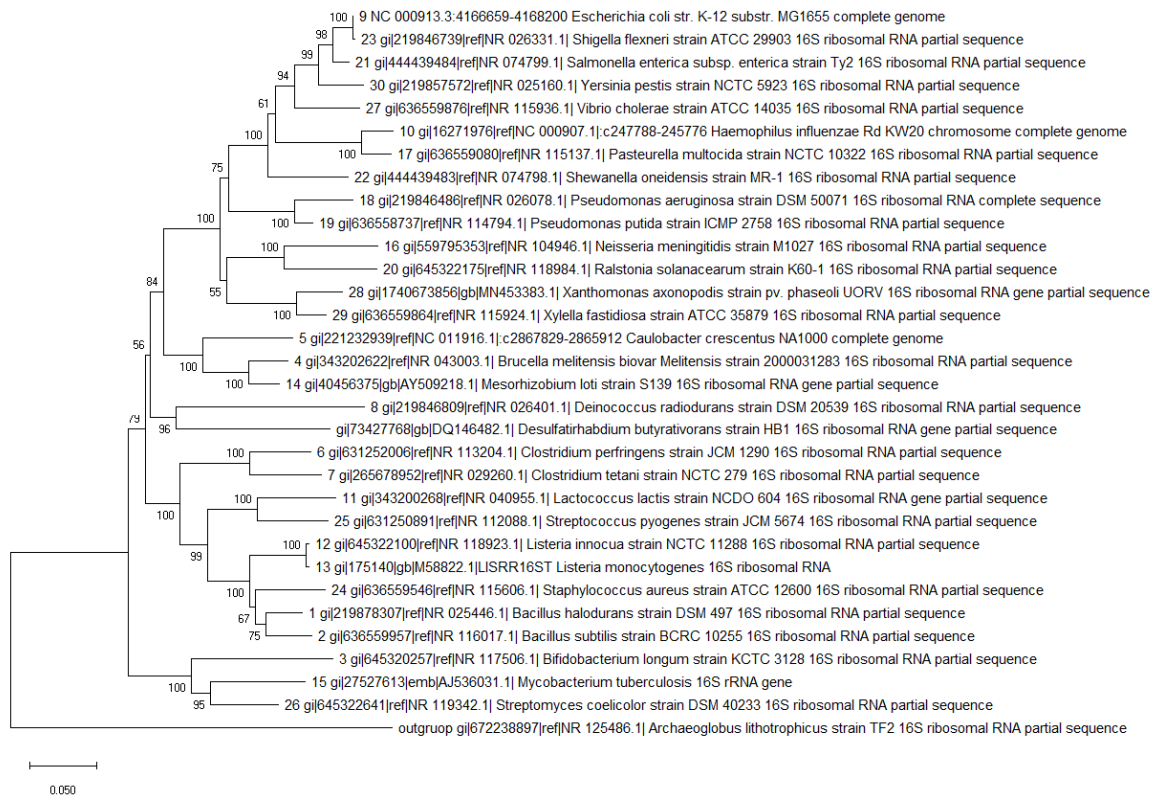


Figure S1.9: Phylogenetic tree of 16S rRNA gene sequences of *Desulfatirhabdium butyrativorans* DSM 18734 and microbial strains belonging to the training set of PhiSpy.

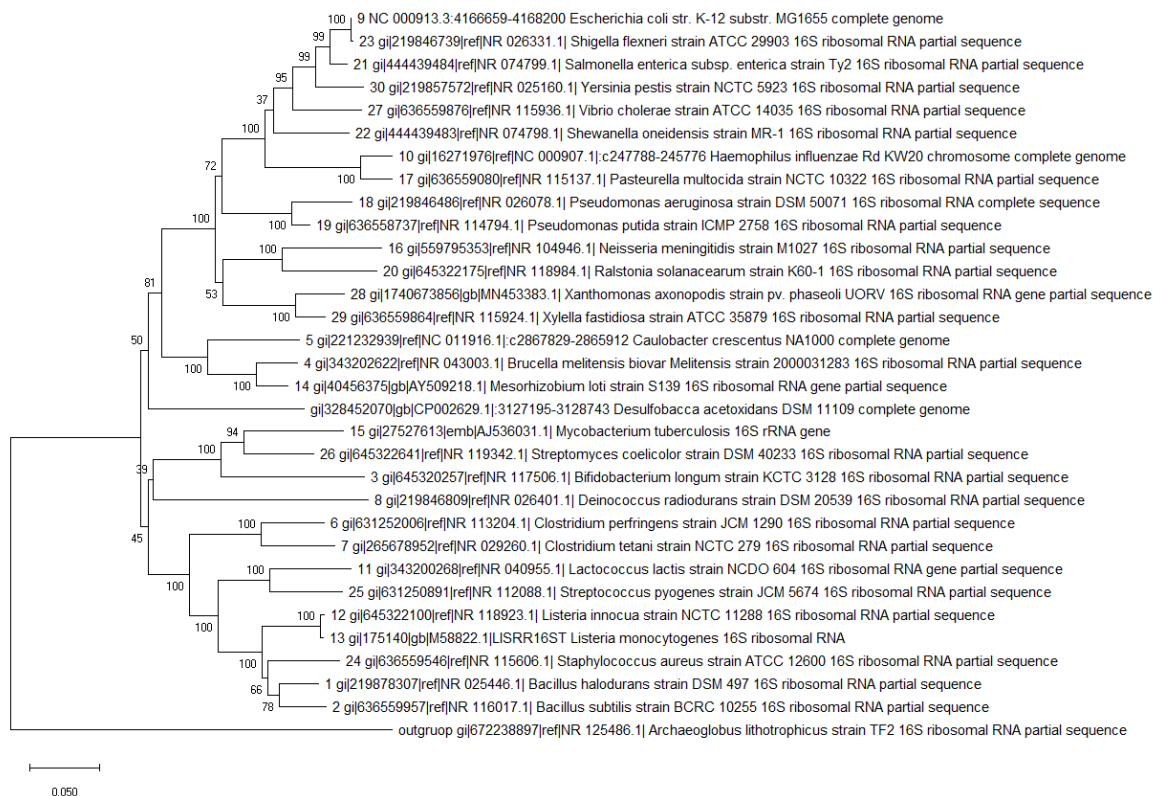


Figure S1.11: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacca acetoxidans* DSM 11109 and microbial strains belonging to the training set of PhiSpy.

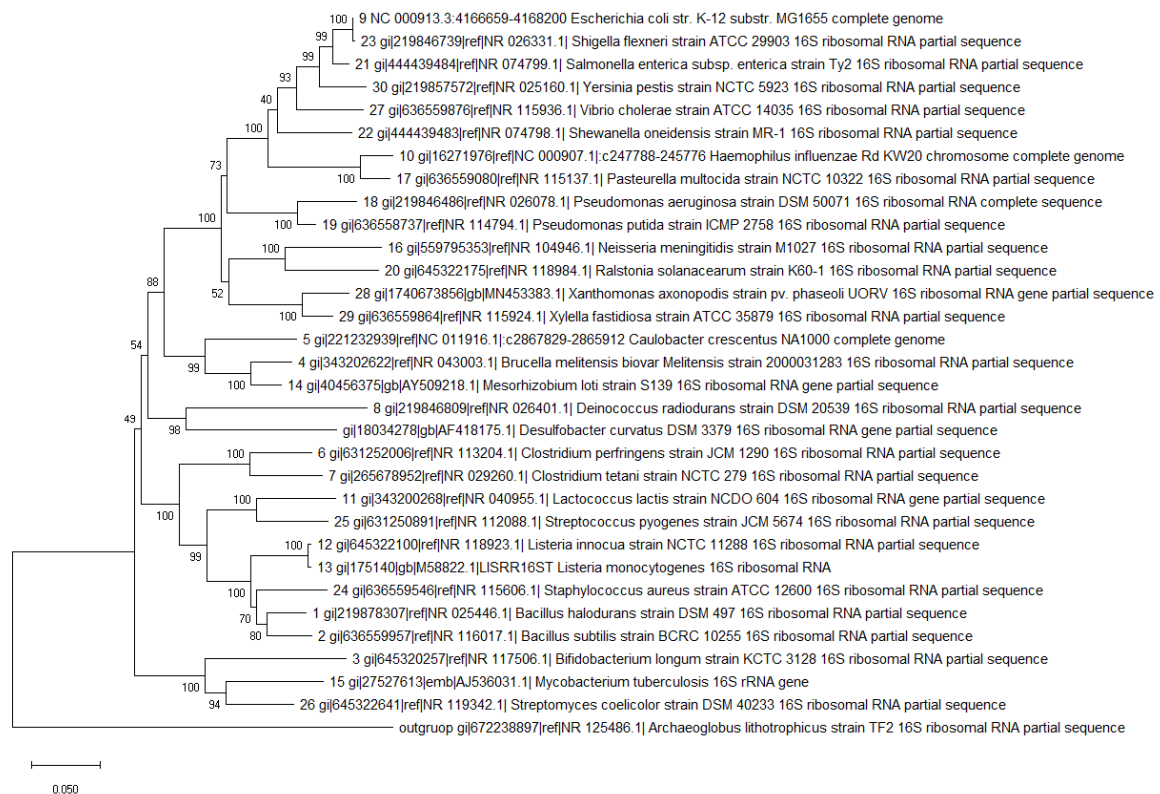


Figure S1.12: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacter curvatus* DSM 3379 and microbial strains belonging to the training set of PhiSpy.

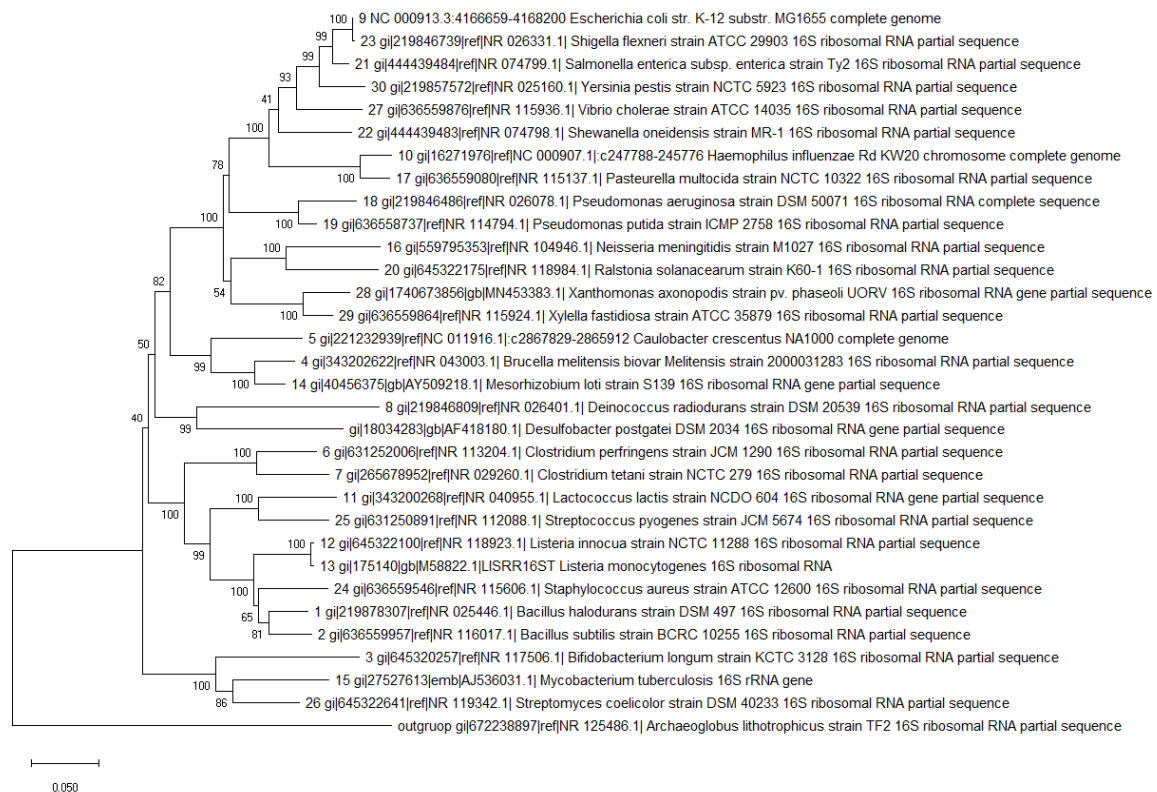


Figure S1.13: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacter postgatei* DSM 2034 and microbial strains belonging to the training set of PhiSpy.

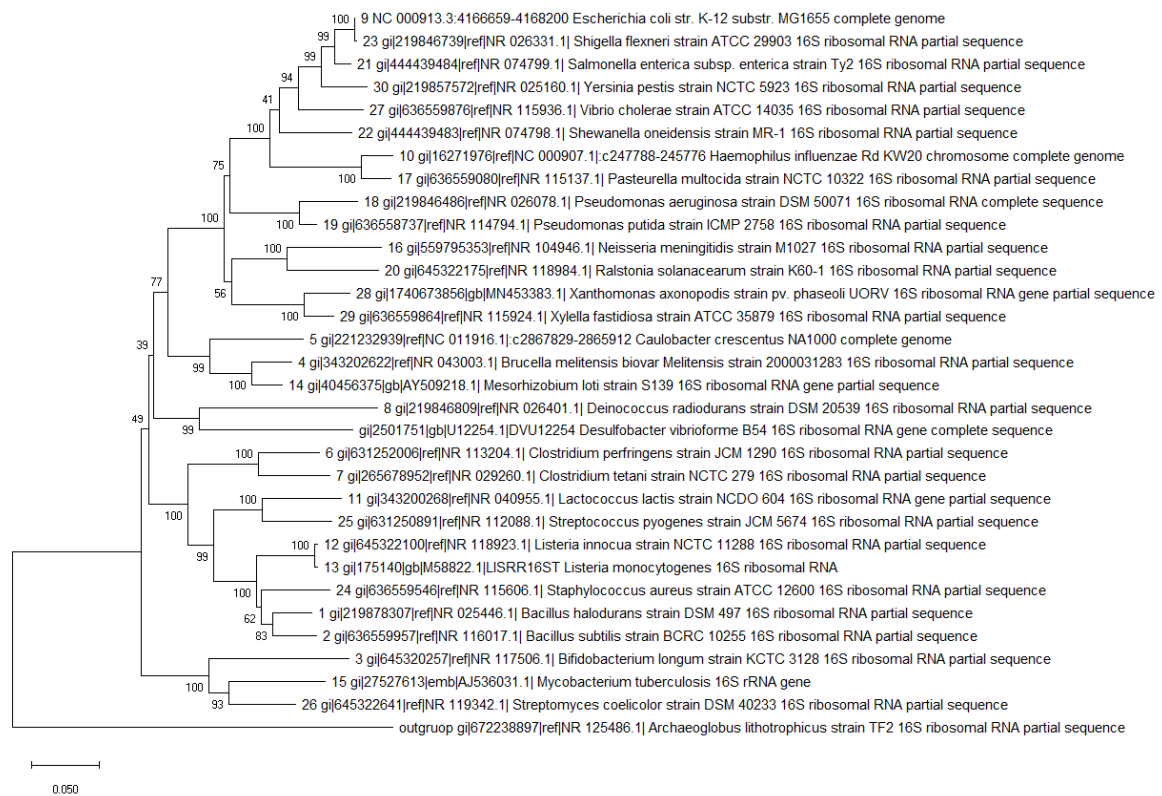


Figure S1.14: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacter vibrioforme* B54 and microbial strains belonging to the training set of PhiSpy.

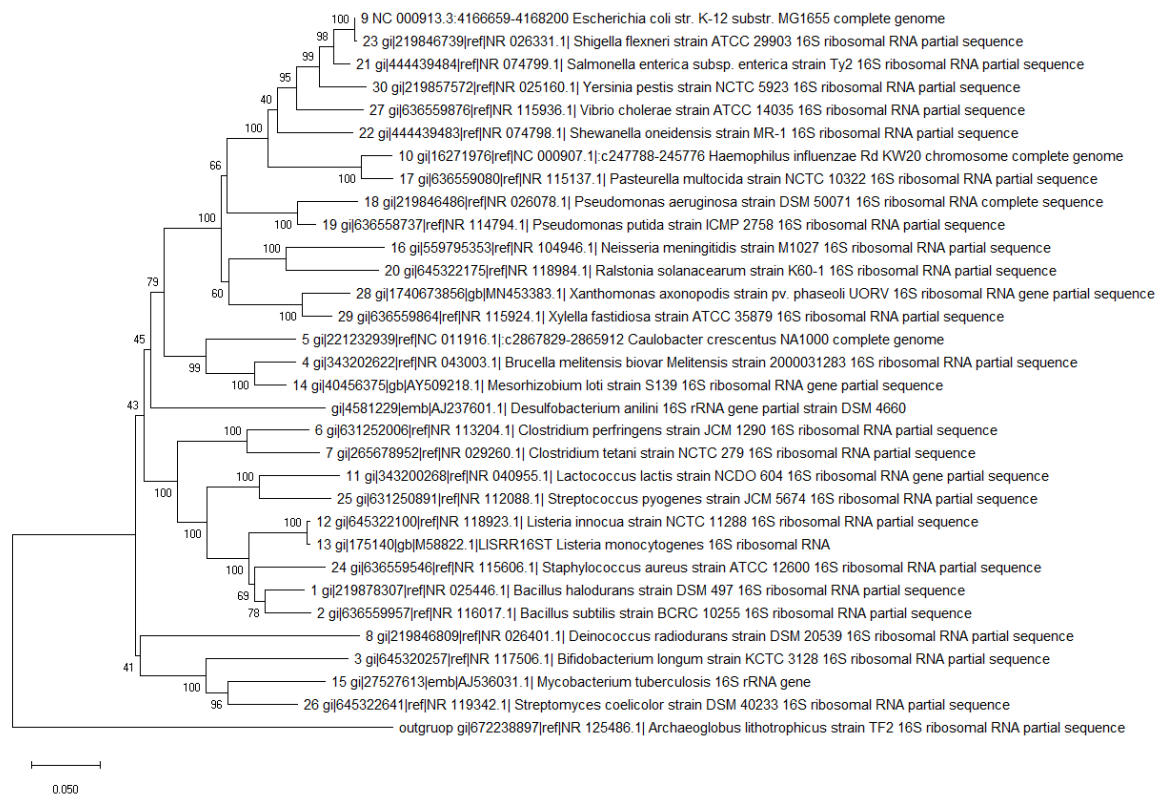


Figure S1.15: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacterium anilini* and microbial strains belonging to the training set of PhiSpy.

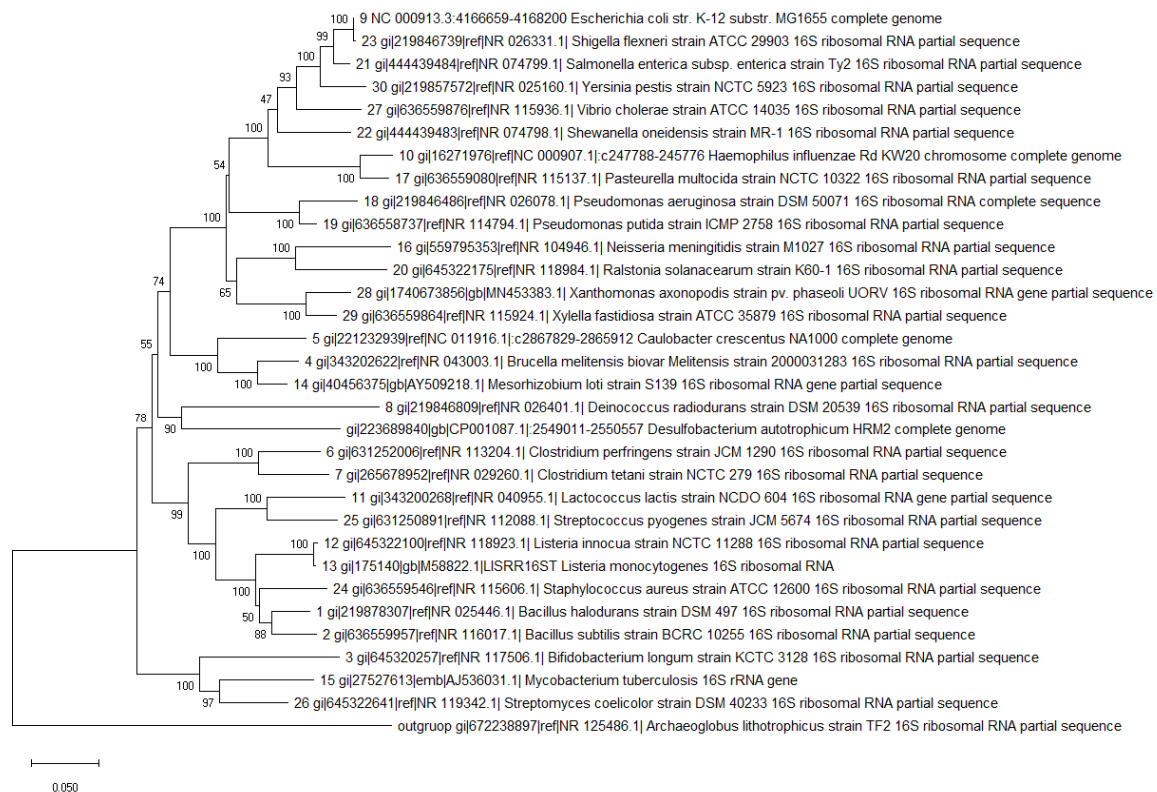


Figure S1.16: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacterium autotrophicum* HRM2 and microbial strains belonging to the training set of PhiSpy.

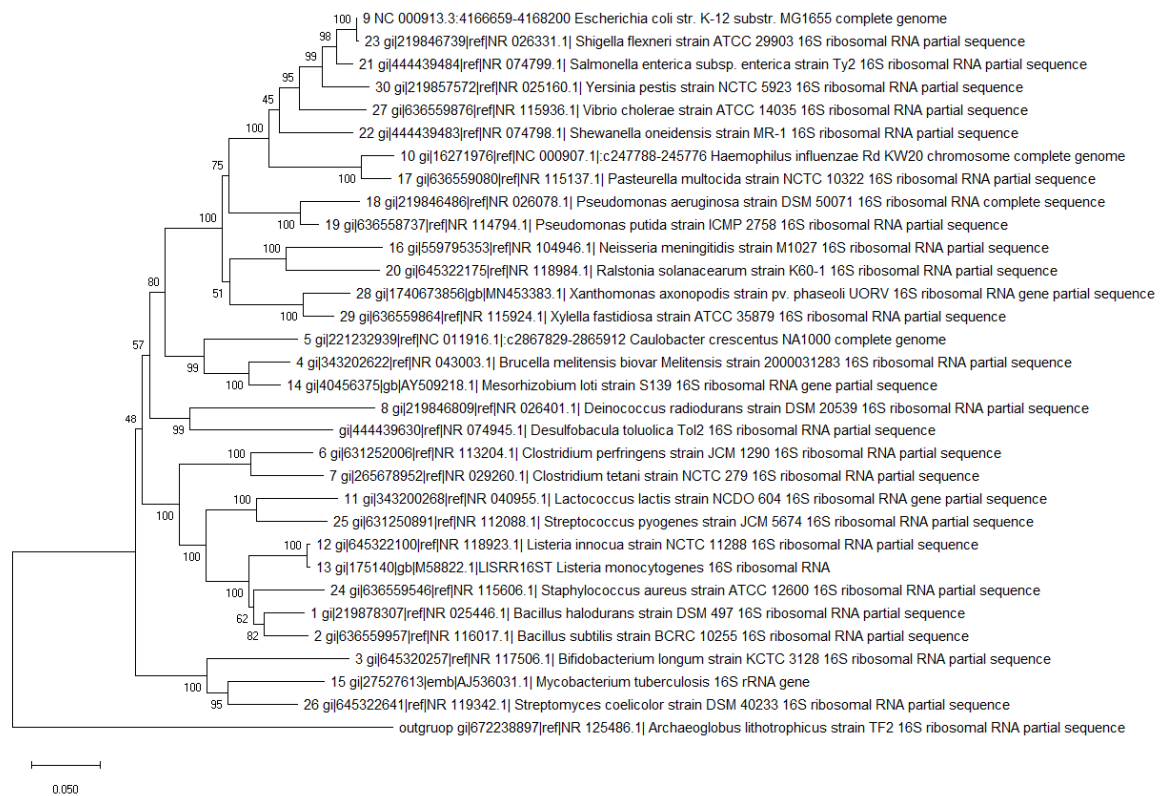


Figure S1.17: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobacula toluolica* Tol2 and microbial strains belonging to the training set of PhiSpy.

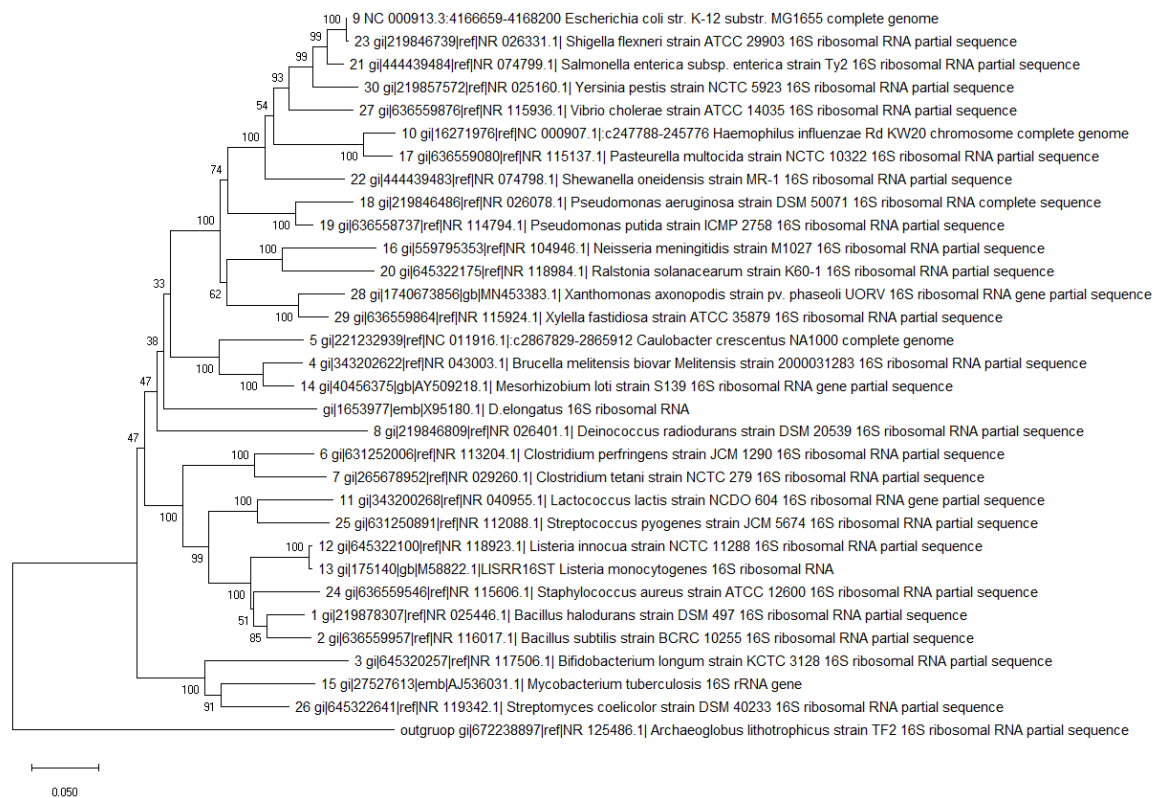


Figure S1.18: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobulbus elongatus* and microbial strains belonging to the training set of PhiSpy.

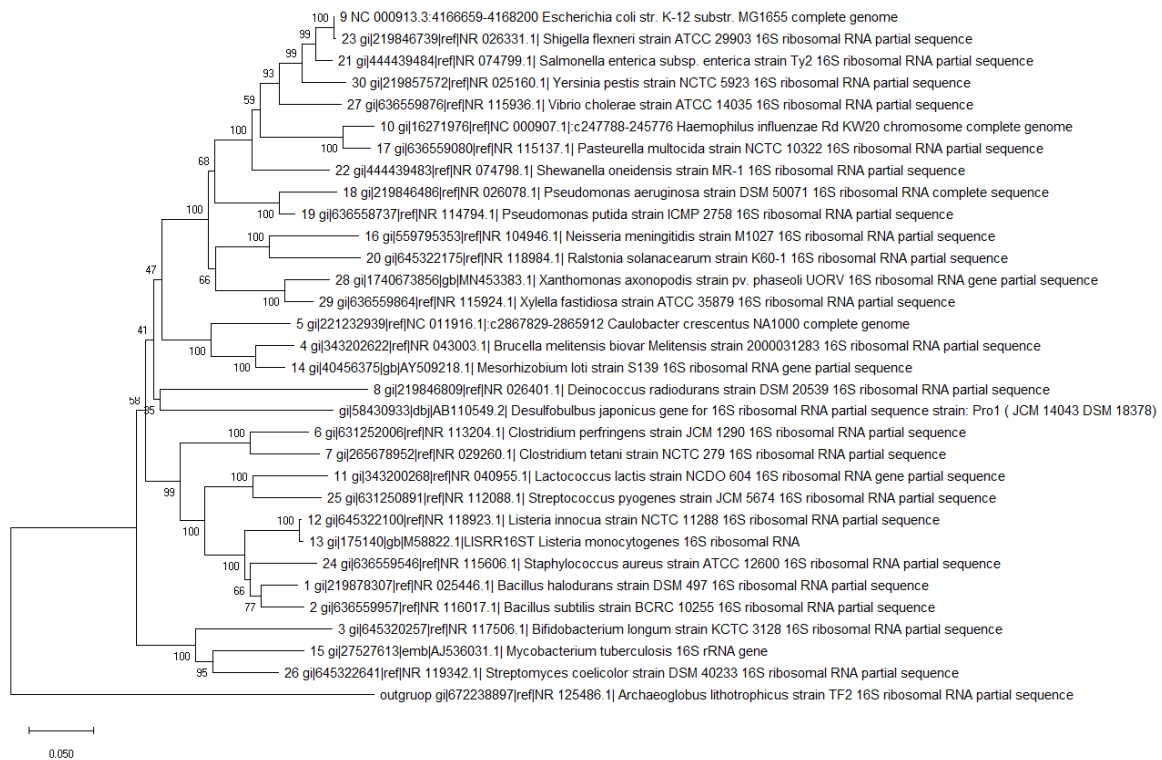


Figure S1.19: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobulbus japonicus* DSM 18378 and microbial strains belonging to the training set of PhiSpy.

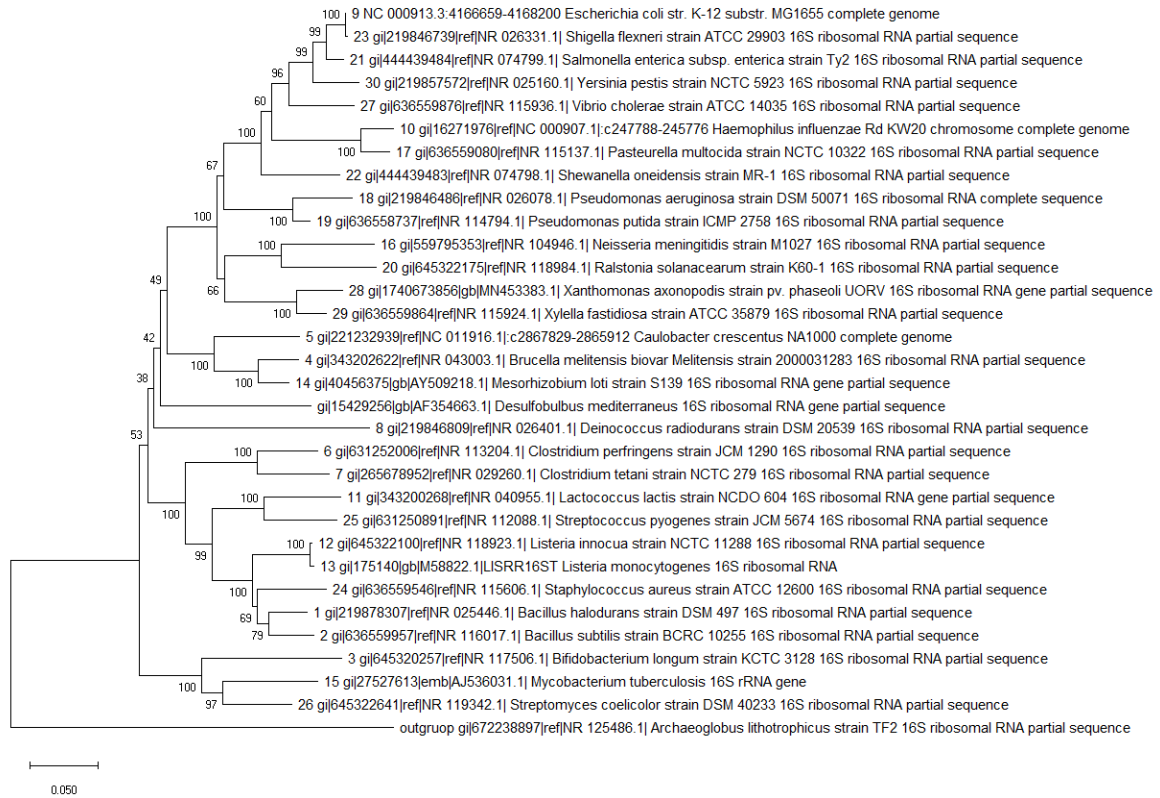


Figure S1.20: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobulbus mediterraneus* and microbial strains belonging to the training set of PhiSpy.

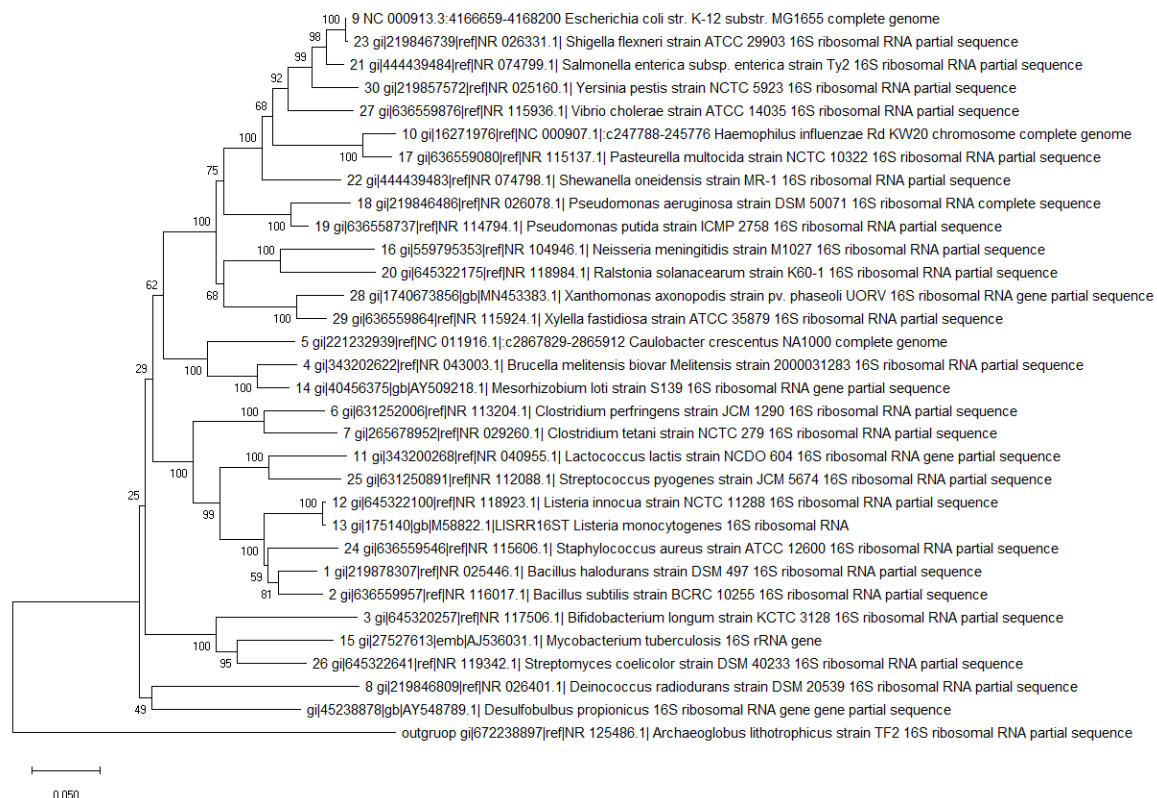


Figure S1.21: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobulbus propionicus* type strain 1pr3 and microbial strains belonging to the training set of PhiSpy.

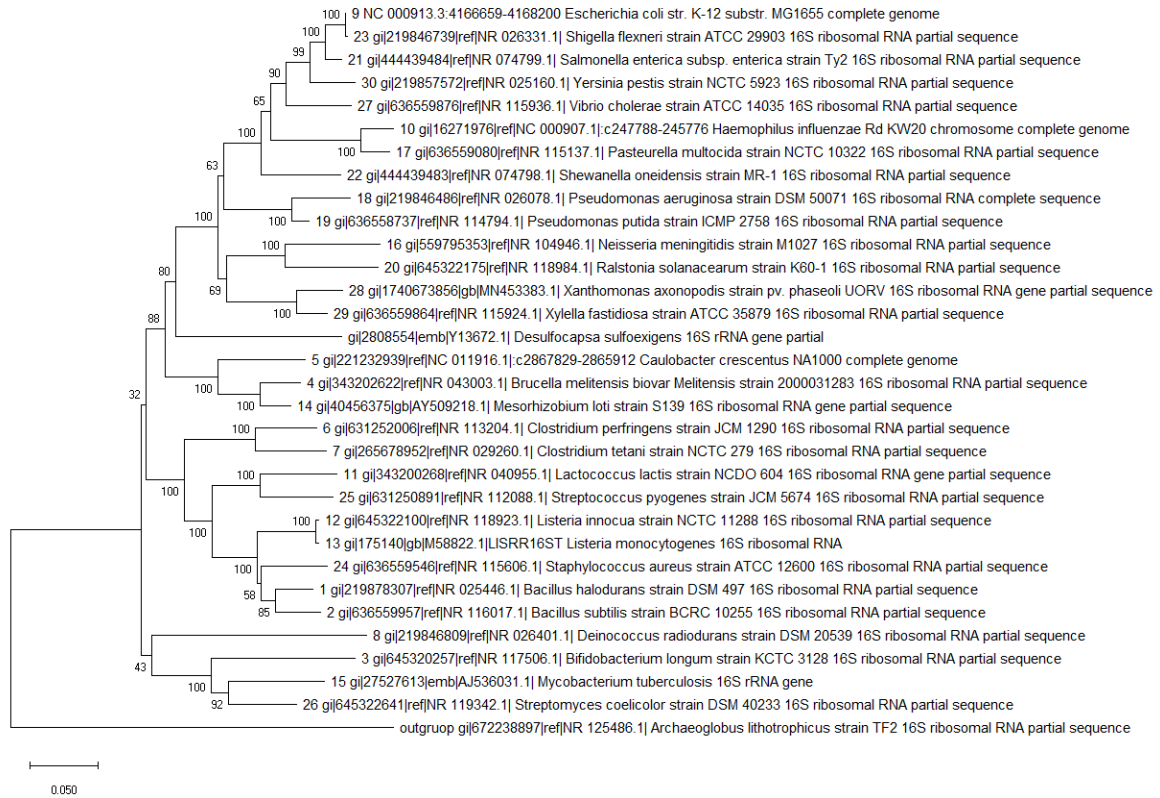


Figure S1.22: Phylogenetic tree of 16S rRNA gene sequences of *Desulfocapsa sulfexigens* DSM 10523 and microbial strains belonging to the training set of PhiSpy.

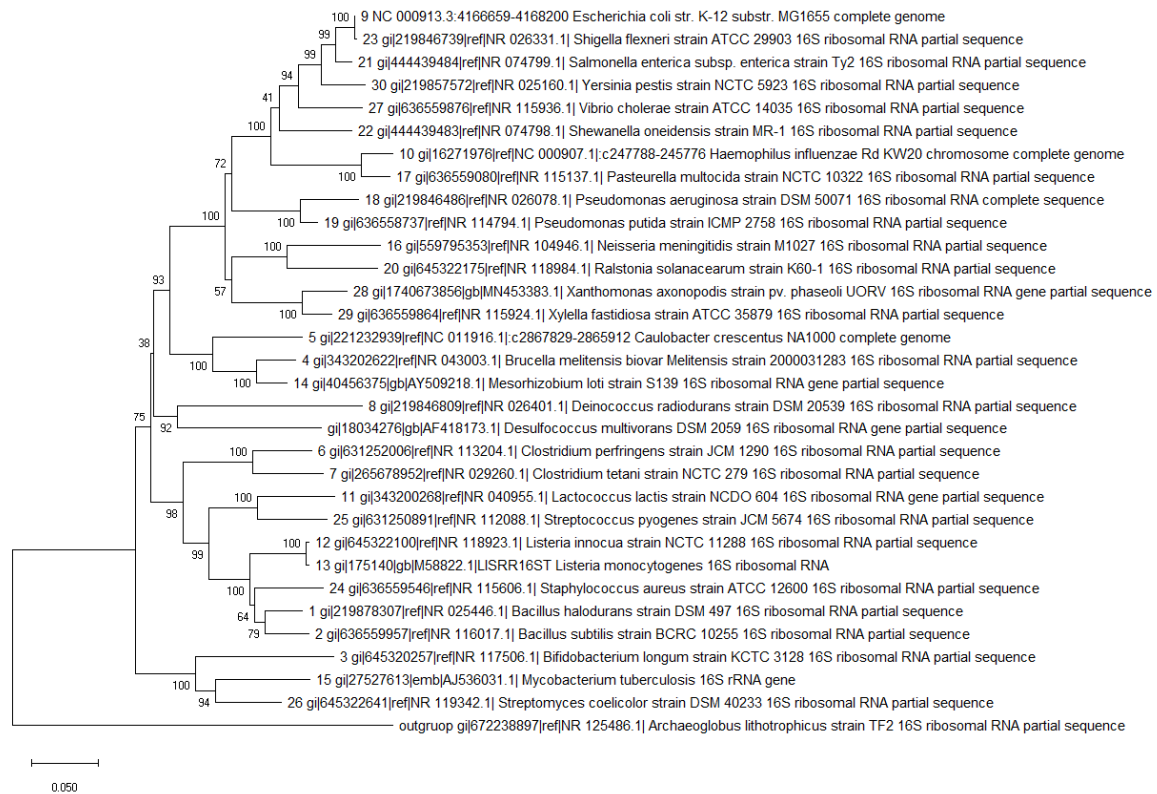


Figure S1.23: Phylogenetic tree of 16S rRNA gene sequences of *Desulfococcus multivorans* DSM 2059 and microbial strains belonging to the training set of PhiSpy.

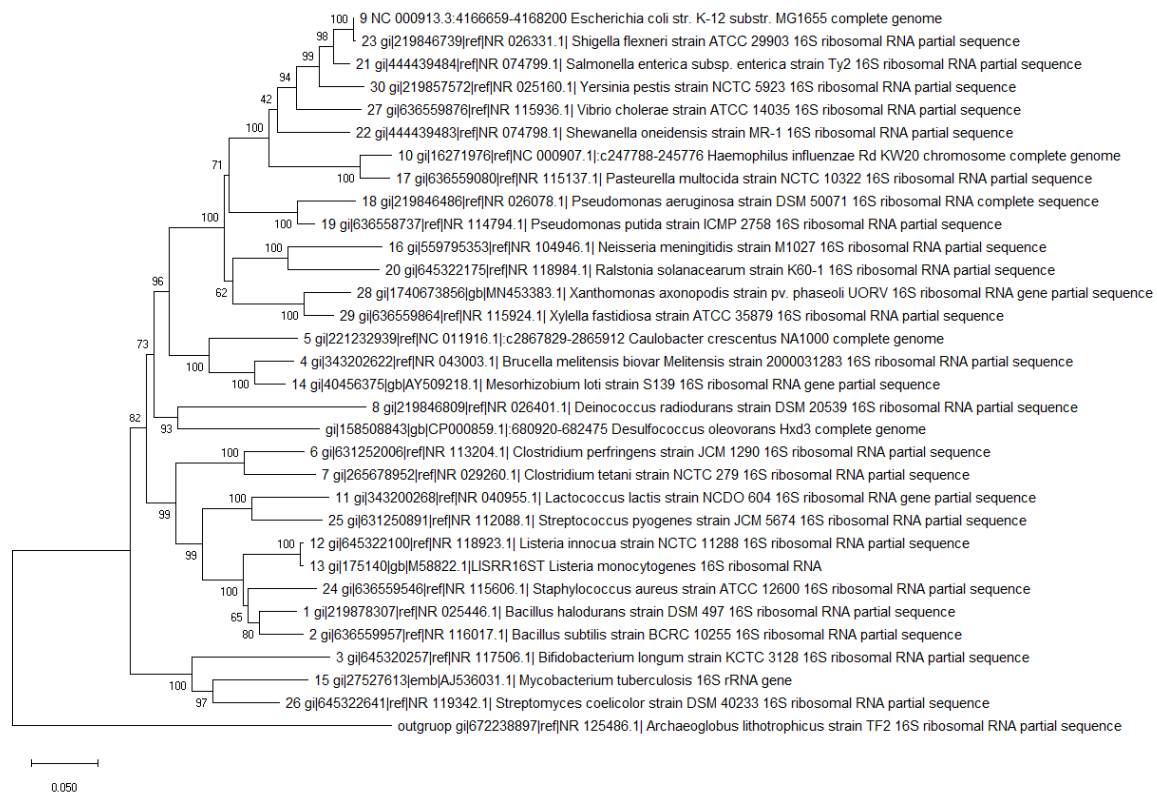


Figure S1.24: Phylogenetic tree of 16S rRNA gene sequences of *Desulfococcus oleovorans* Hxd3 and microbial strains belonging to the training set of PhiSpy.

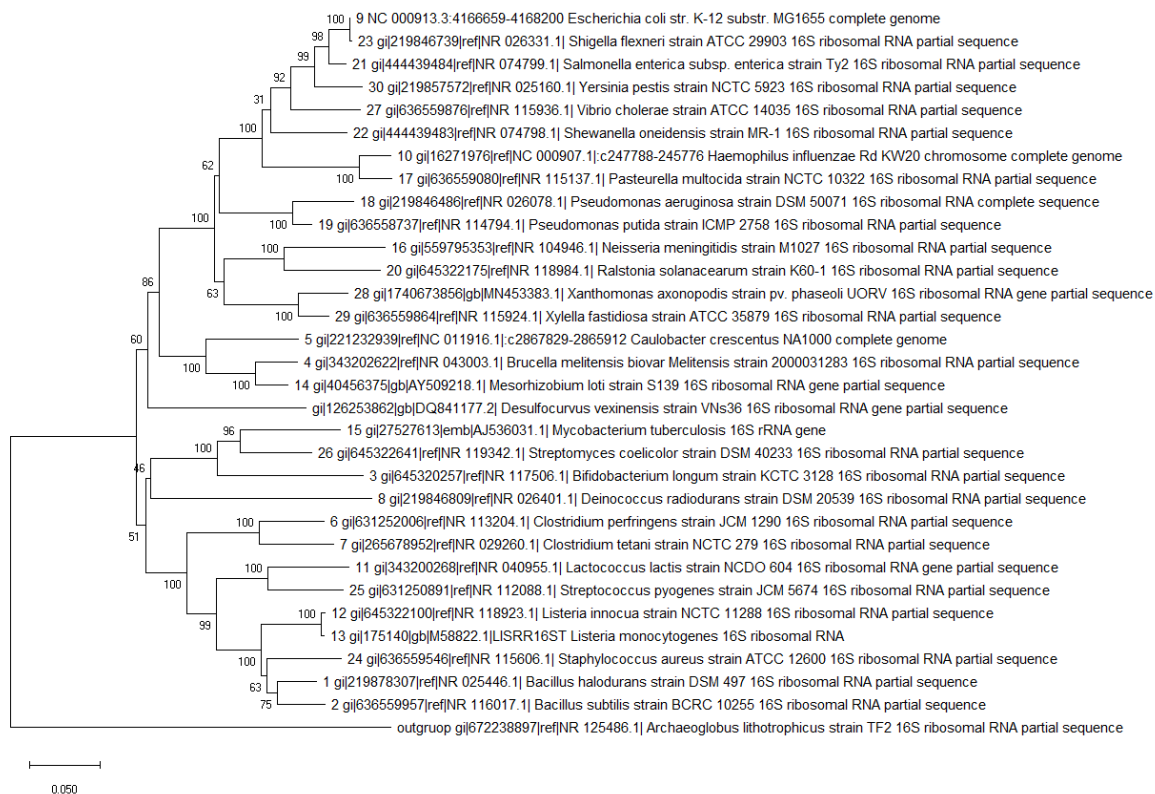


Figure S1.25: Phylogenetic tree of 16S rRNA gene sequences of *Desulfocurvus vexinensis* and microbial strains belonging to the training set of PhiSpy.

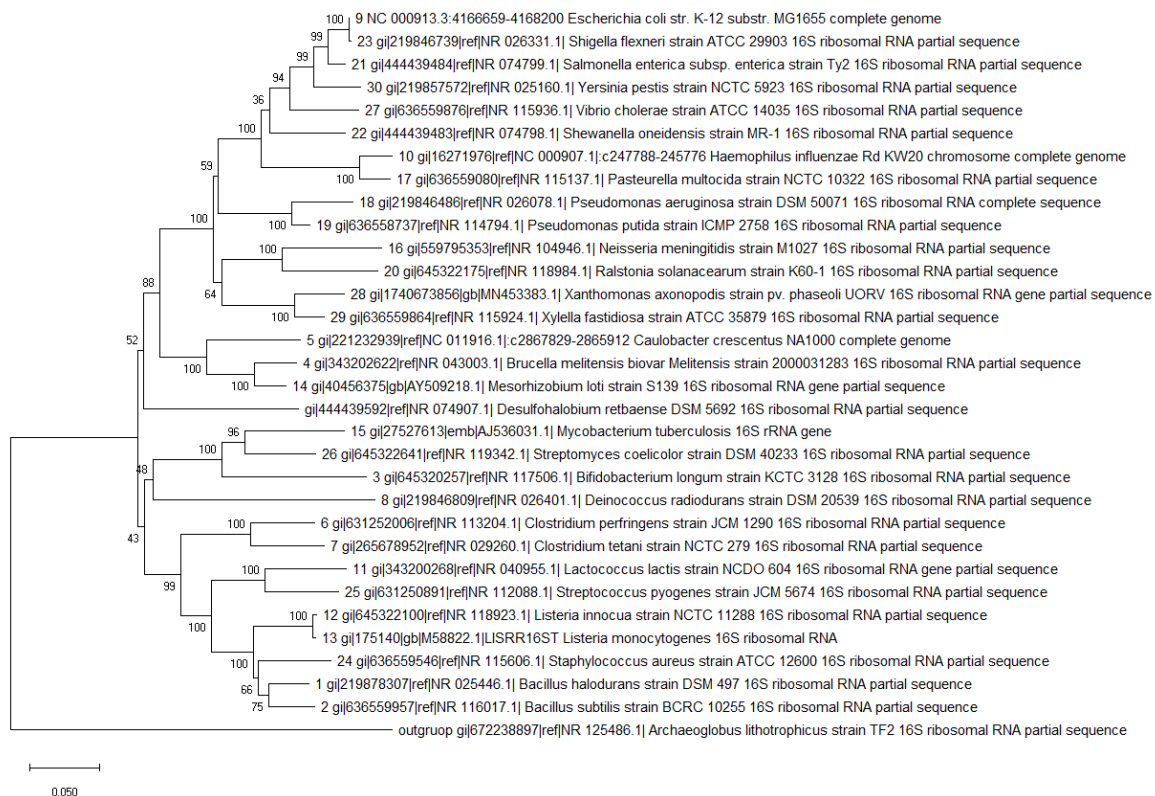


Figure S1.26: Phylogenetic tree of 16S rRNA gene sequences of *Desulfobalobium retbaense* DSM 5692 and microbial strains belonging to the training set of PhiSpy.

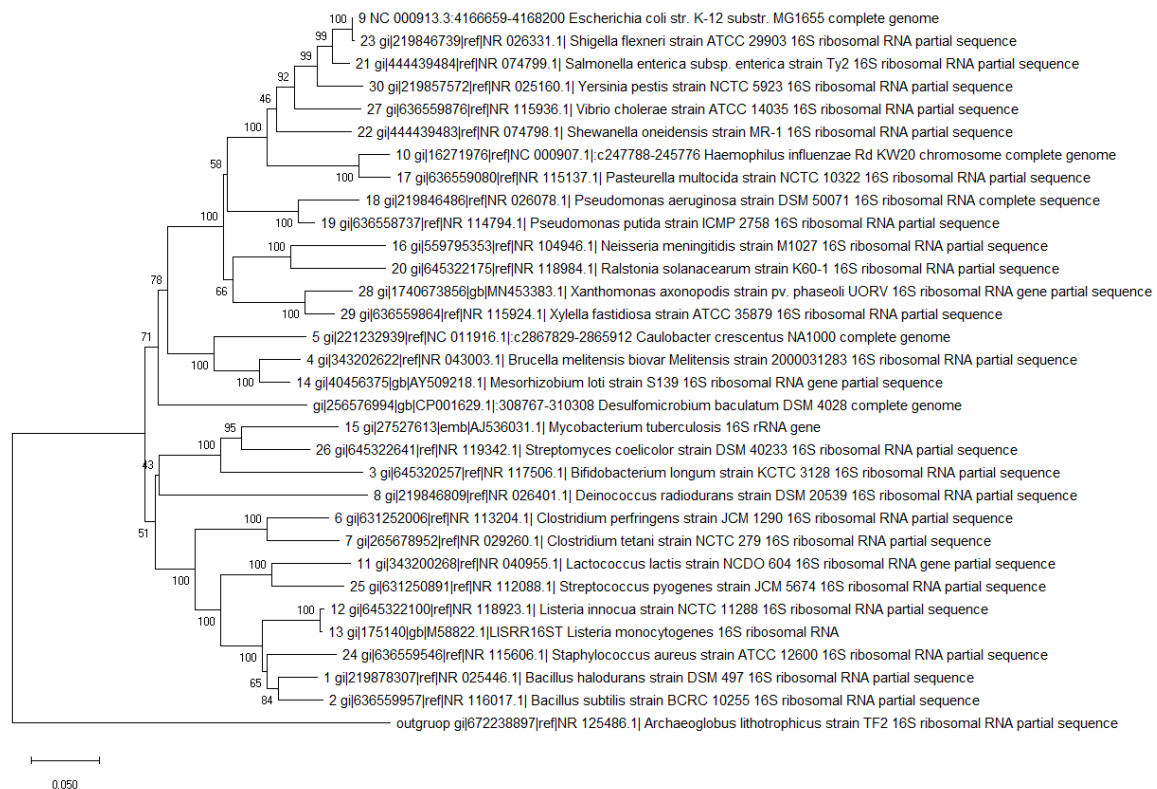


Figure S1.27: Phylogenetic tree of 16S rRNA gene sequences of *Desulfomicrobium baculatum* DSM 4028 and microbial strains belonging to the training set of PhiSpy.

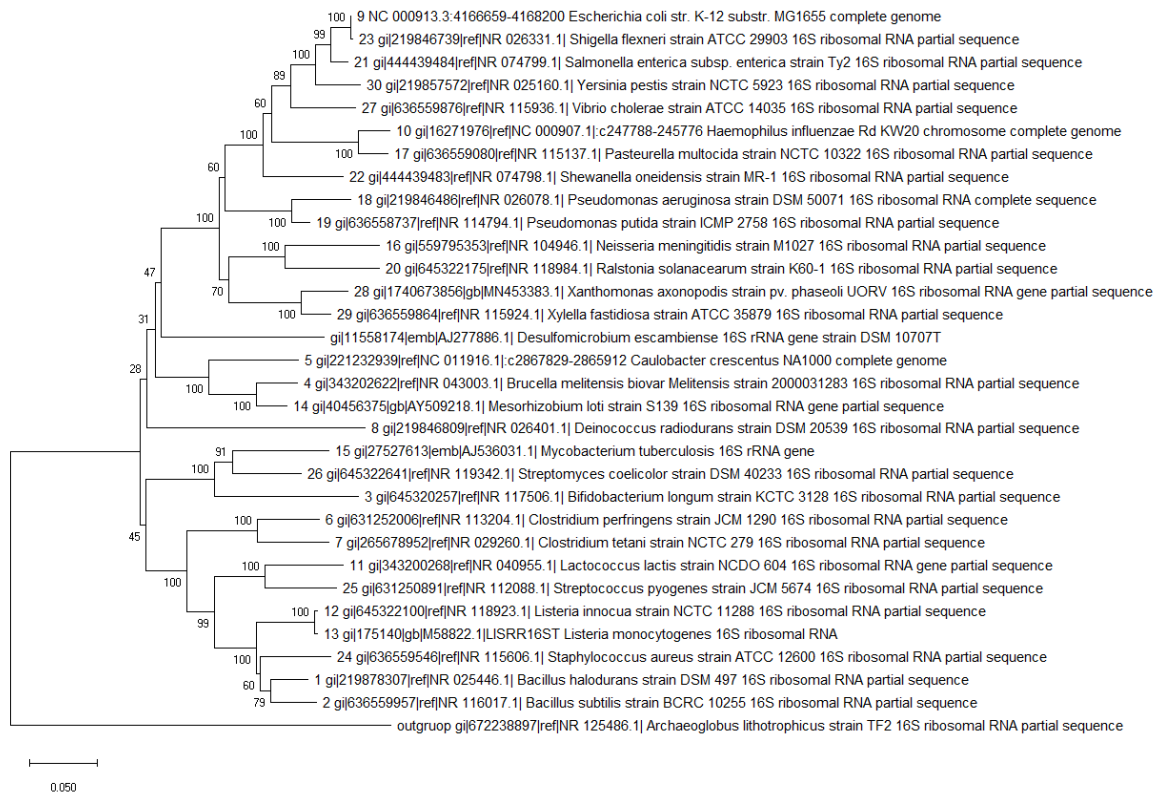


Figure S1.28: Phylogenetic tree of 16S rRNA gene sequences of *Desulfomicrobium escambiense* and microbial strains belonging to the training set of PhiSpy.

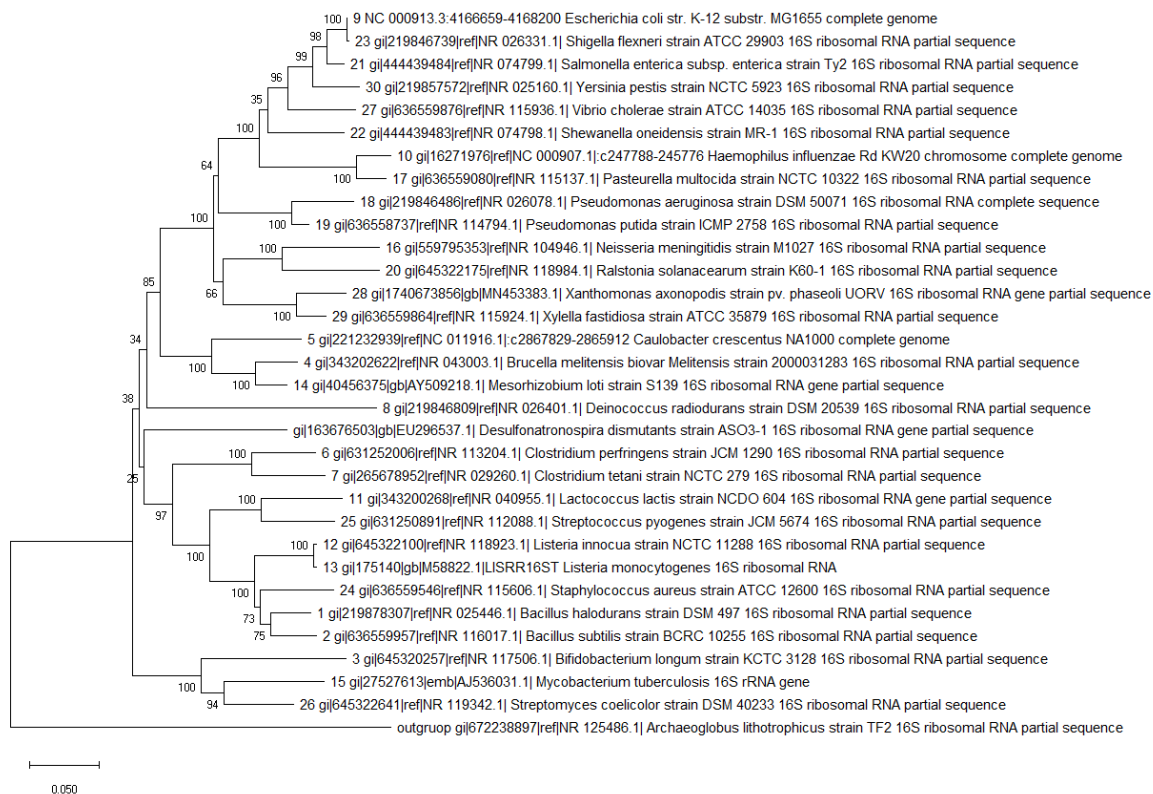


Figure S1.29: Phylogenetic tree of 16S rRNA gene sequences of *Desulfonatronospira dismutans* strain ASO3-1 and microbial strains belonging to the training set of PhiSpy.

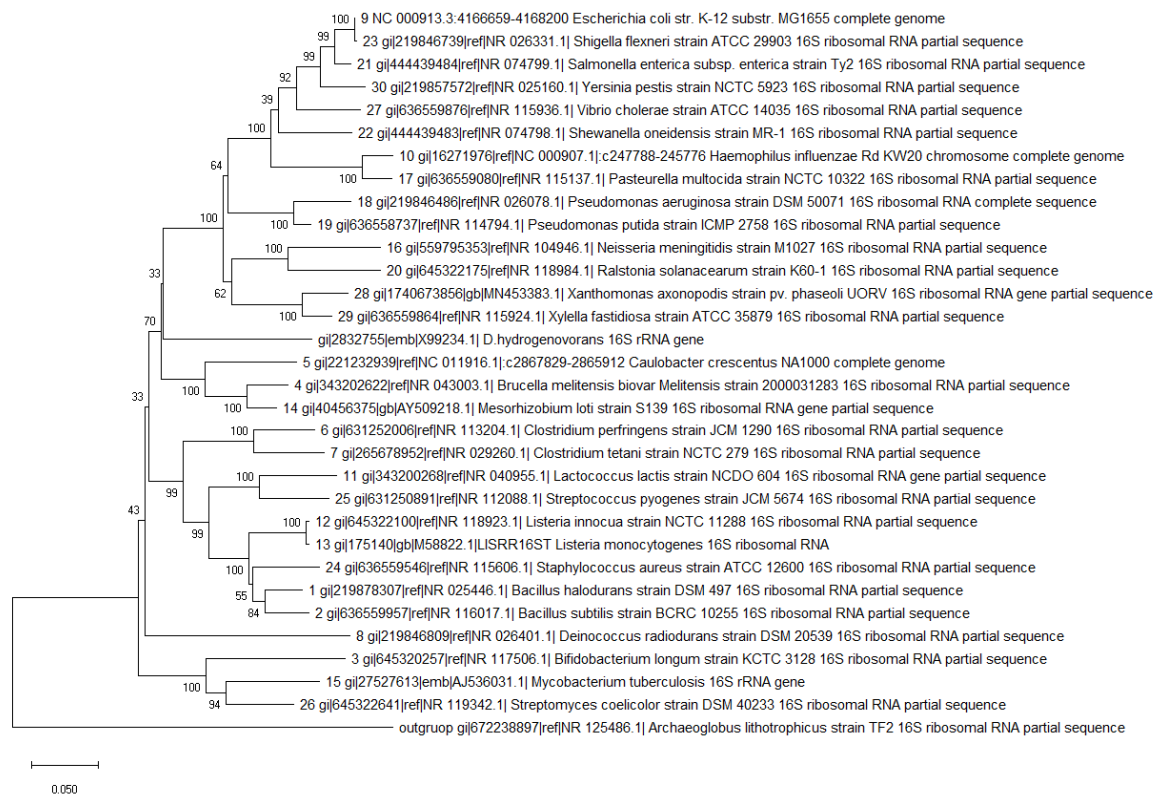


Figure S1.30: Phylogenetic tree of 16S rRNA gene sequences of *Desulfonatronovibrio hydrogenovorans* DSM 9292 and microbial strains belonging to the training set of PhiSpy.

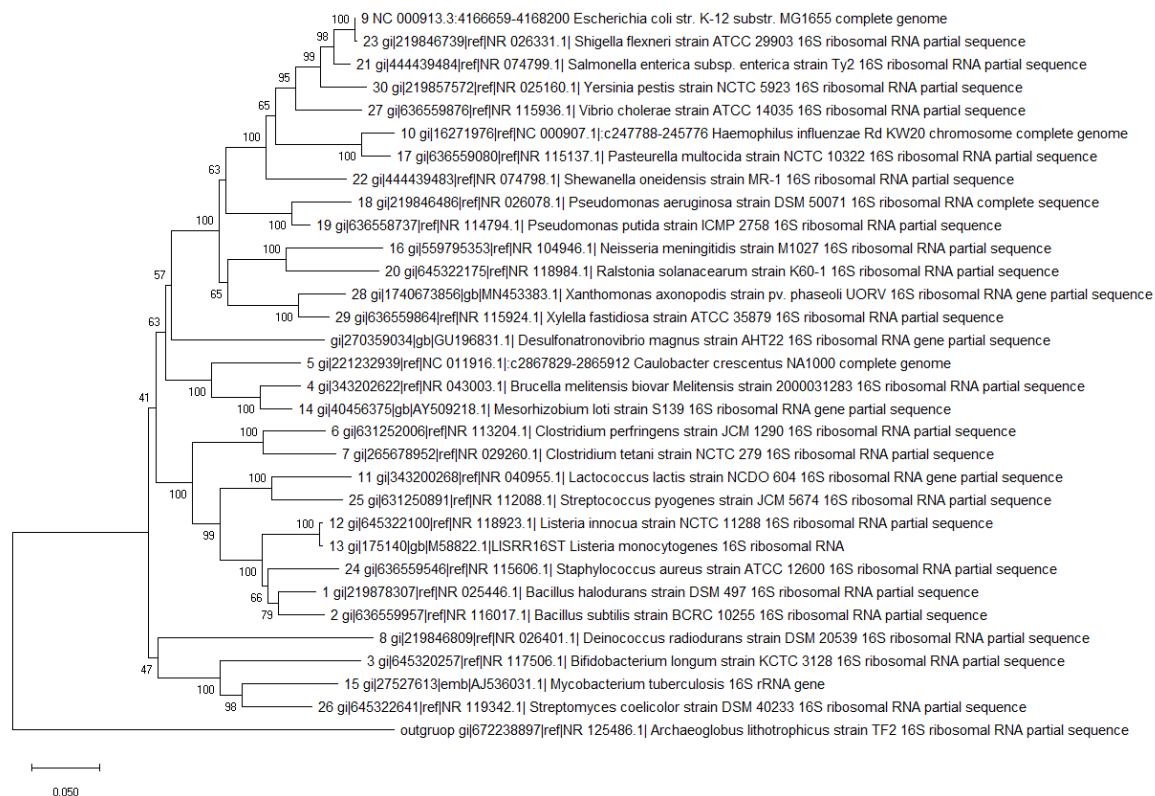


Figure S1.31: Phylogenetic tree of 16S rRNA gene sequences of *Desulfonatronovibrio magnus* strain AHT22 and microbial strains belonging to the training set of PhiSpy.

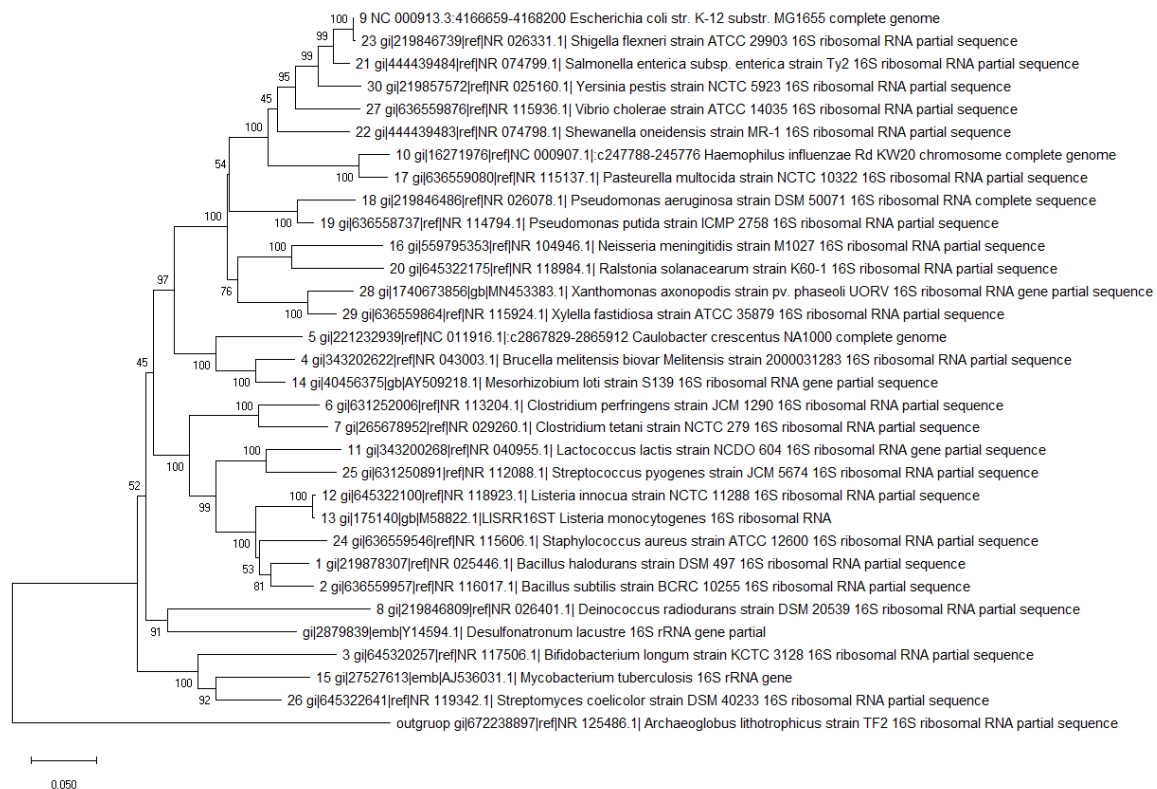


Figure S1.32: Phylogenetic tree of 16S rRNA gene sequences of *Desulfonatronum lacustre* and microbial strains belonging to the training set of PhiSpy.

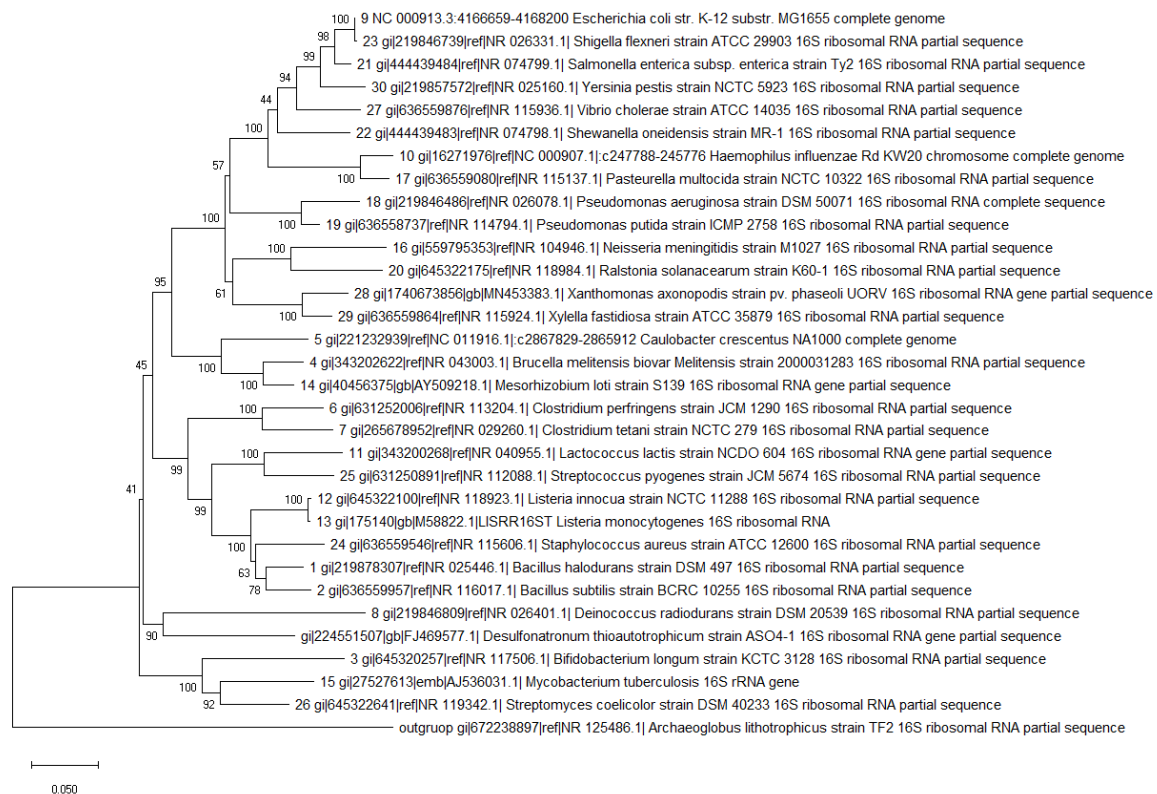


Figure S1.33: Phylogenetic tree of 16S rRNA gene sequences of *Desulfonatronum thioautotrophicum* strain ASO4-1 and microbial strains belonging to the training set of PhiSpy.

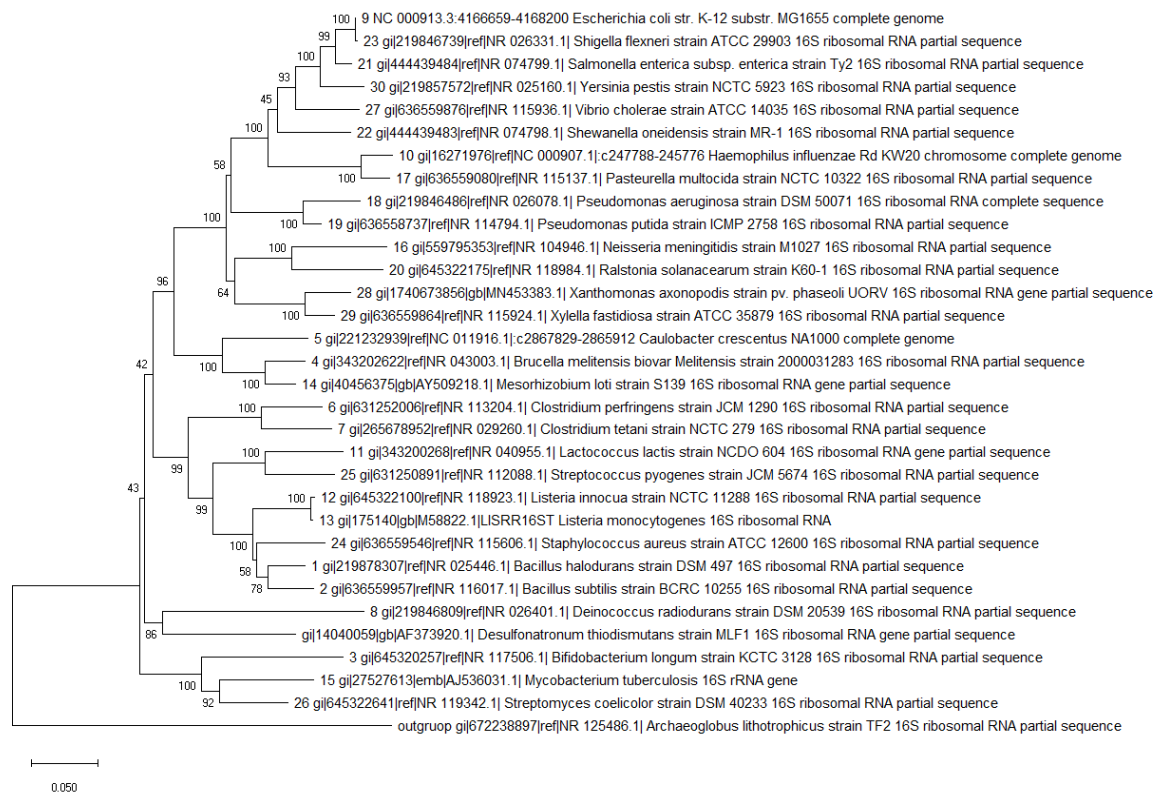


Figure S1.34: Phylogenetic tree of 16S rRNA gene sequences of *Desulfonatronum thiodismutans* and microbial strains belonging to the training set of PhiSpy.

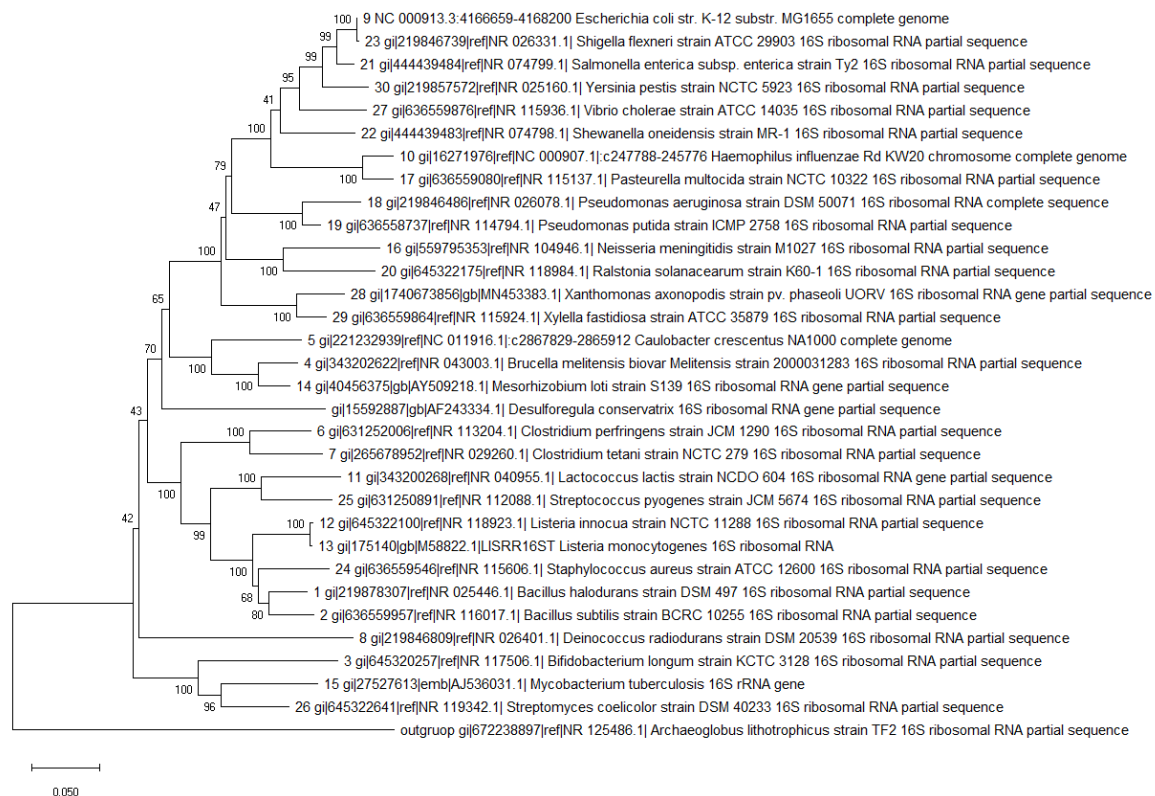


Figure S1.35: Phylogenetic tree of 16S rRNA gene sequences of *Desulforegula conservatrix* and microbial strains belonging to the training set of PhiSpy.

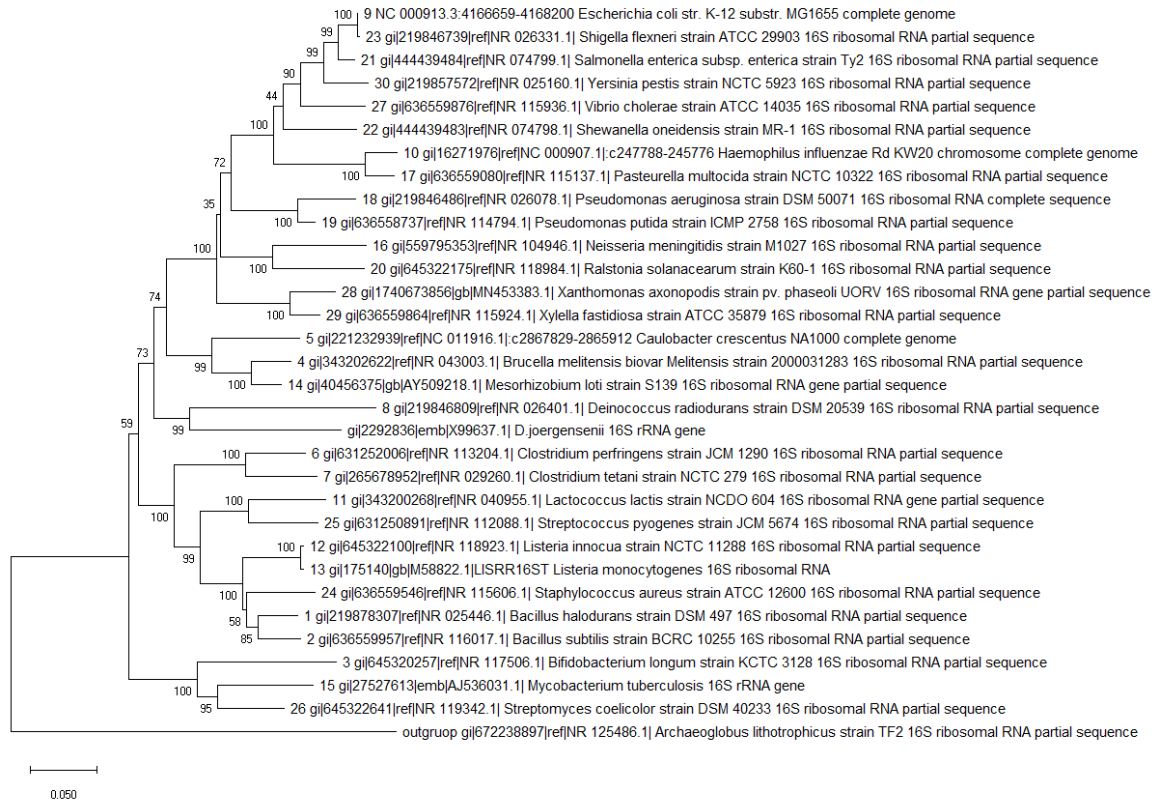


Figure S1.36: Phylogenetic tree of 16S rRNA gene sequences of *Desulfospira joergensenii* DSM 10085 and microbial strains belonging to the training set of PhiSpy.

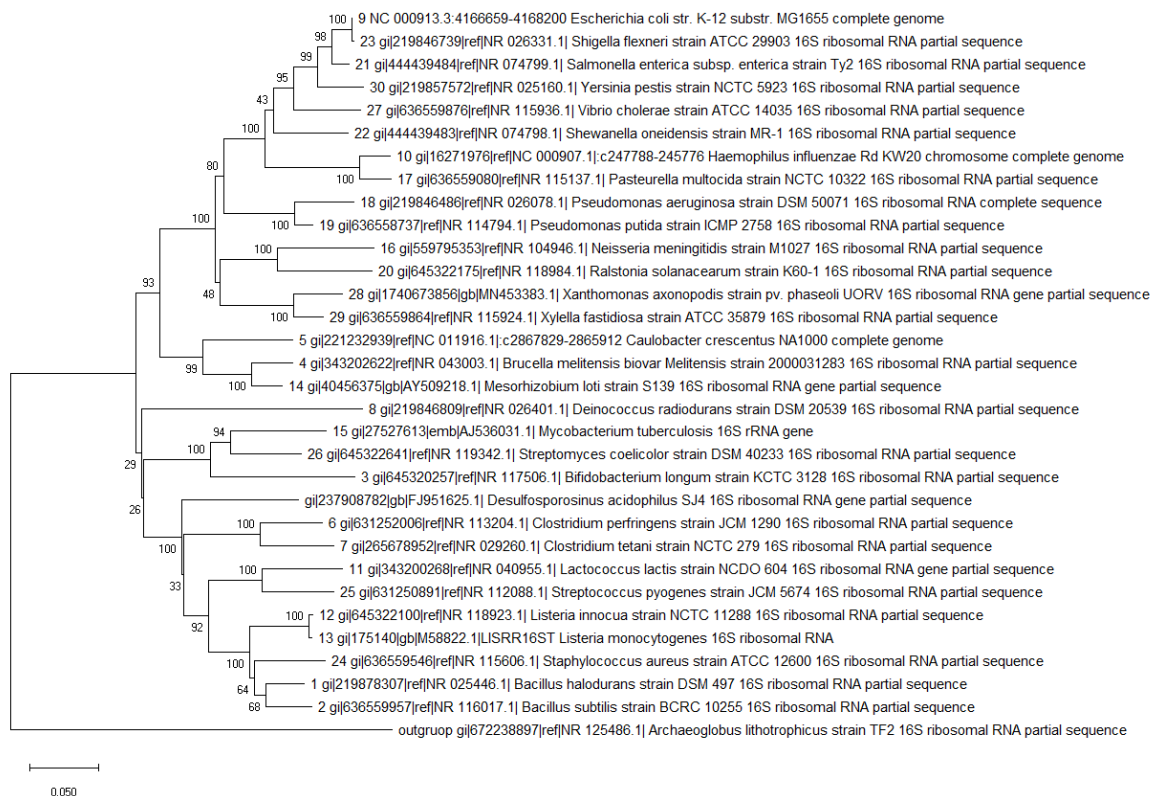


Figure S1.37: Phylogenetic tree of 16S rRNA gene sequences of *Desulfosporosinus acidiphilus* SJ4 and microbial strains belonging to the training set of PhiSpy.

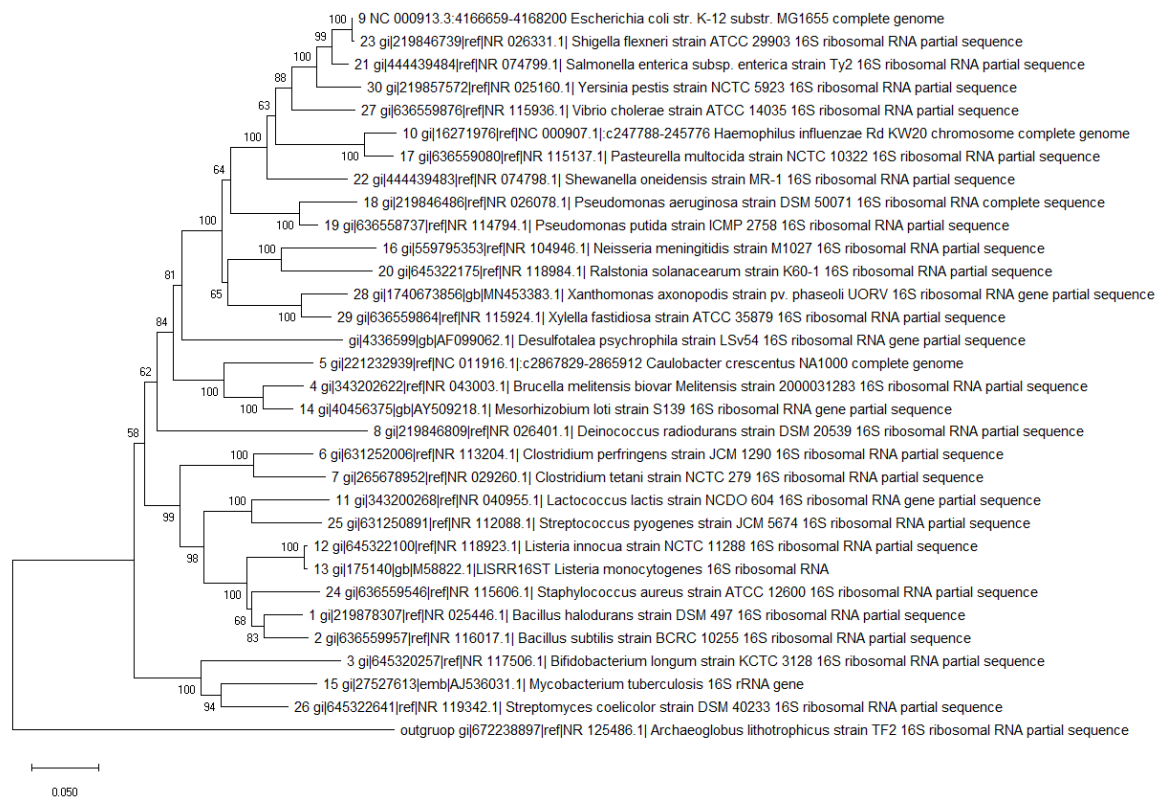


Figure S1.38: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotalea psychrophila* strain LSv54 and microbial strains belonging to the training set of PhiSpy.

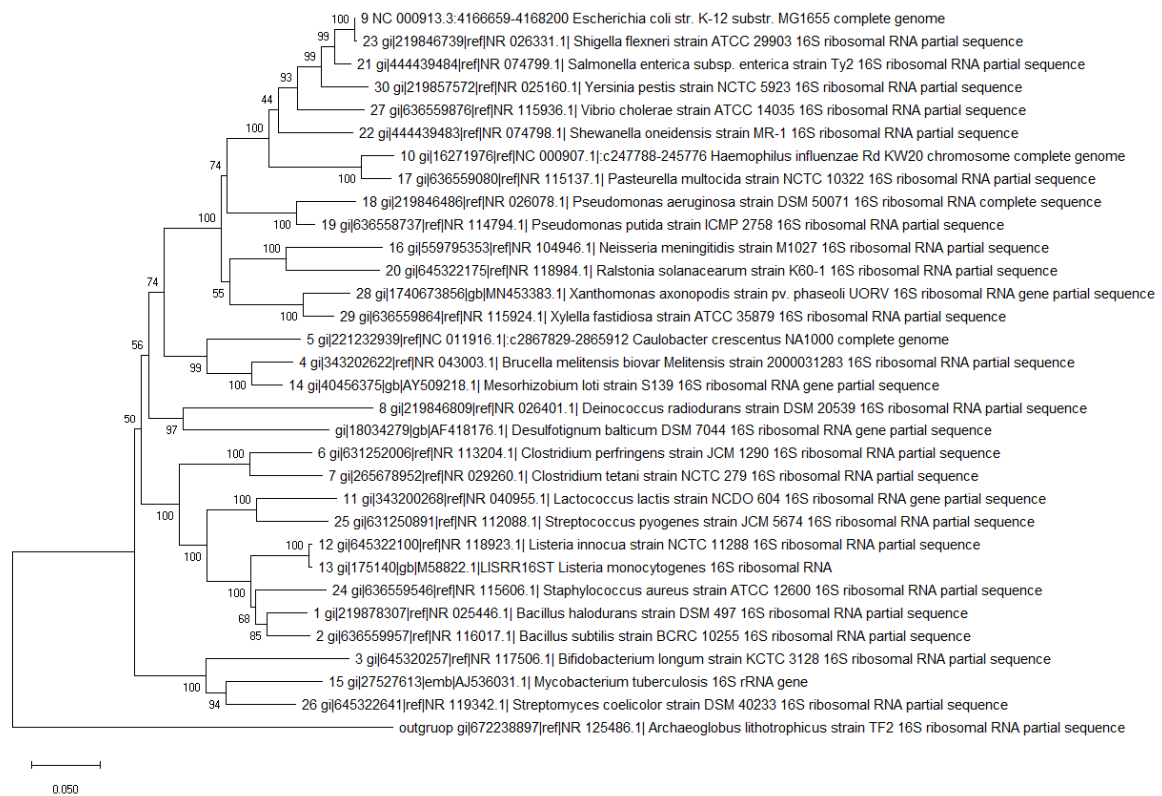


Figure S1.39: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotignum balticum* DSM 7044 and microbial strains belonging to the training set of PhiSpy.

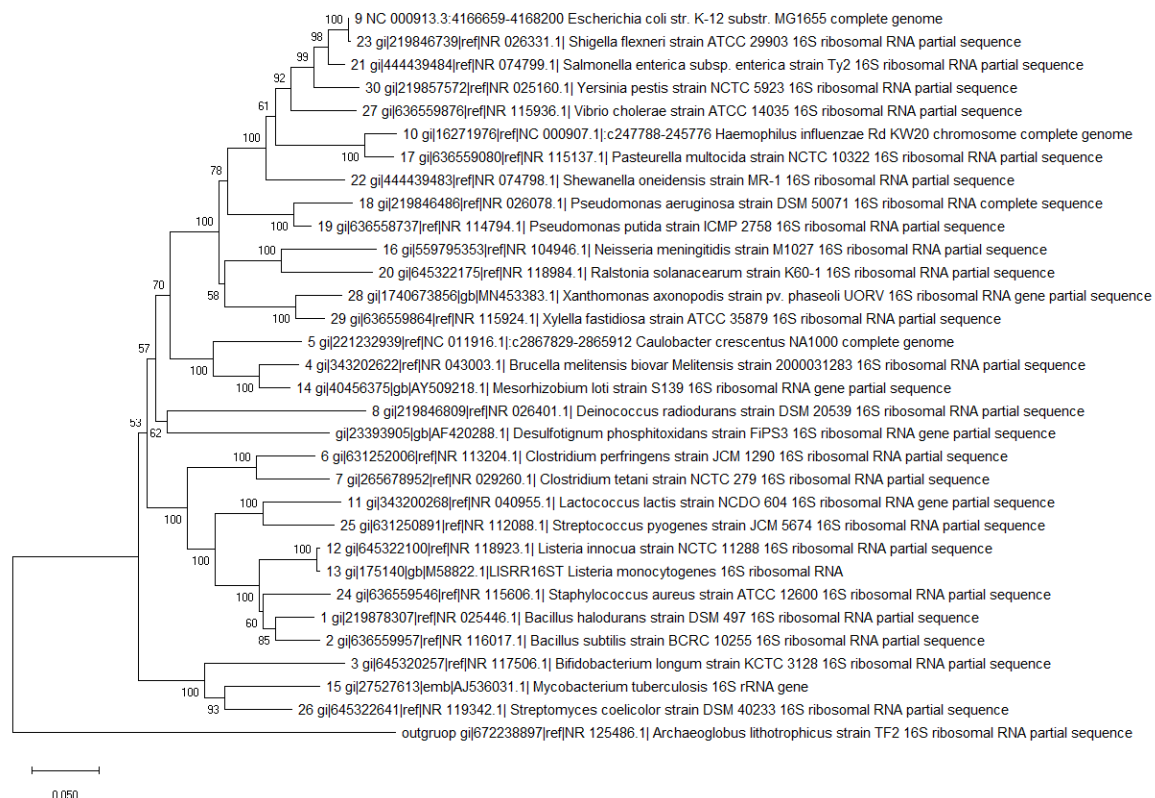


Figure S1.40: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotignum phosphitoxidans* DSM 13687 and microbial strains belonging to the training set of PhiSpy.

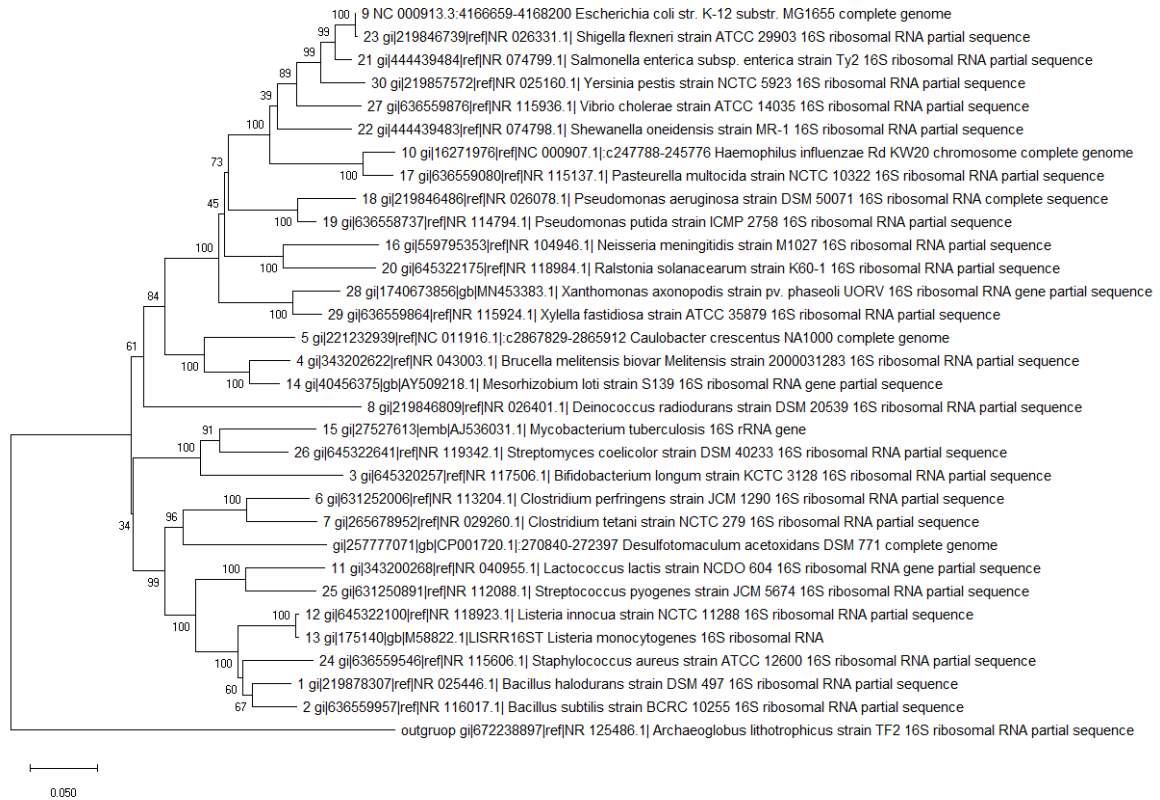


Figure S1.41: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotomaculum acetoxidans* DSM 771 and microbial strains belonging to the training set of PhiSpy.

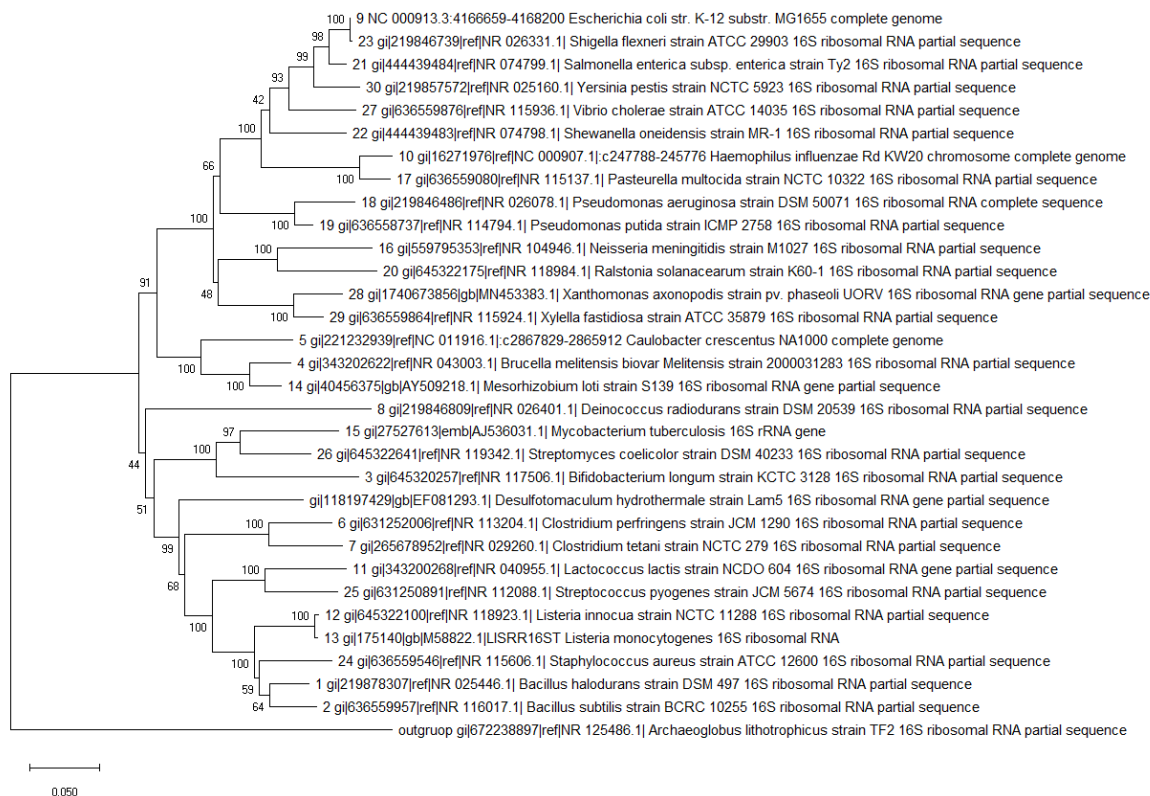


Figure S1.42: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotomaculum hydrothermale* strain Lam5 and microbial strains belonging to the training set of PhiSpy.

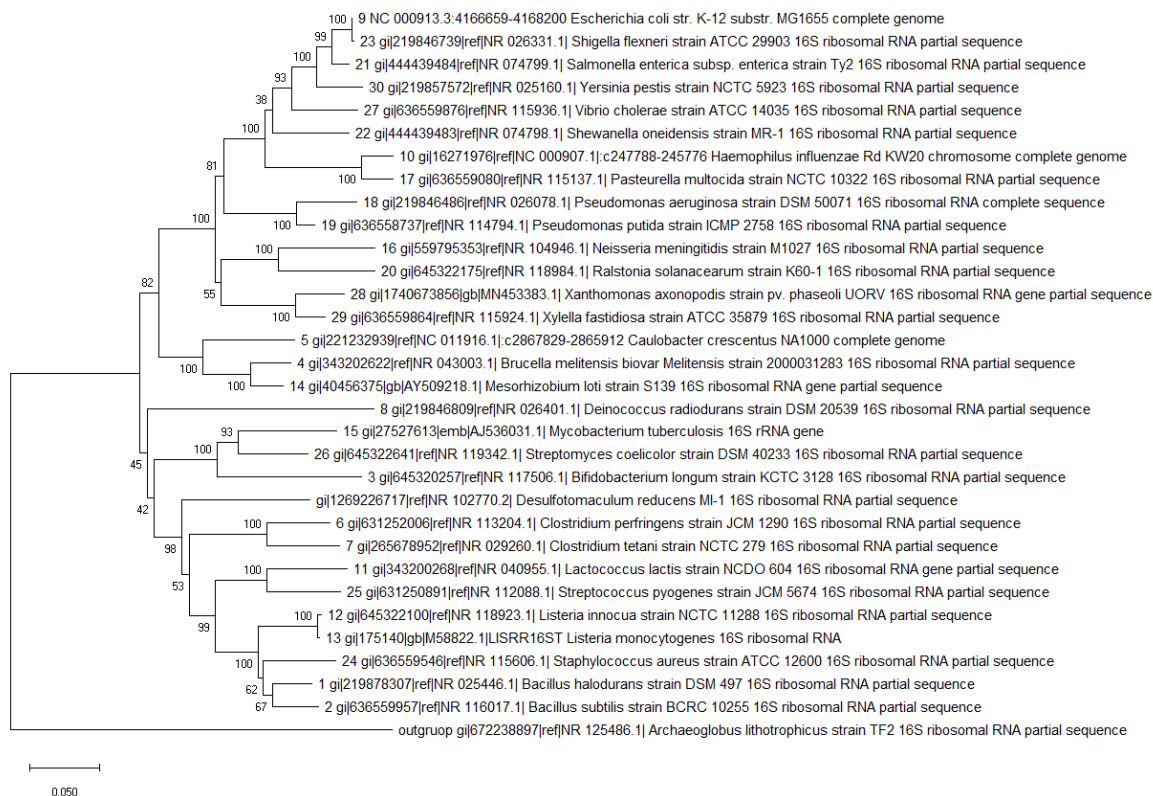


Figure S1.43: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotomaculum reducens* MI-1 and microbial strains belonging to the training set of PhiSpy.

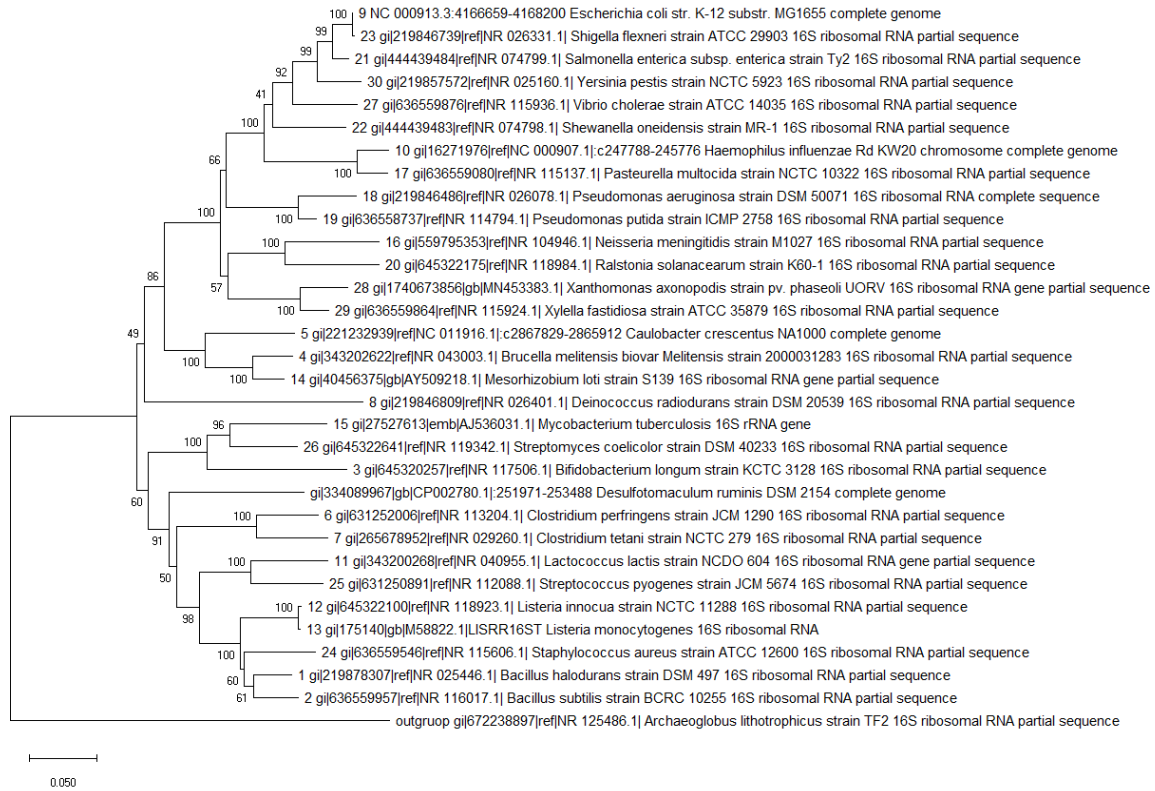


Figure S1.44: Phylogenetic tree of 16S rRNA gene sequences of *Desulfotomaculum ruminis* DSM 2154 and microbial strains belonging to the training set of PhiSpy.

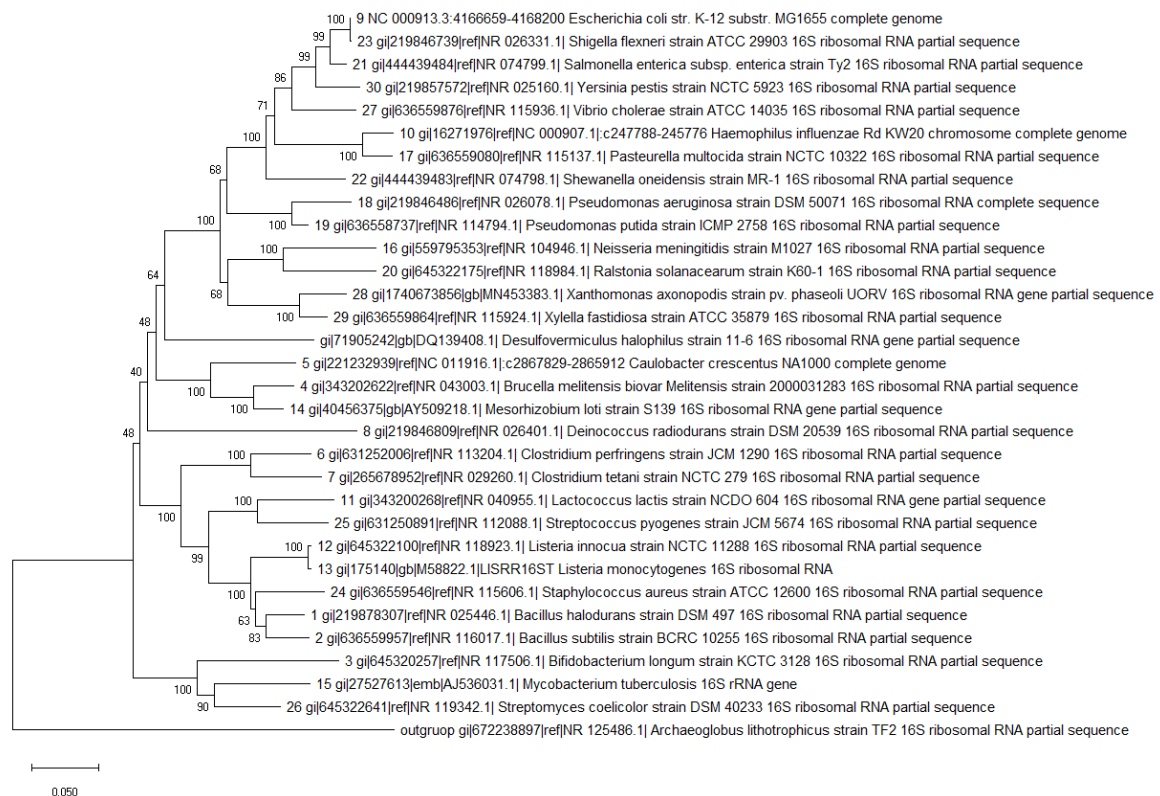


Figure S1.45: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovermiculus halophilus* and microbial strains belonging to the training set of PhiSpy.

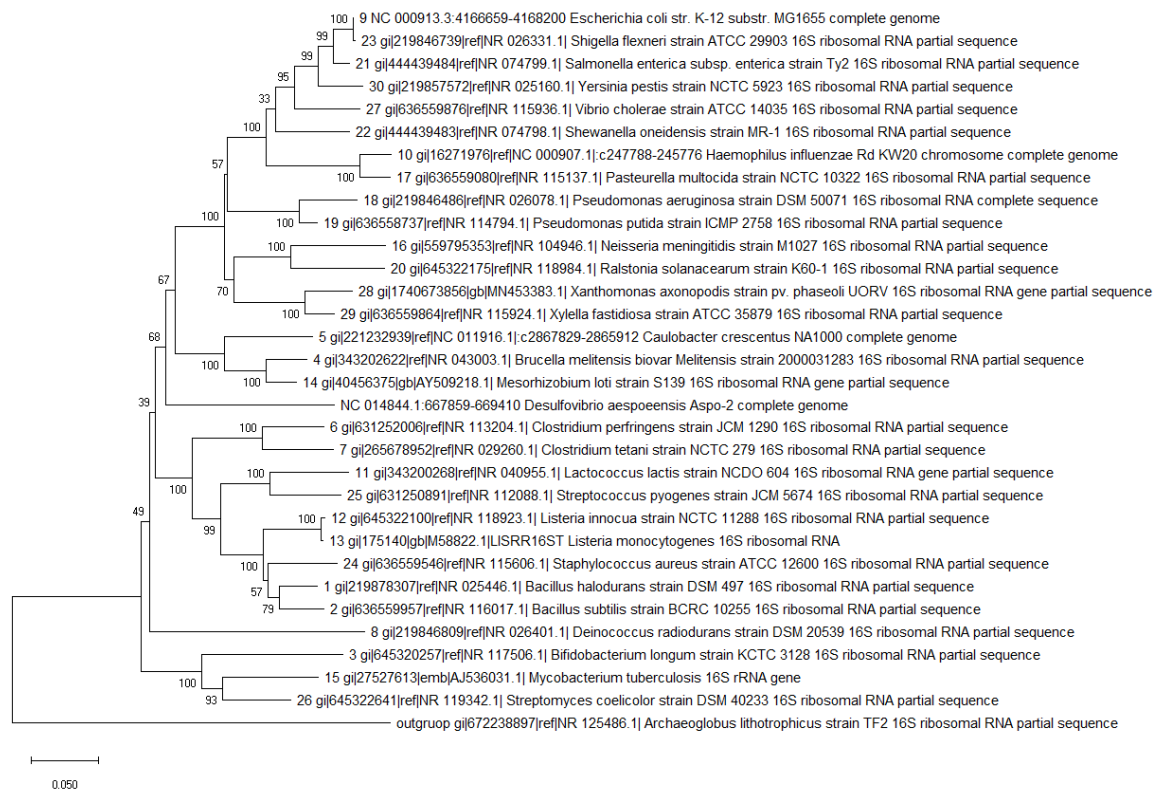


Figure S1.46: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio aespoeensis* Aspo-2 and microbial strains belonging to the training set of PhiSpy.

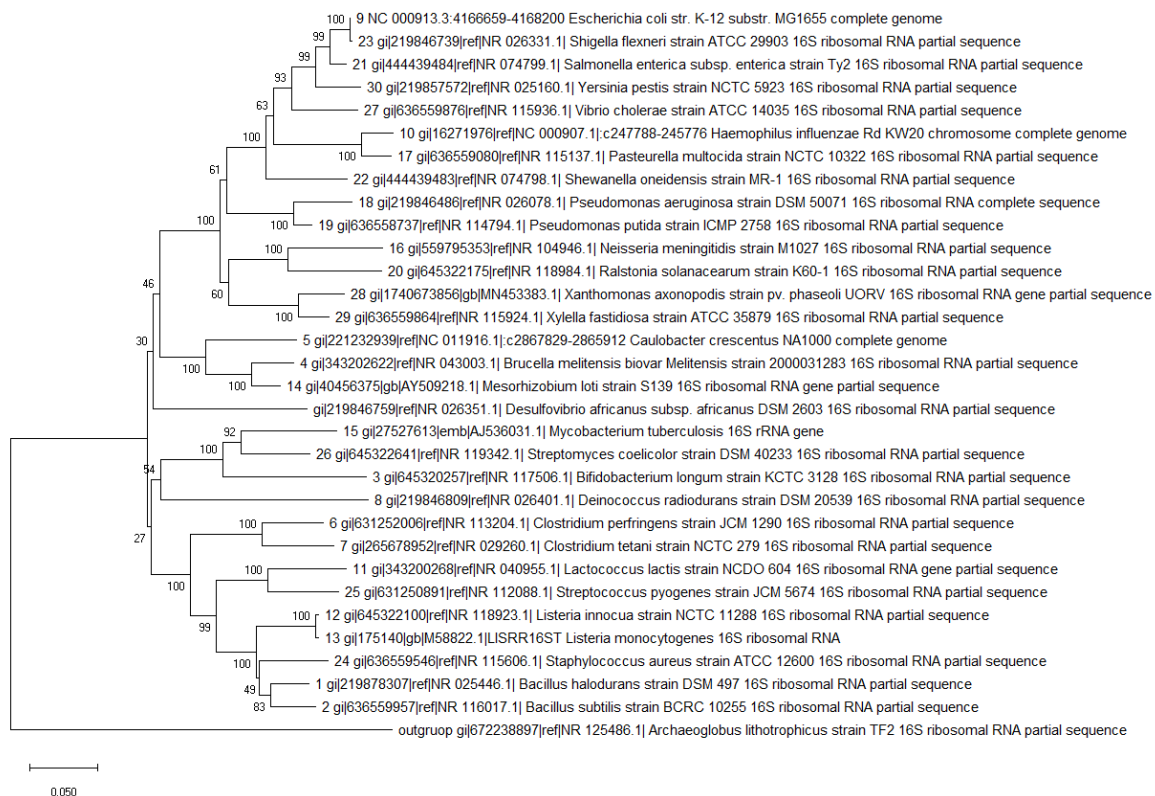


Figure S1.47: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio africanus subsp. africanus* DSM 2603 and microbial strains belonging to the training set of PhiSpy.

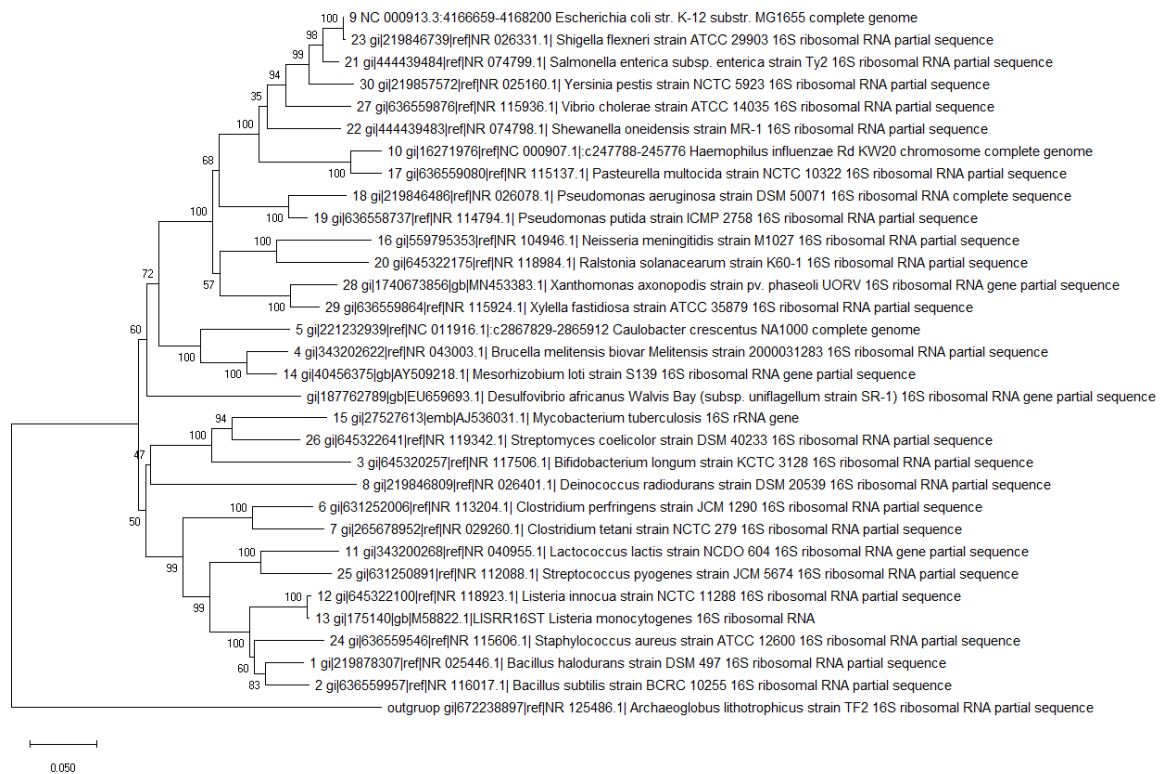


Figure S1.48: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio africanus* Walvis Bay and microbial strains belonging to the training set of PhiSpy.

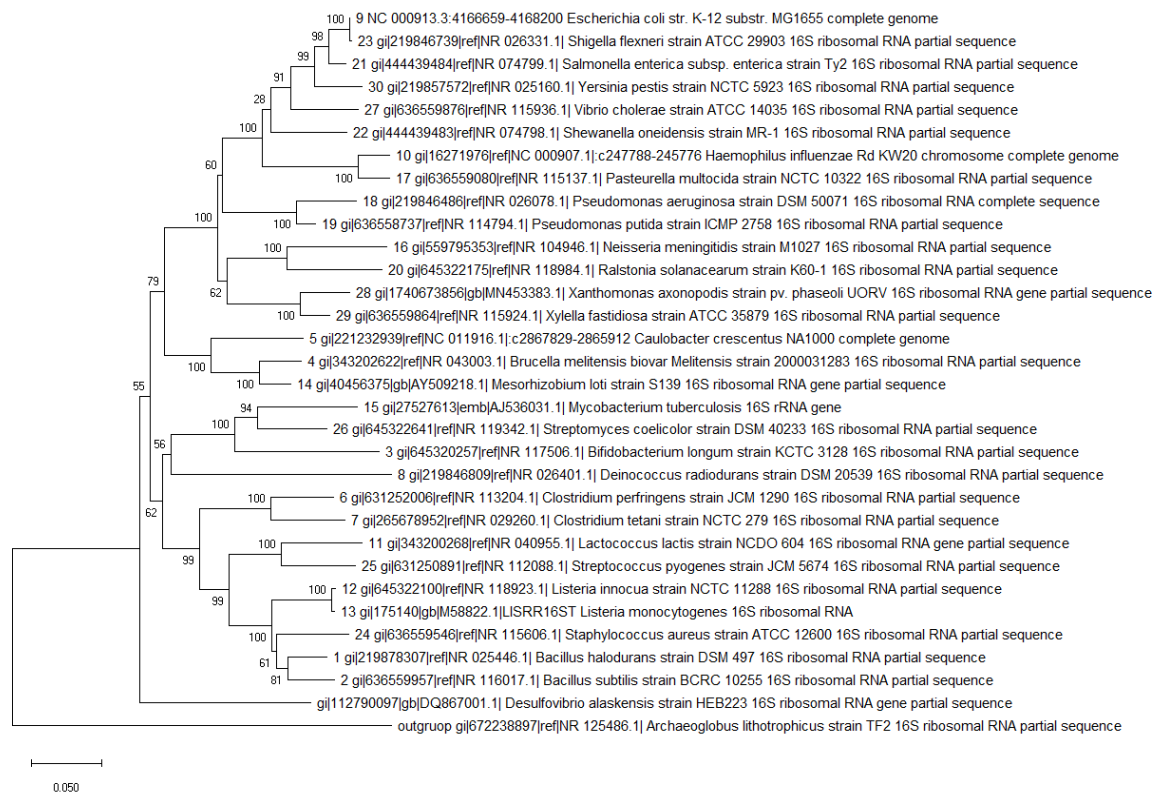


Figure S1.49: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio alaskensis* and microbial strains belonging to the training set of PhiSpy.

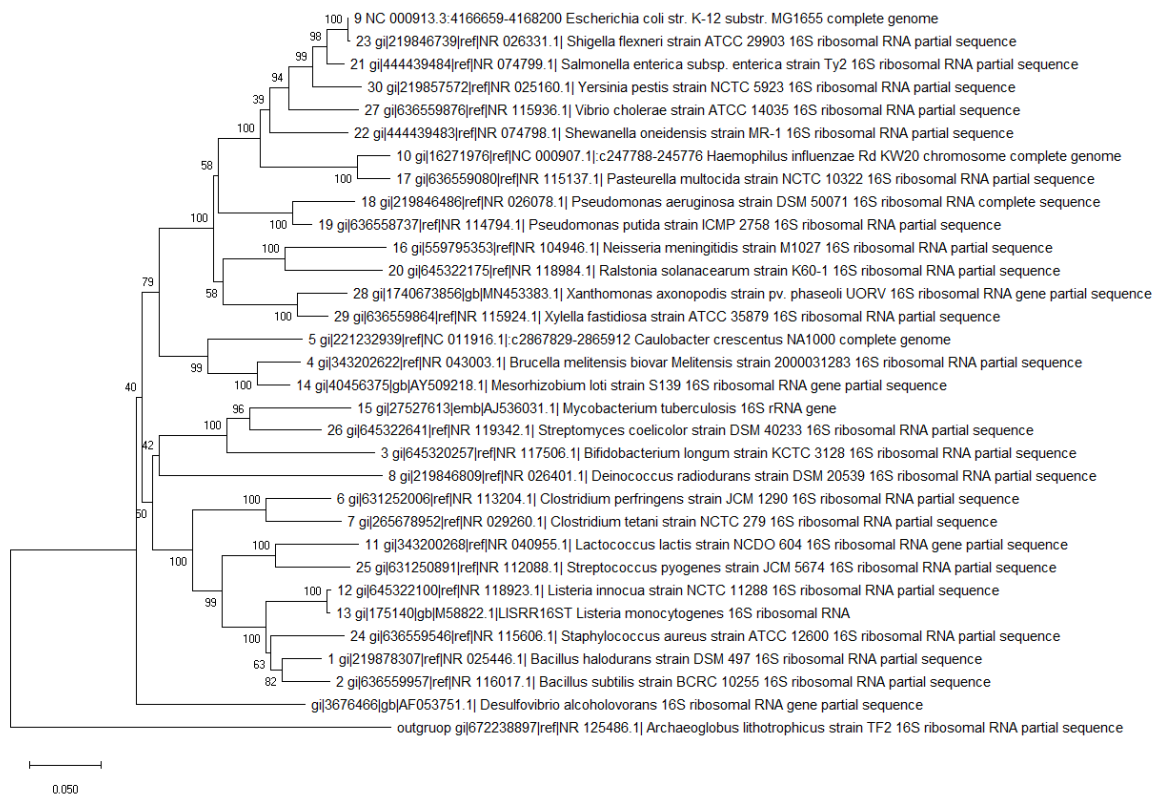


Figure S1.50: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio alcoholivorans* and microbial strains belonging to the training set of PhiSpy.

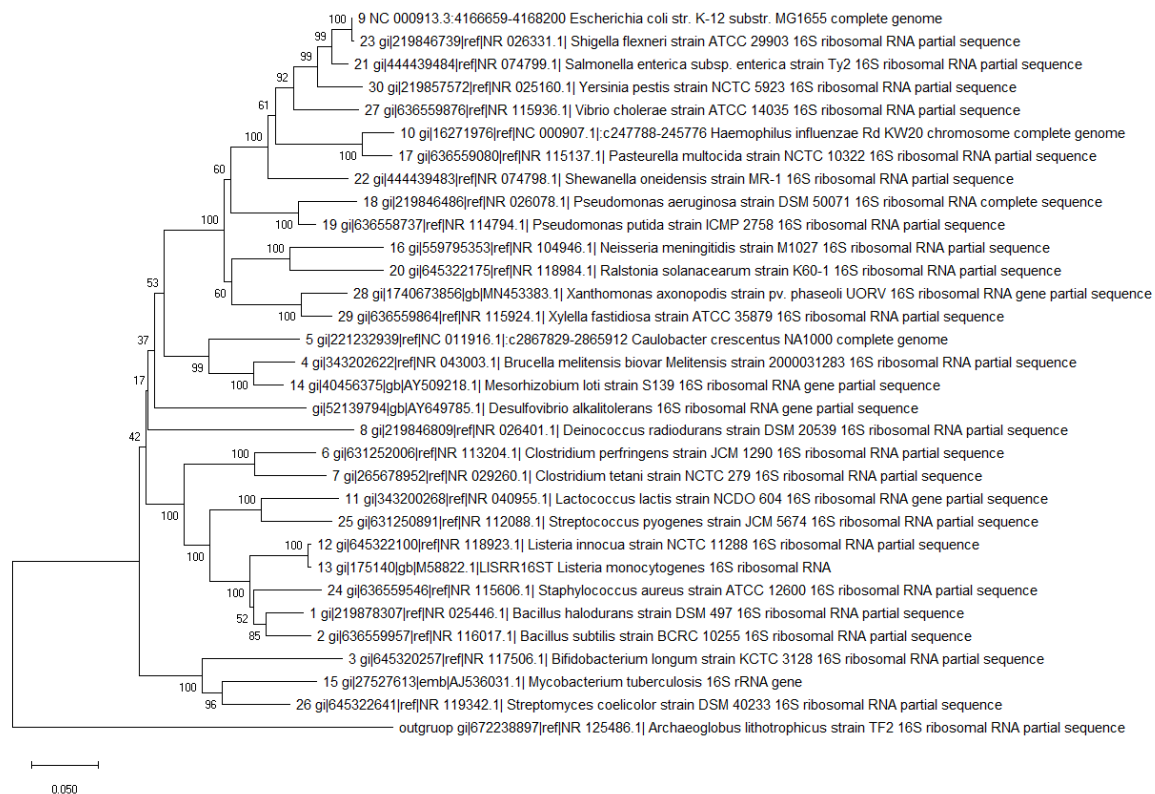


Figure S1.51: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio alkalitolerans* and microbial strains belonging to the training set of PhiSpy.

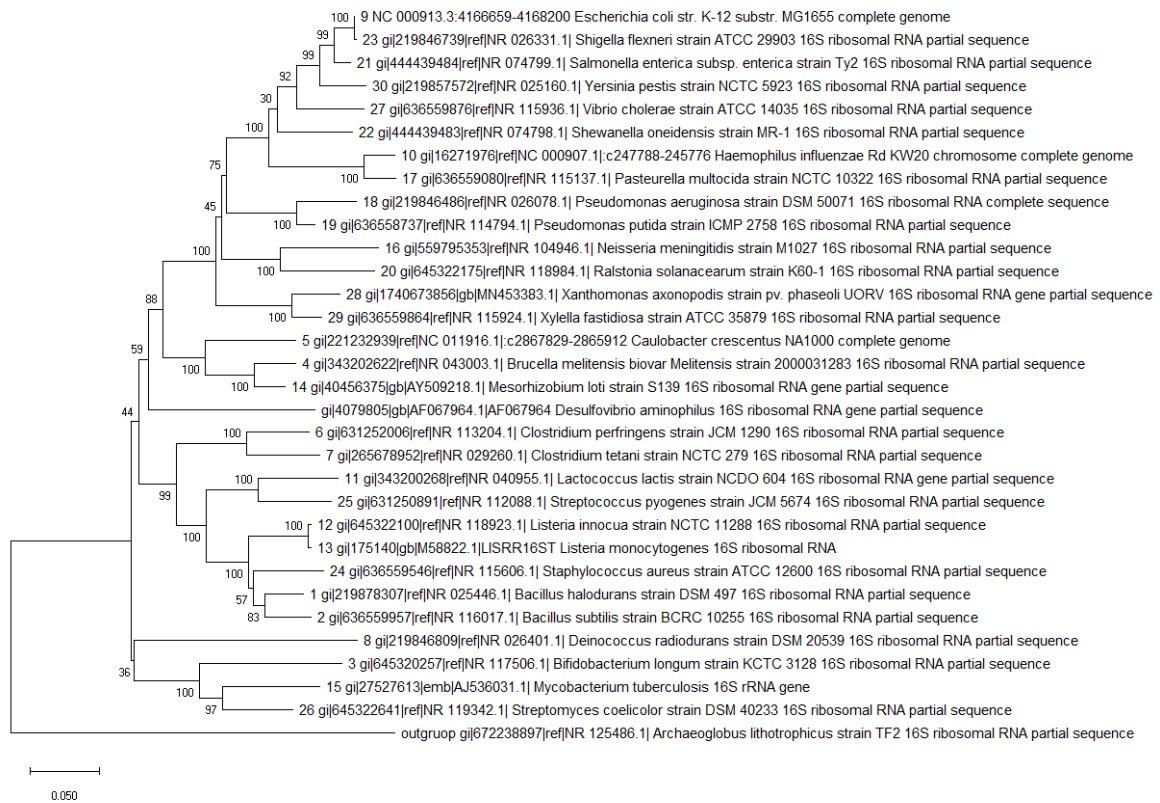


Figure S1.52: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio aminophilus* DSM 12254 and microbial strains belonging to the training set of PhiSpy.

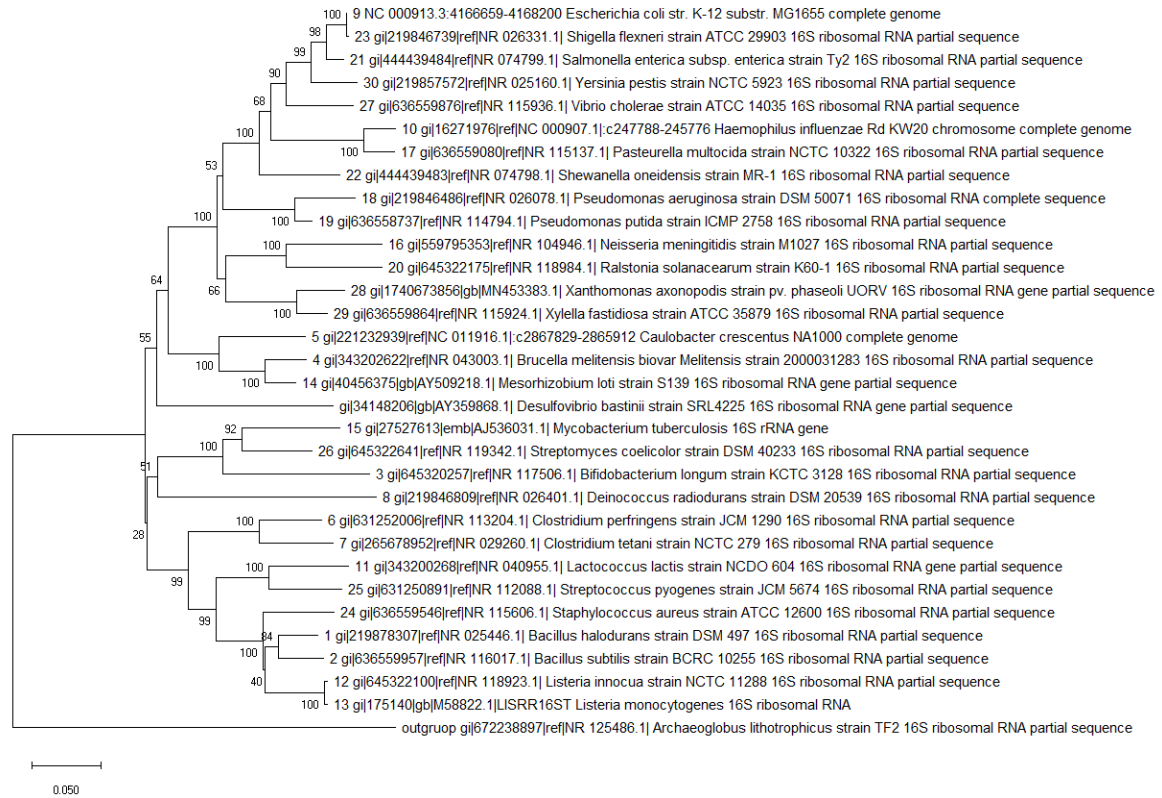


Figure S1.53: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio bastinii* strain SRL4225 and microbial strains belonging to the training set of PhiSpy.

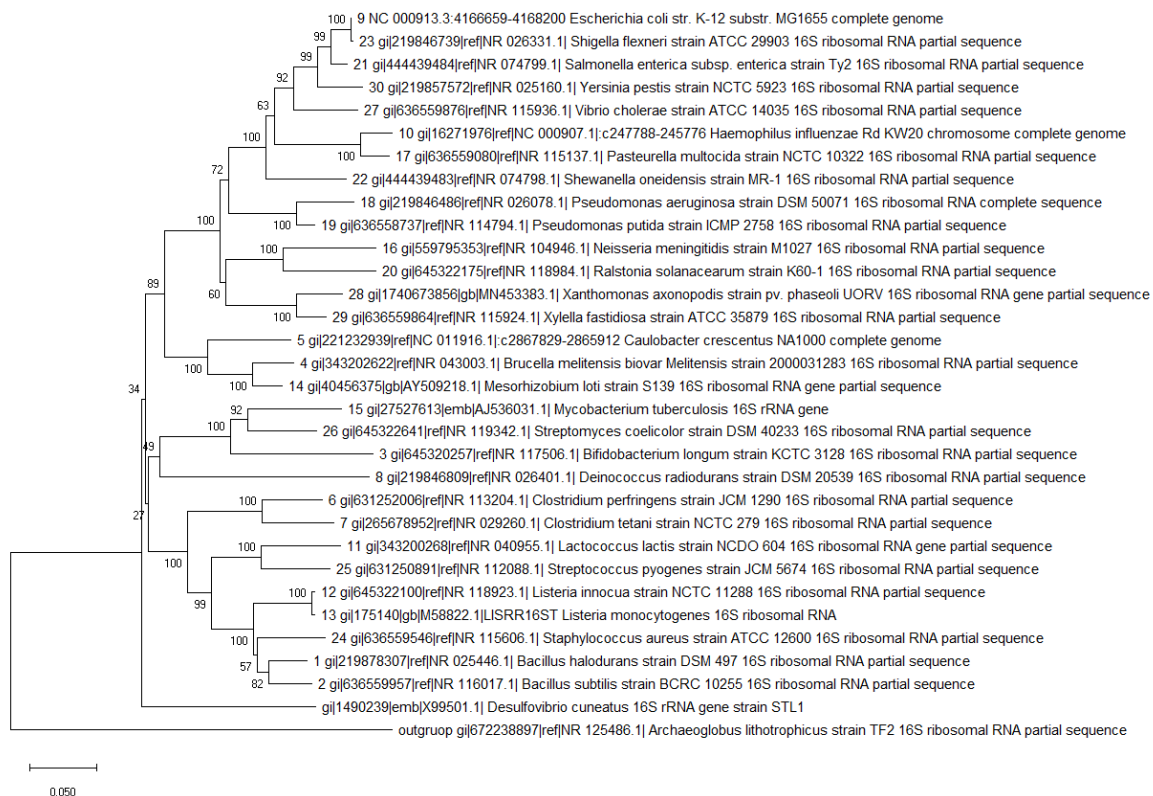


Figure S1.54: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio cuneatus* DSM 11391 and microbial strains belonging to the training set of PhiSpy.

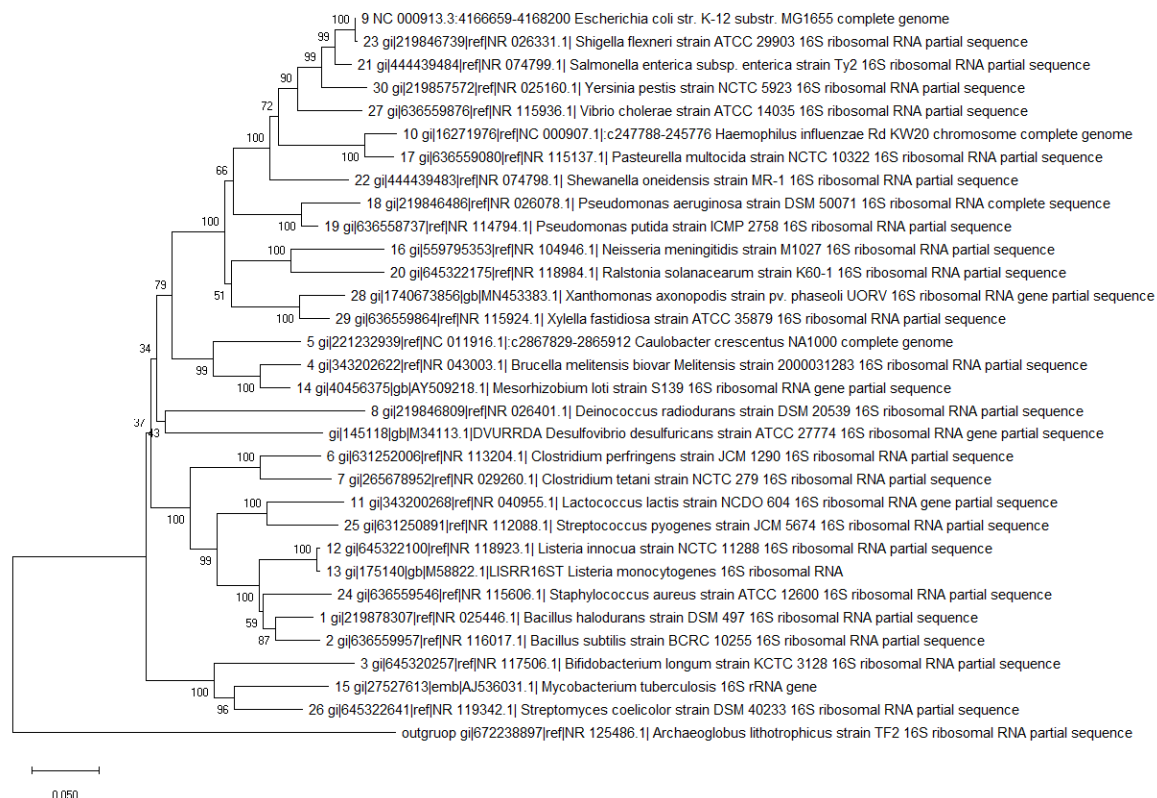


Figure S1.55: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio desulfuricans* 642 and microbial strains belonging to the training set of PhiSpy.

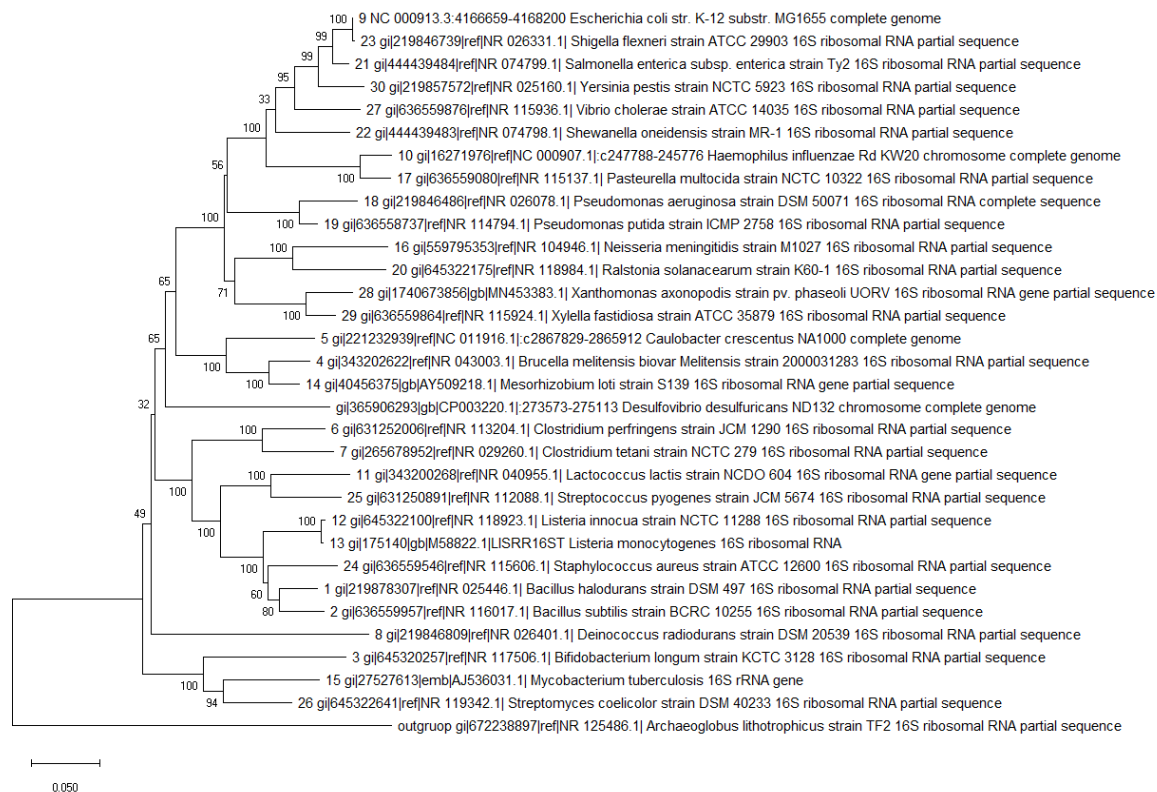


Figure S1.56: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio desulfuricans* ND132 and microbial strains belonging to the training set of PhiSpy.

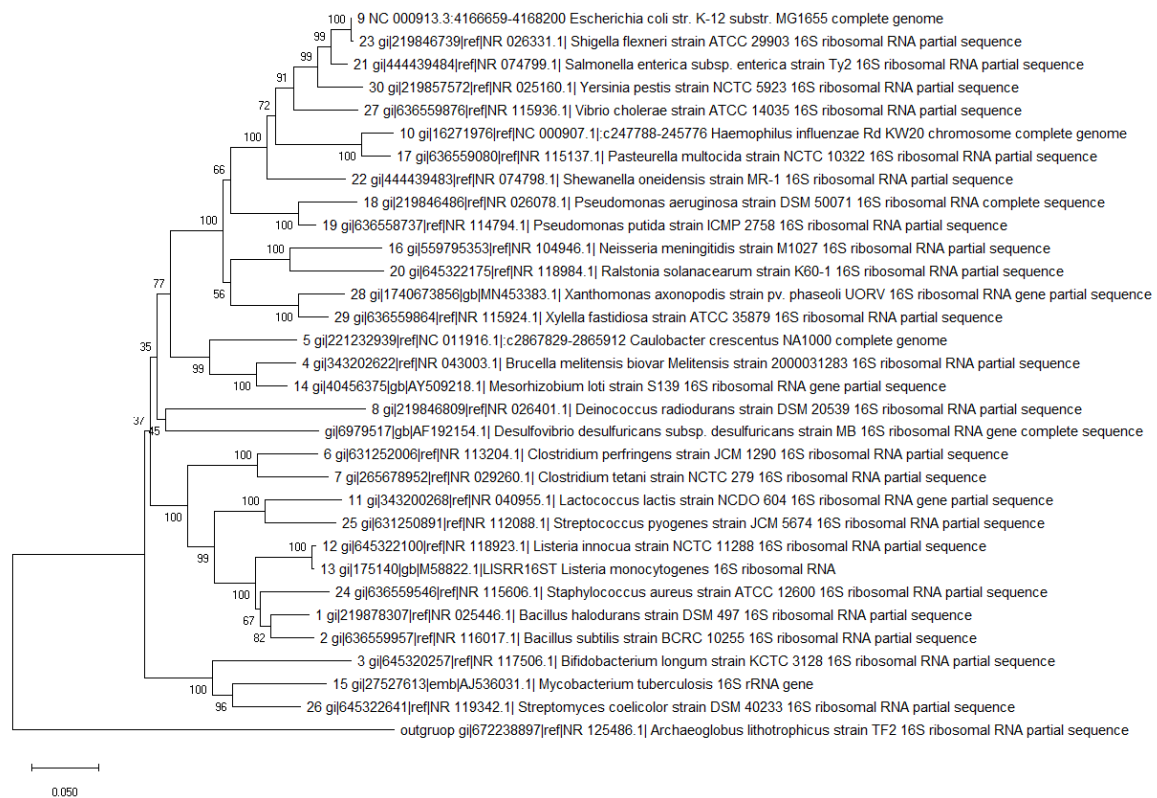


Figure S1.57: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio desulfuricans* subsp. *desulfuricans* strain MB and microbial strains belonging to the training set of PhiSpy.

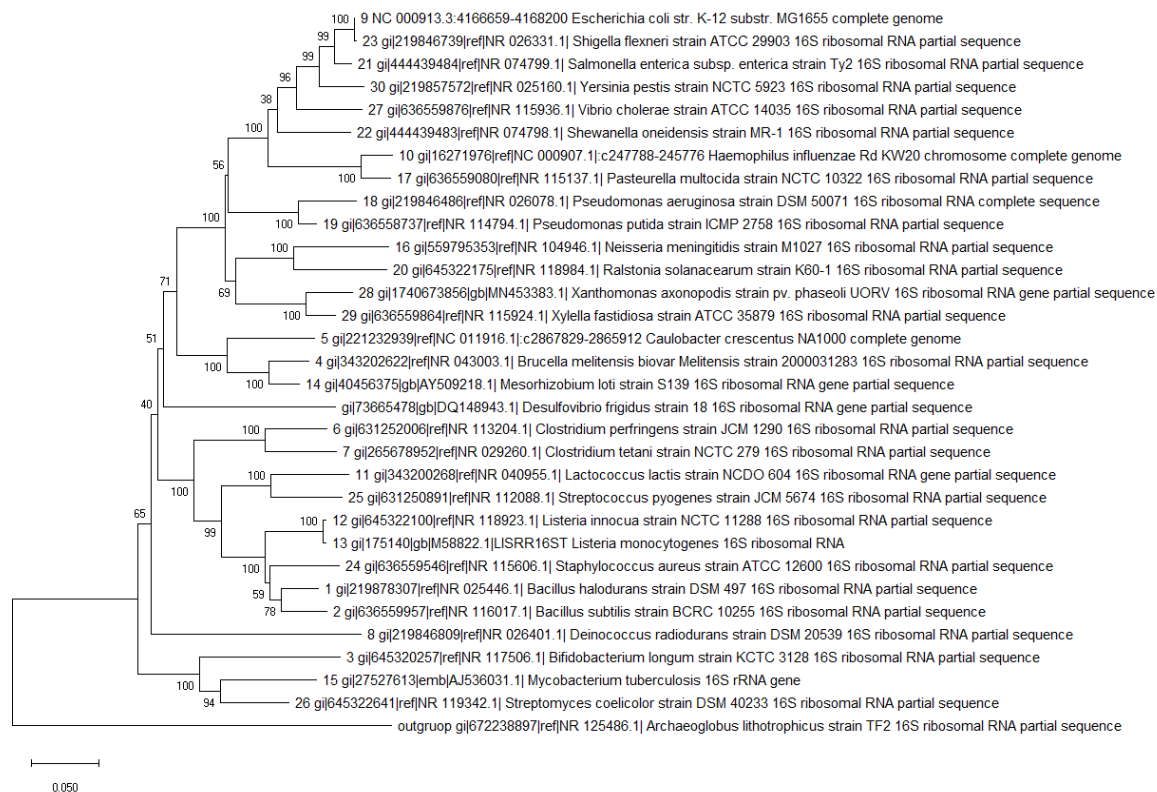


Figure S1.58: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio frigidus* DSM 17176 and microbial strains belonging to the training set of PhiSpy.

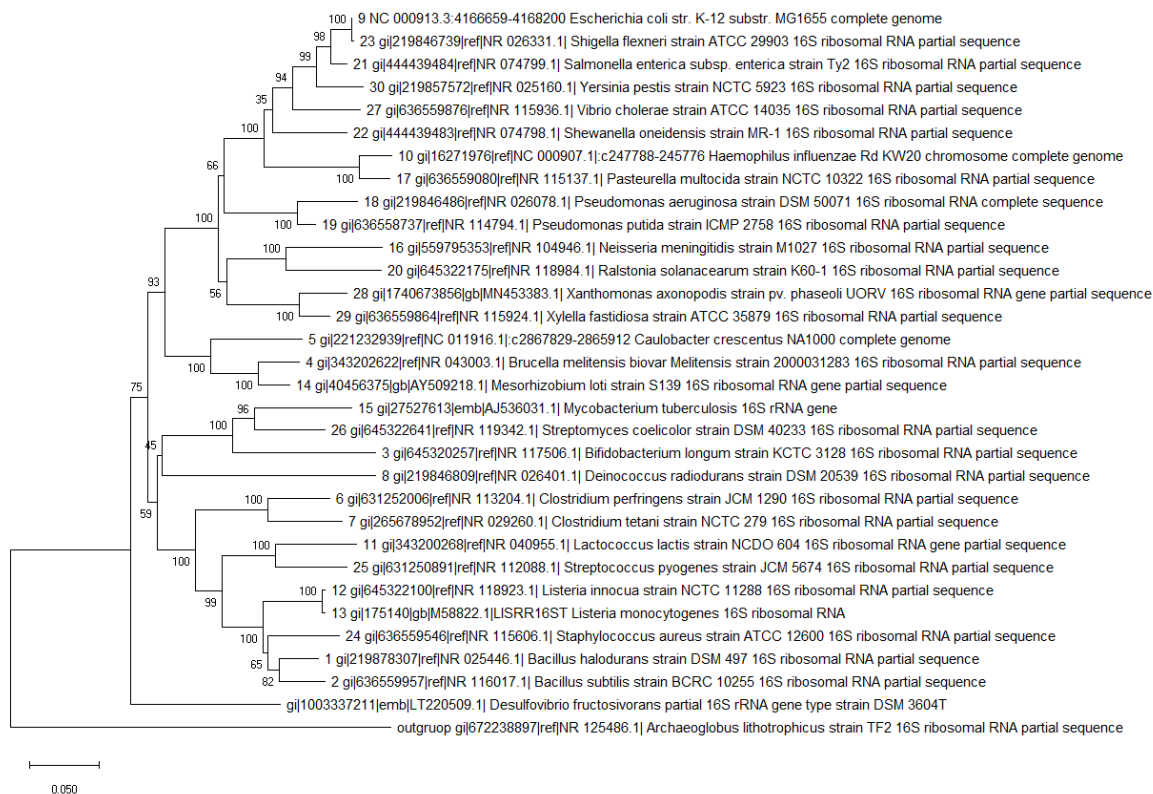


Figure S1.59: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio fructosivorans* JJ and microbial strains belonging to the training set of PhiSpy.

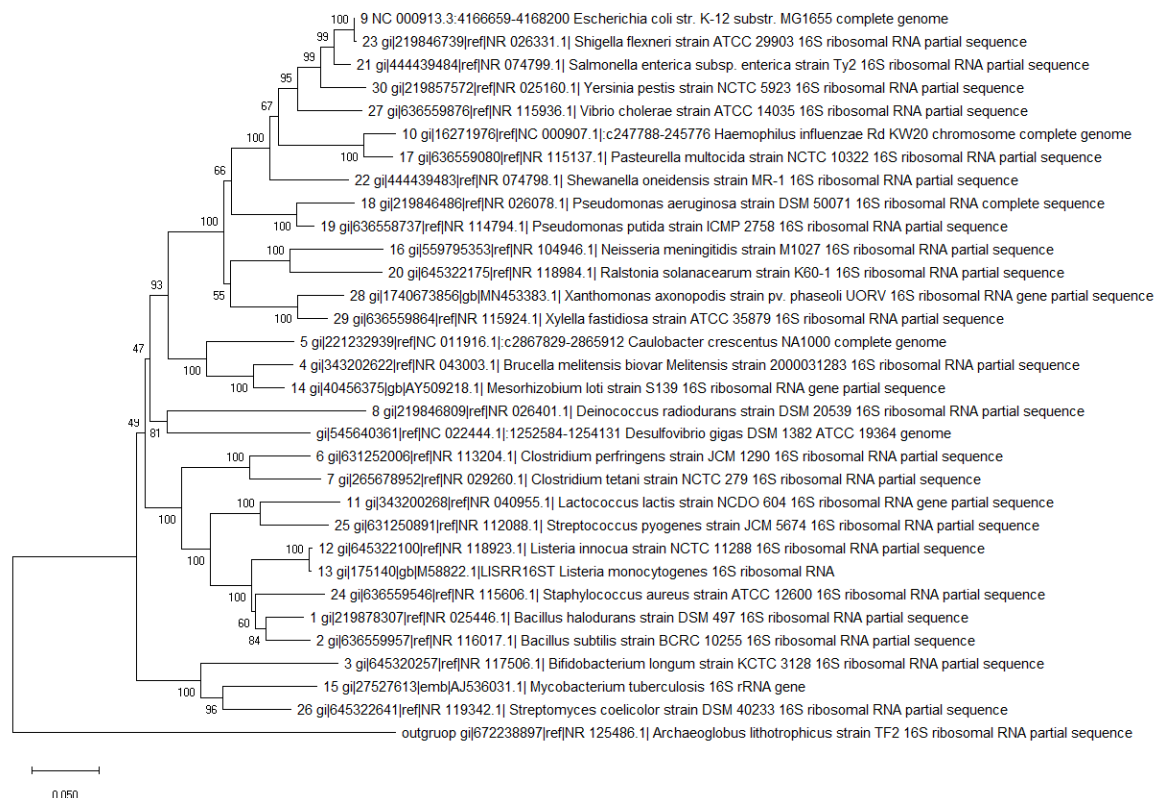


Figure S1.60: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio gigas* DSM 1382 and microbial strains belonging to the training set of PhiSpy.

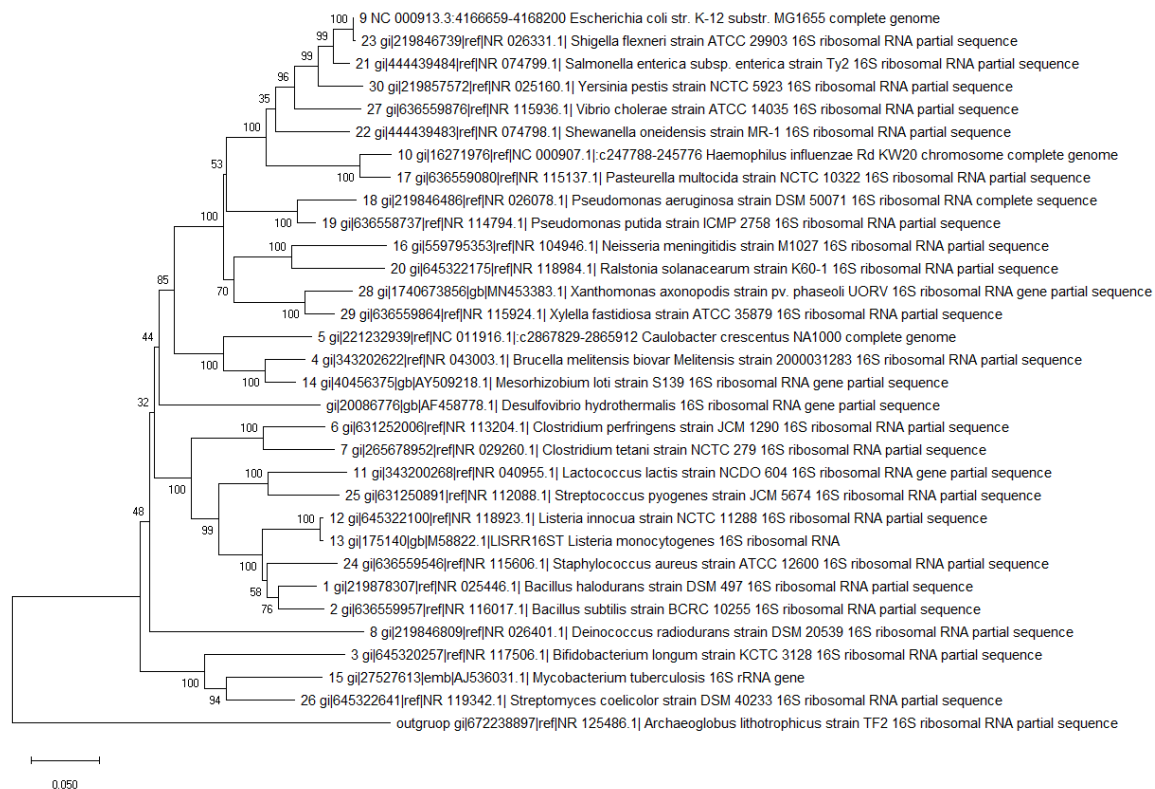


Figure S1.61: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio hydrothermalis* DSM 14728 and microbial strains belonging to the training set of PhiSpy.

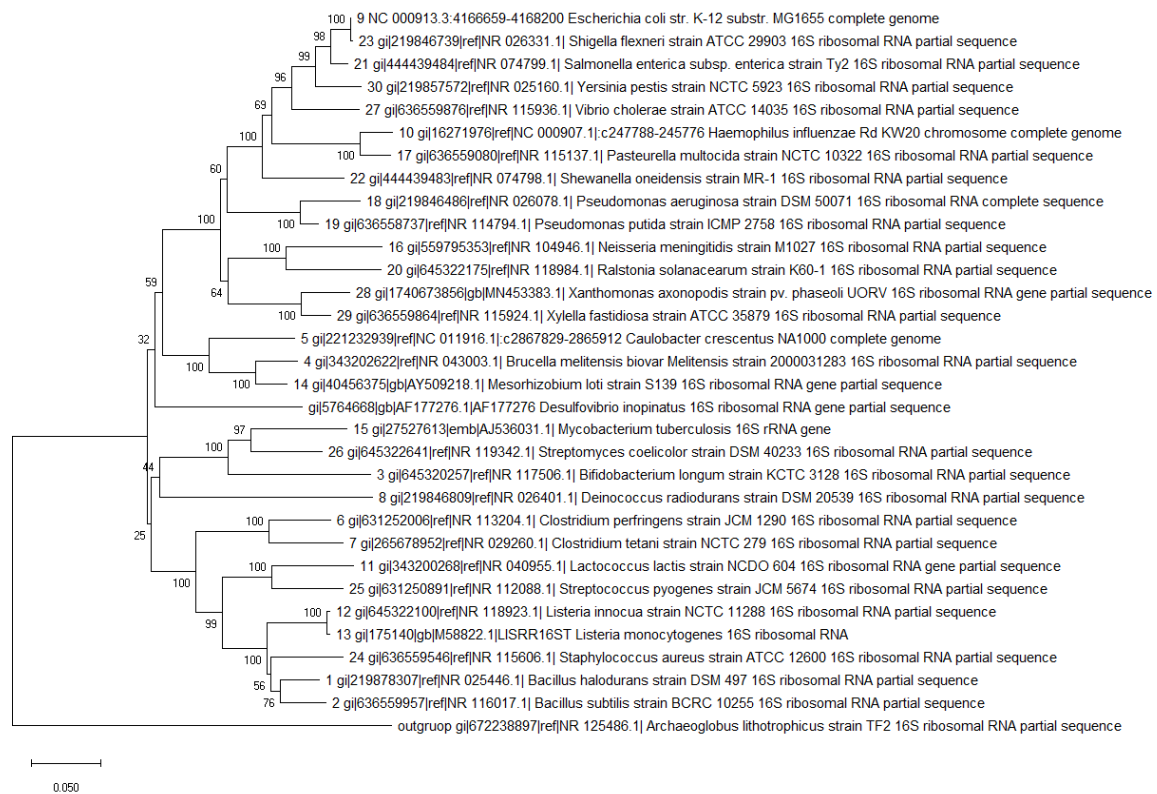


Figure S1.62: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio inopinatus* DSM 10711 and microbial strains belonging to the training set of PhiSpy.

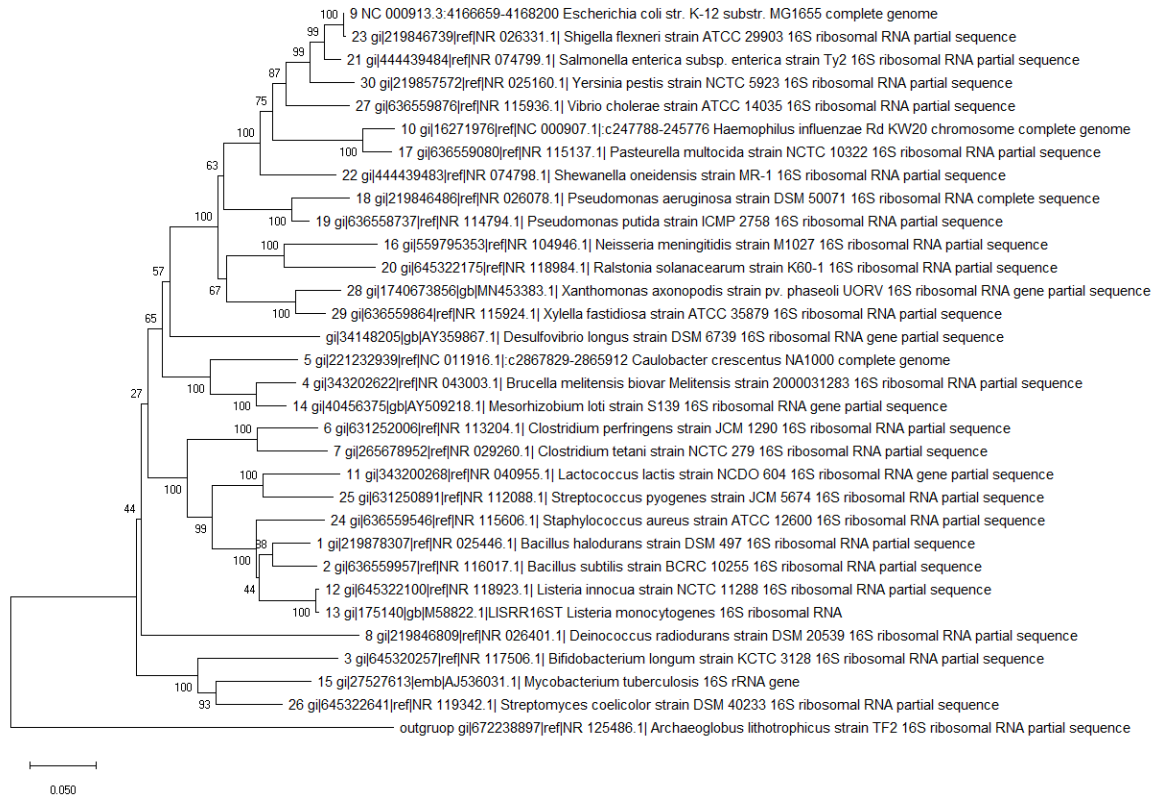


Figure S1.63: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio longus* strain DSM 6739 and microbial strains belonging to the training set of PhiSpy.

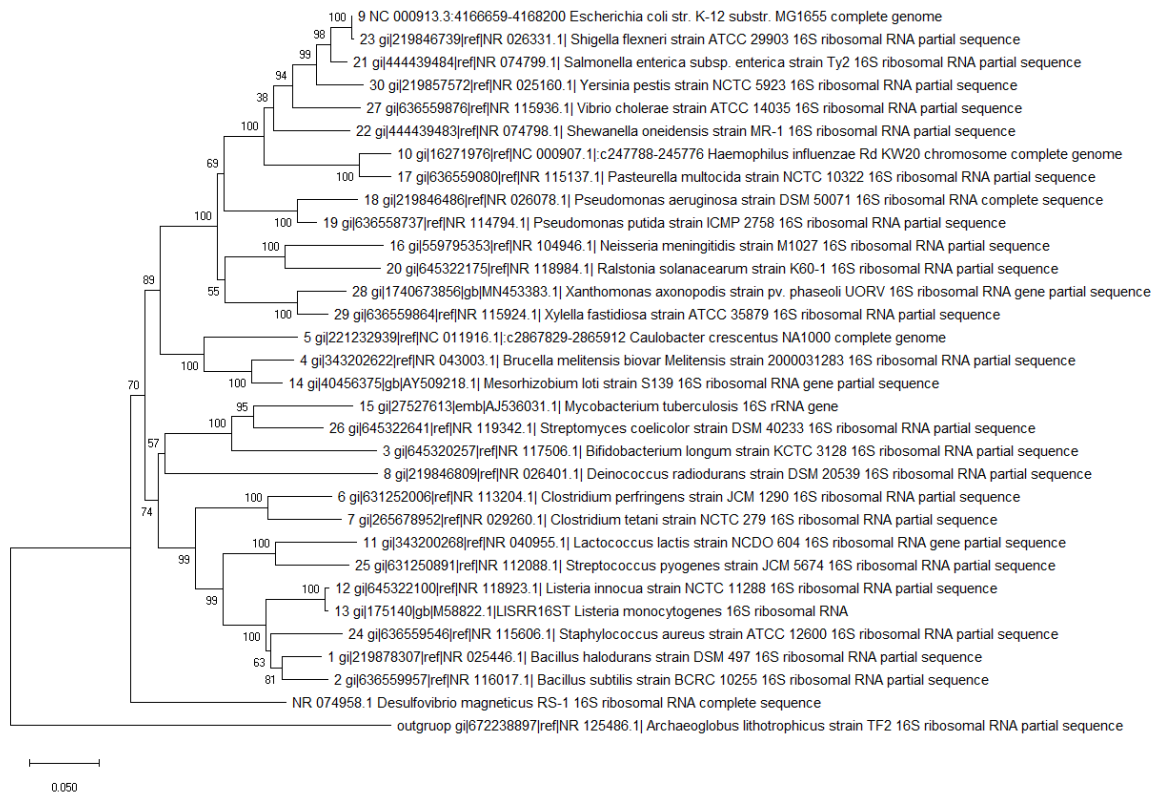


Figure S1.64: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio magneticus* RS-1 and microbial strains belonging to the training set of PhiSpY.

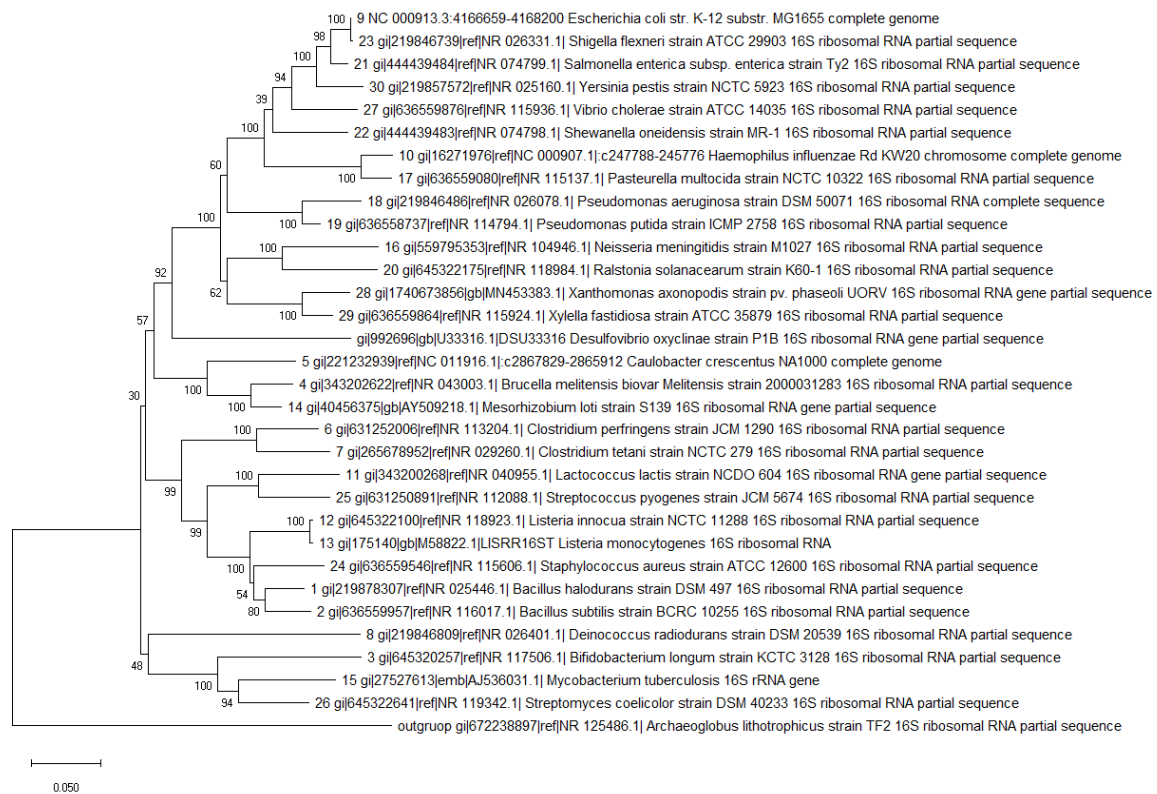


Figure S1.65: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio oxyclinae* strain P1B and microbial strains belonging to the training set of PhiSpy.

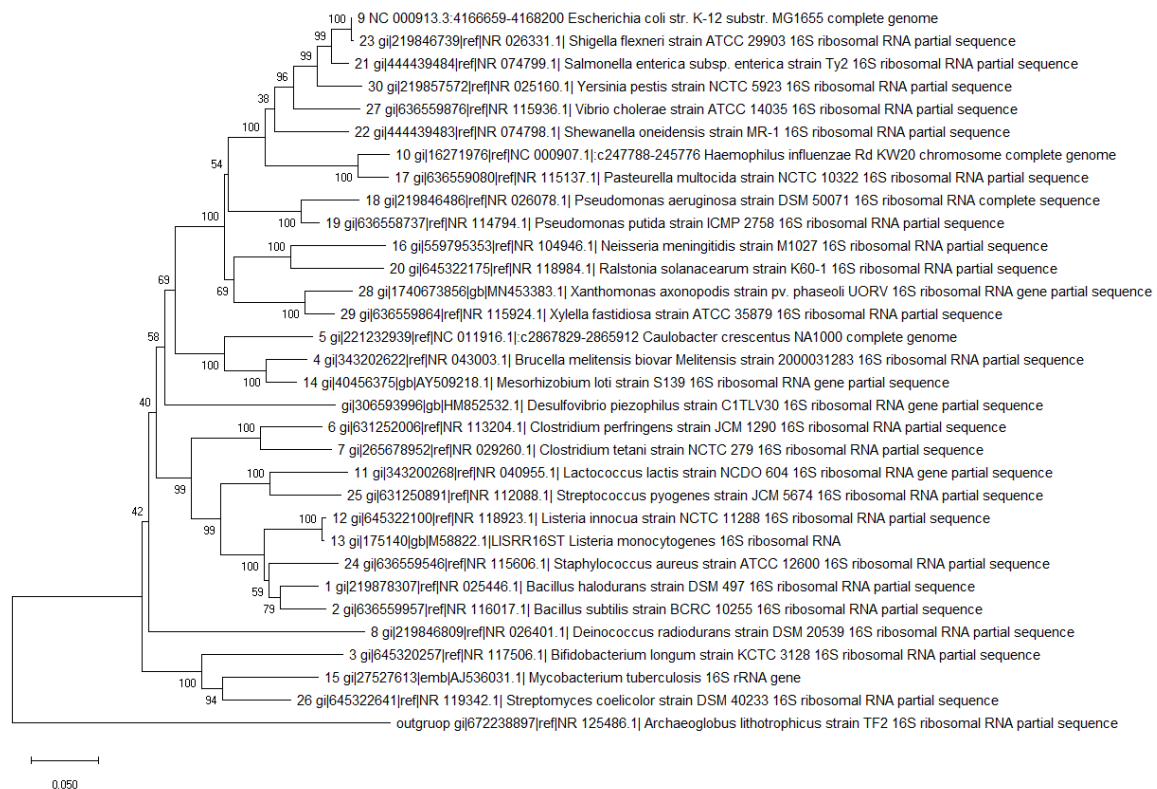


Figure S1.66: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio piezophilus* strain C1TLV30 and microbial strains belonging to the training set of PhiSpy.

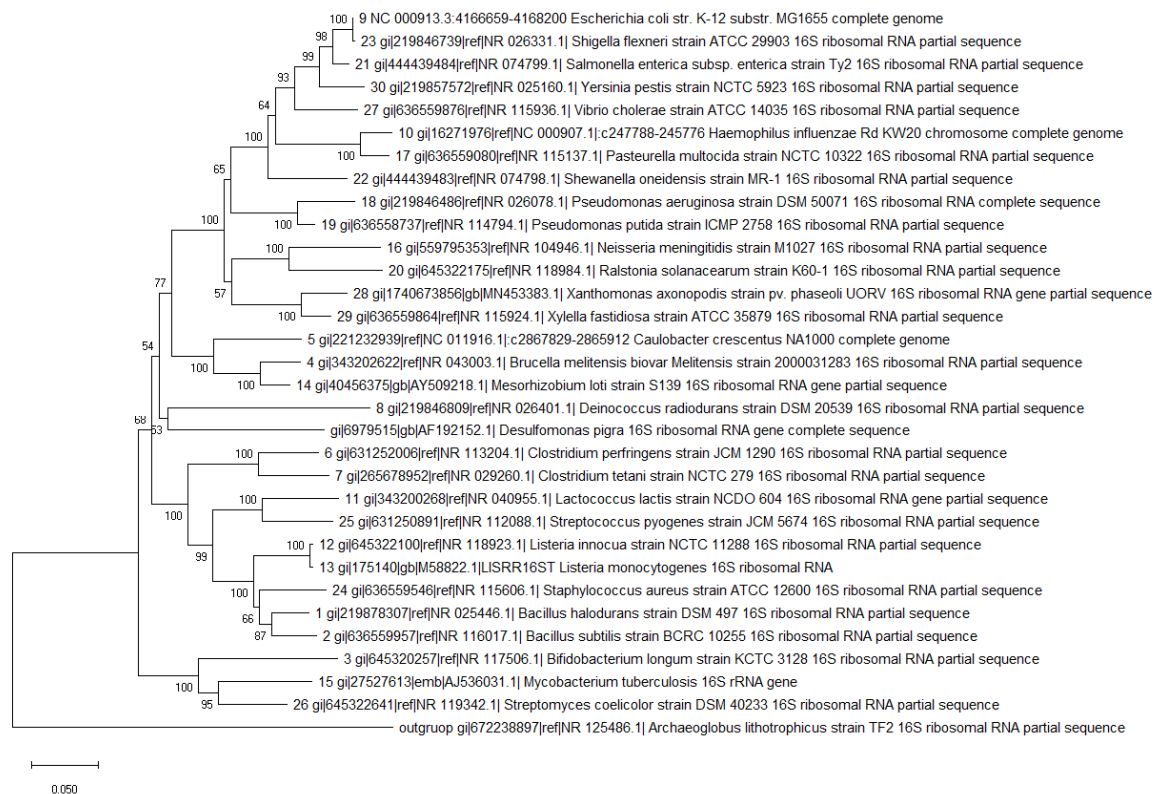


Figure S1.67: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio piger* ATCC 29098 and microbial strains belonging to the training set of PhiSpy.

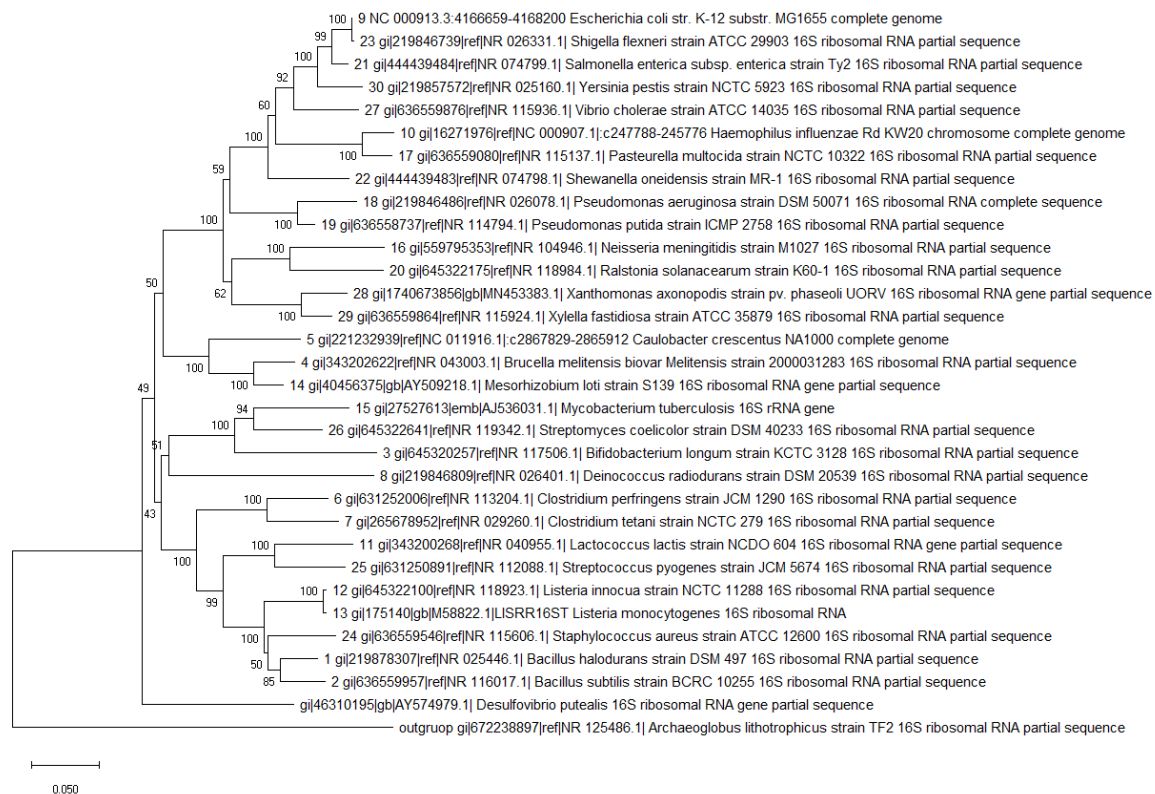


Figure S1.68: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio putealis* DSM 16056 and microbial strains belonging to the training set of PhiSpy.

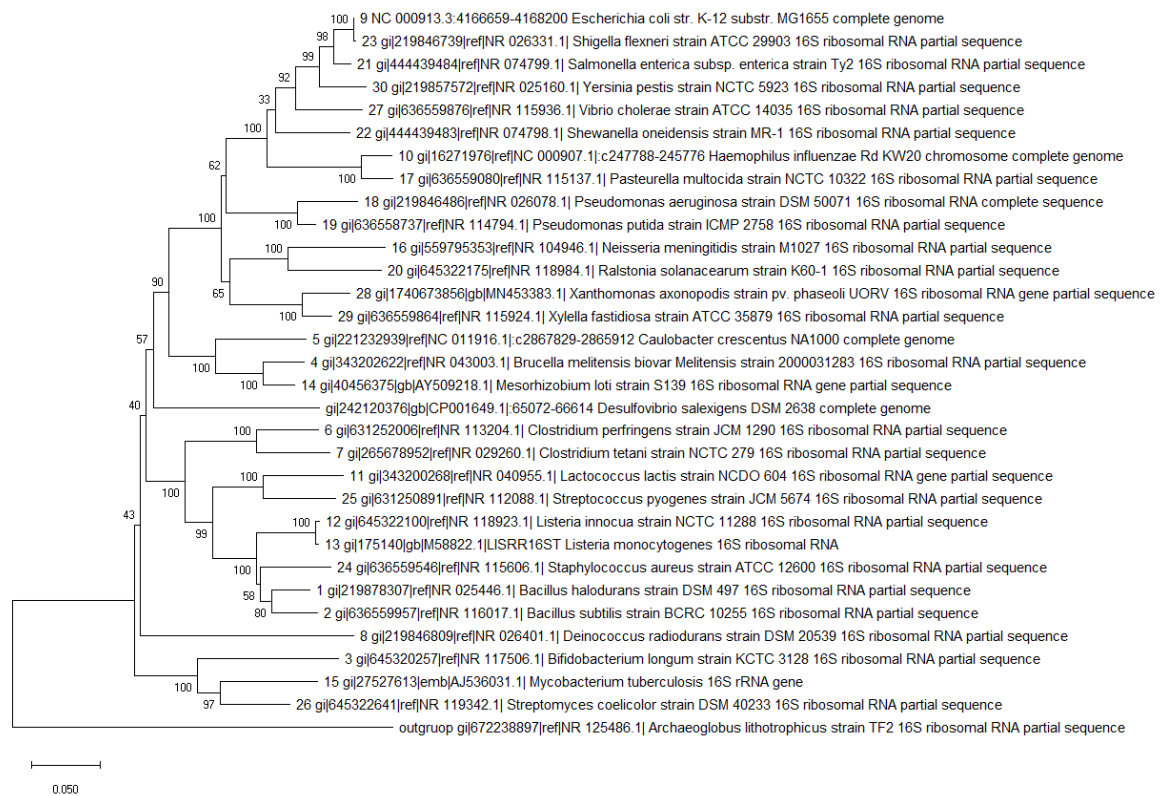


Figure S1.69: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio salexigens* and microbial strains belonging to the training set of PhiSpy.

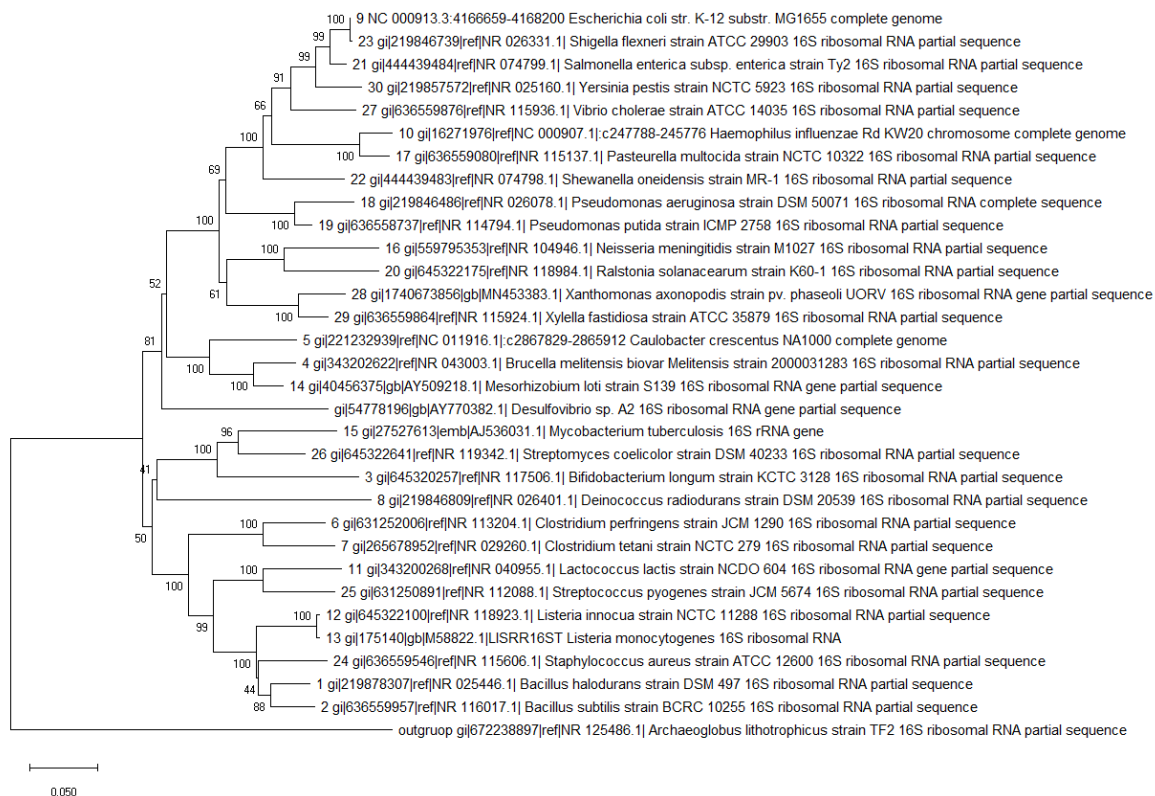


Figure S1.70: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio* sp. A2 and microbial strains belonging to the training set of PhiSpy.

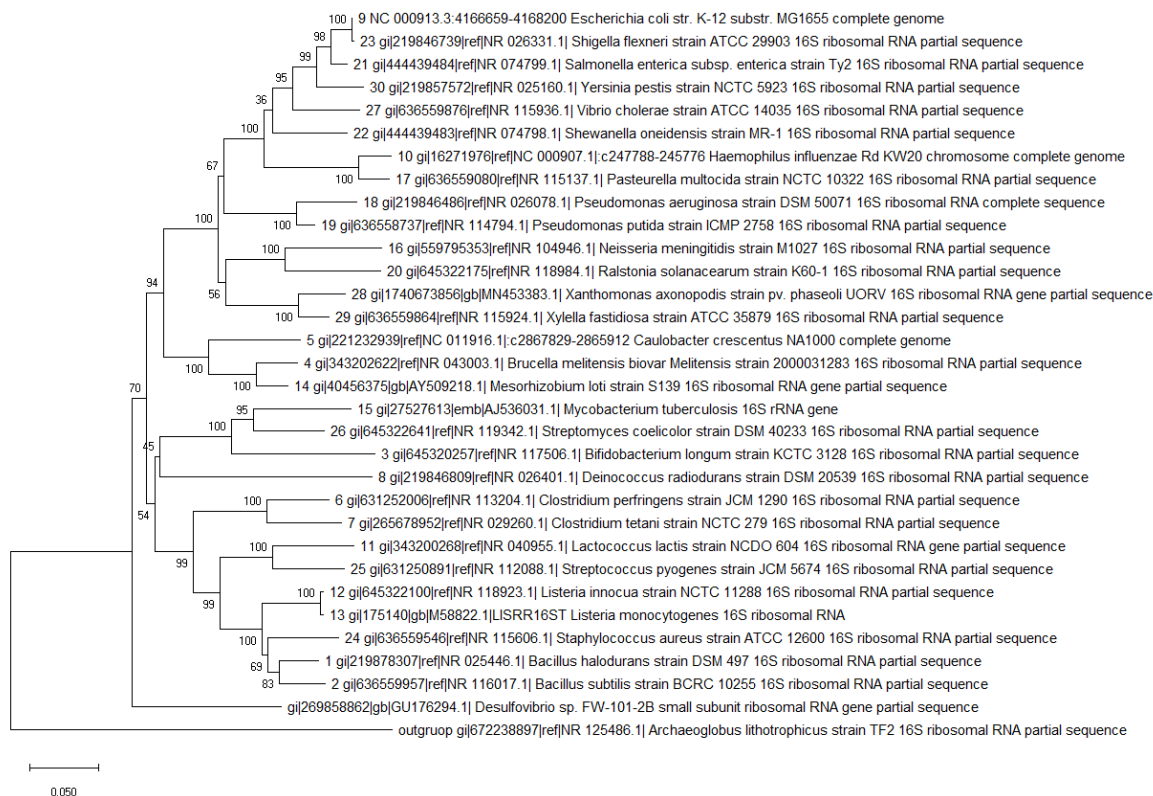


Figure S1.71: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio* sp. FW1012B and microbial strains belonging to the training set of PhiSpy.

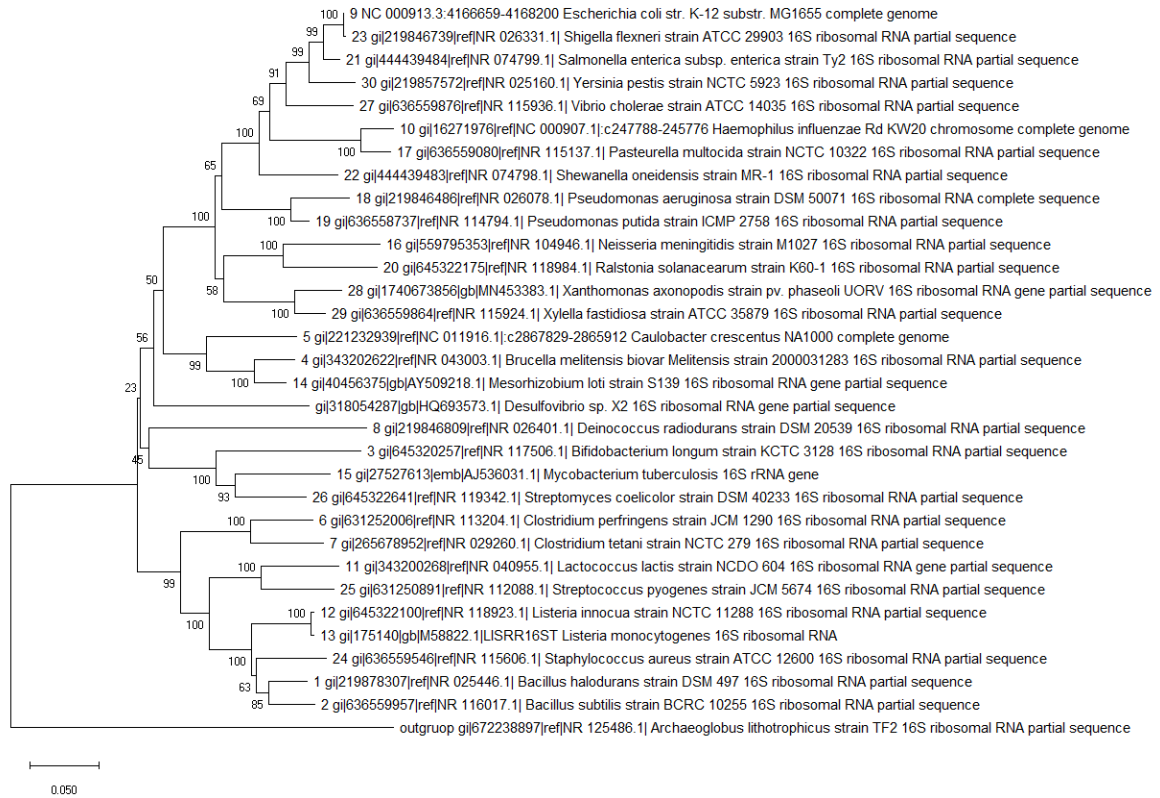


Figure S1.72: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio* sp. X2 and microbial strains belonging to the training set of PhiSpy.

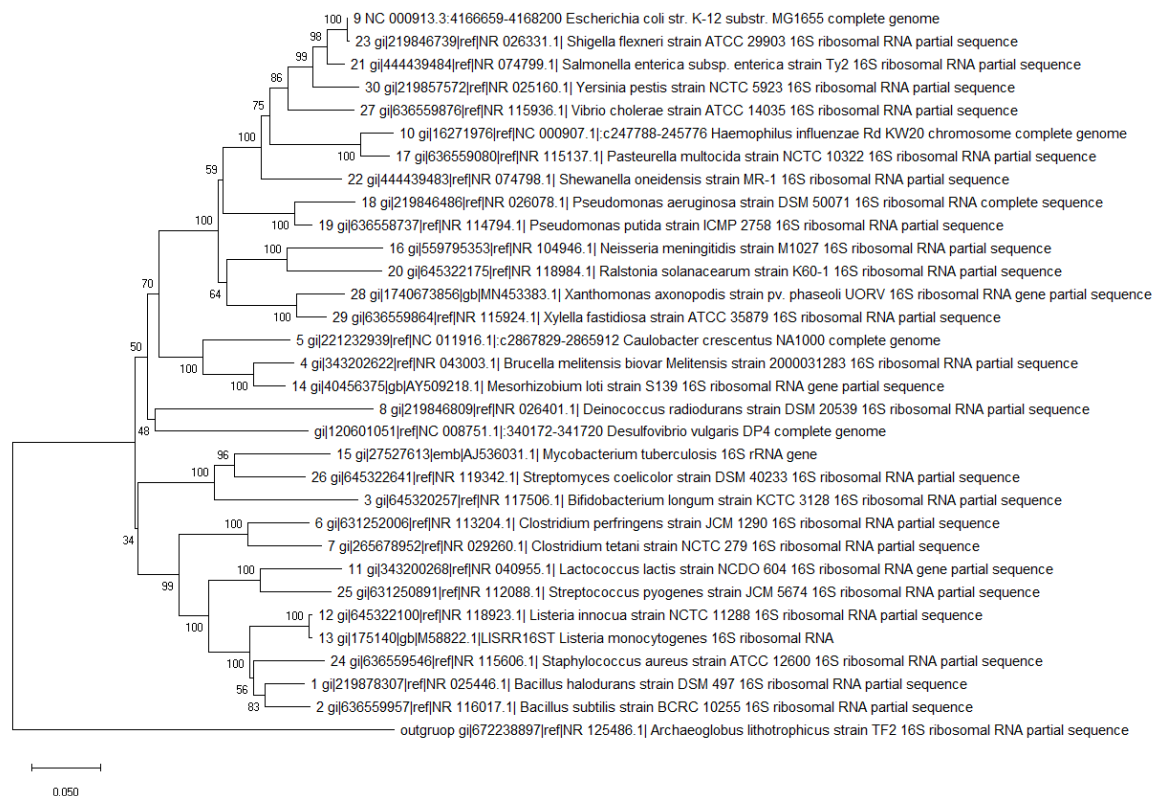


Figure S1.73: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio vulgaris* DP4 and microbial strains belonging to the training set of PhiSpy.

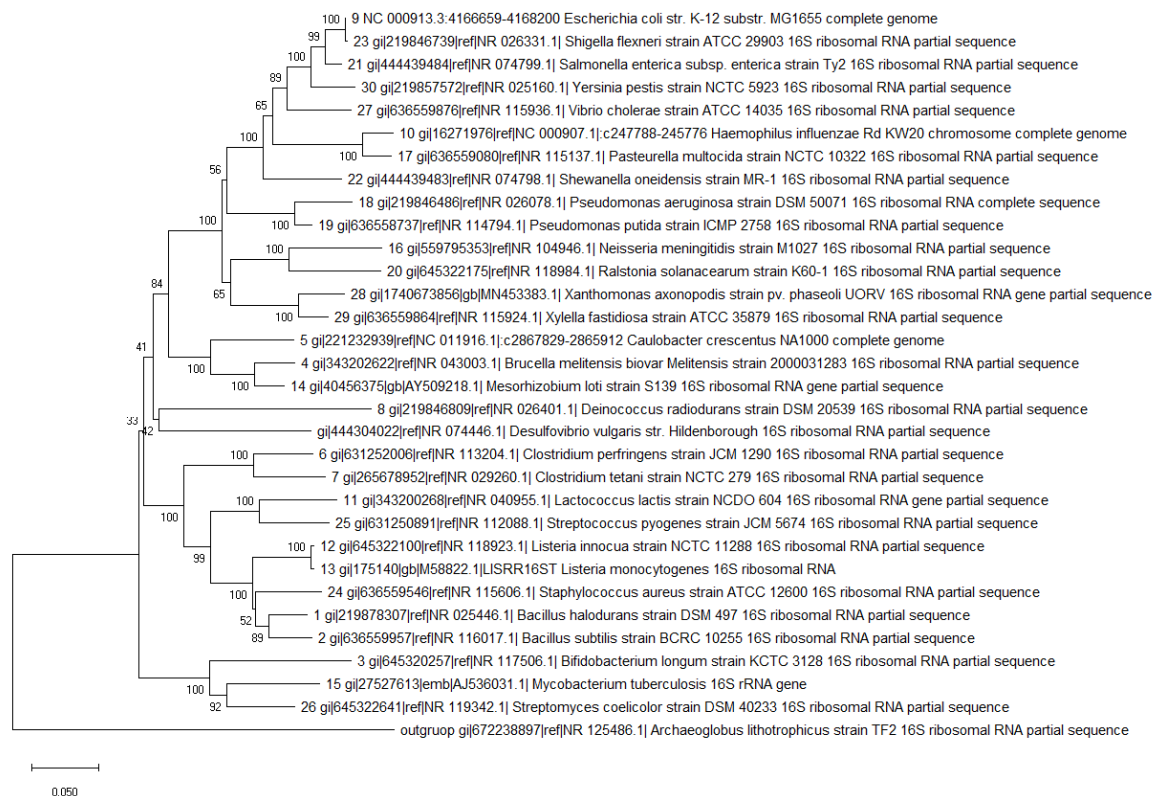


Figure S1.74: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio vulgaris* str. *Hildenborough* and microbial strains belonging to the training set of PhiSpy.

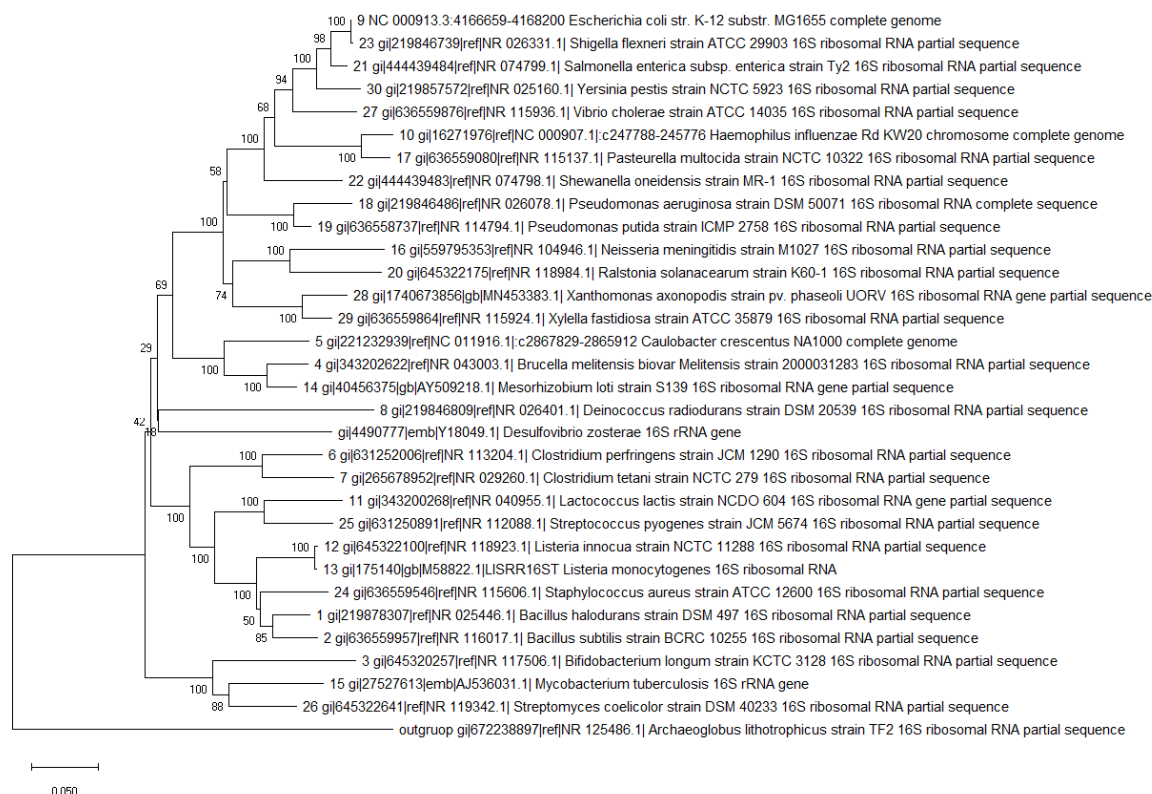


Figure S1.75: Phylogenetic tree of 16S rRNA gene sequences of *Desulfovibrio zosteriae* DSM 11974 and microbial strains belonging to the training set of PhiSpy.

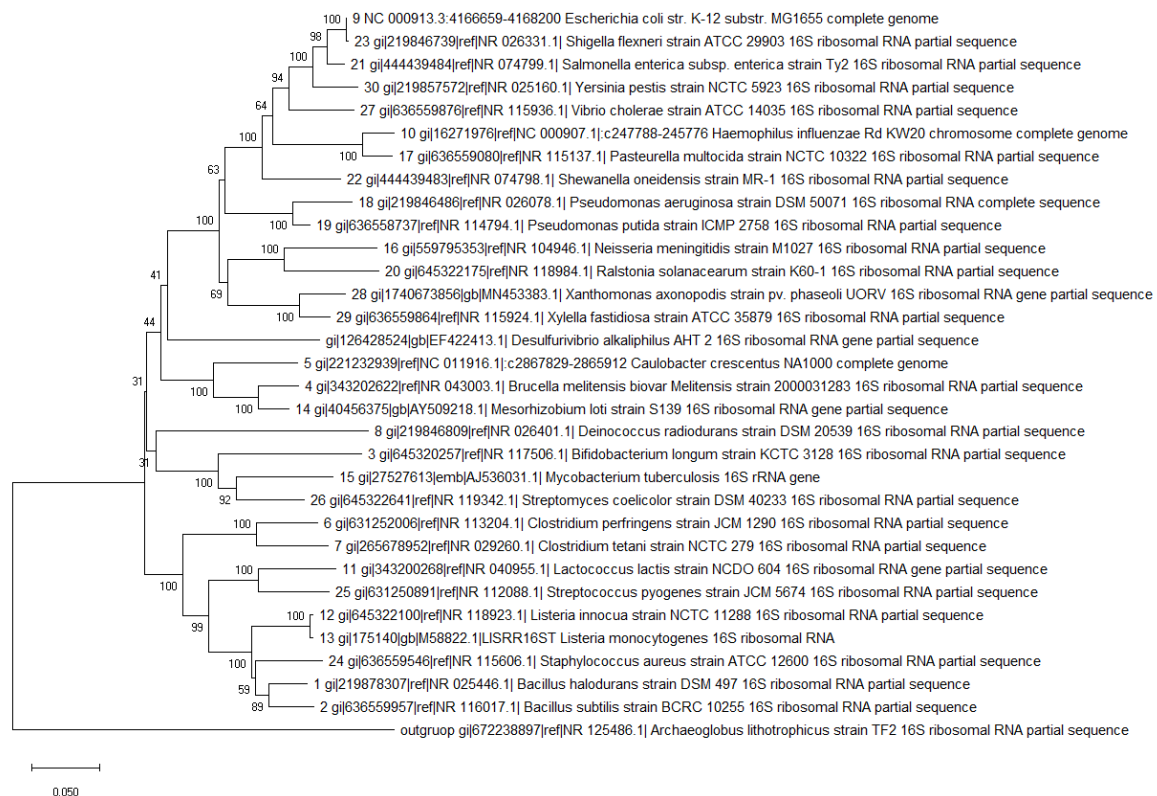


Figure S1.76: Phylogenetic tree of 16S rRNA gene sequences of *Desulfurivibrio alkaliphilus* AHT2 and microbial strains belonging to the training set of PhiSpy.

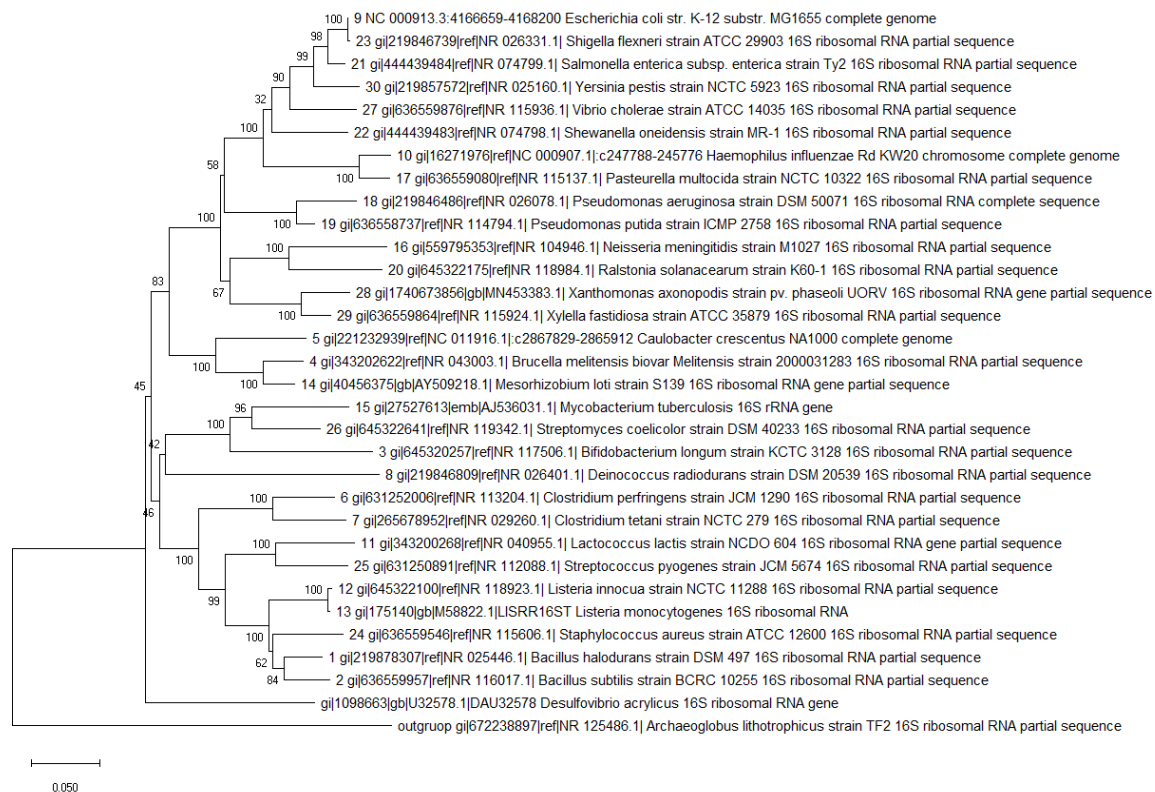


Figure S1.77: Phylogenetic tree of 16S rRNA gene sequences of *Halodesulfovibrio aestuarii* DSM 10141 and microbial strains belonging to the training set of PhiSpy.

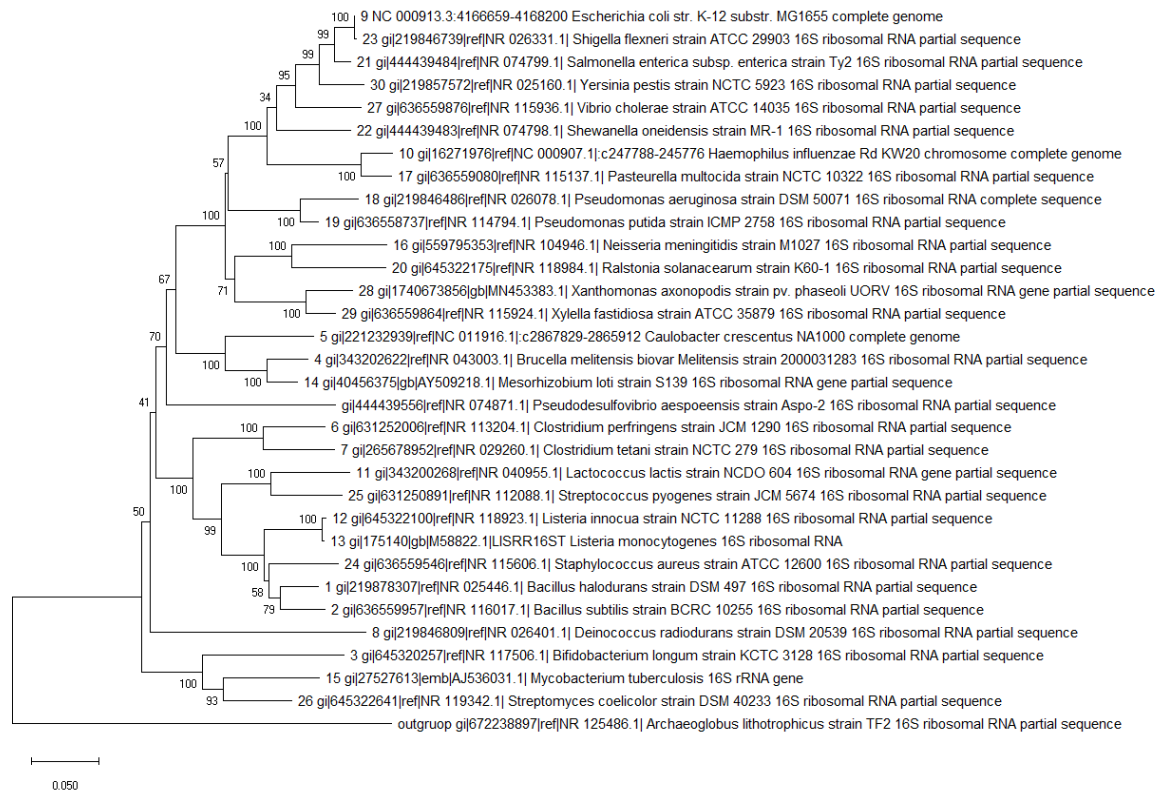


Figure S1.78: Phylogenetic tree of 16S rRNA gene sequences of *Pseudodesulfovibrio aespoensis* strain Aspo-2 and microbial strains belonging to the training set of PhiSpy.

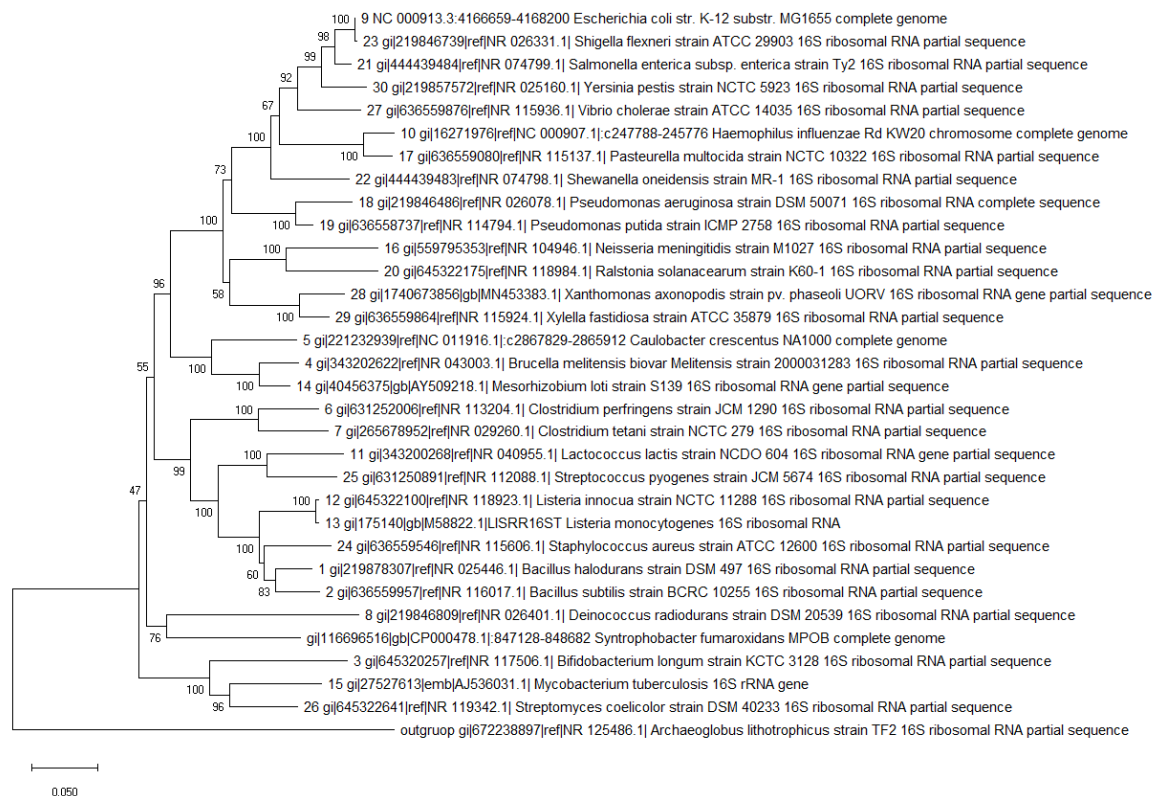


Figure S1.79: Phylogenetic tree of 16S rRNA gene sequences of *Syntrophobacter fumaroxidans* MPOB and microbial strains belonging to the training set of PhiSpy.

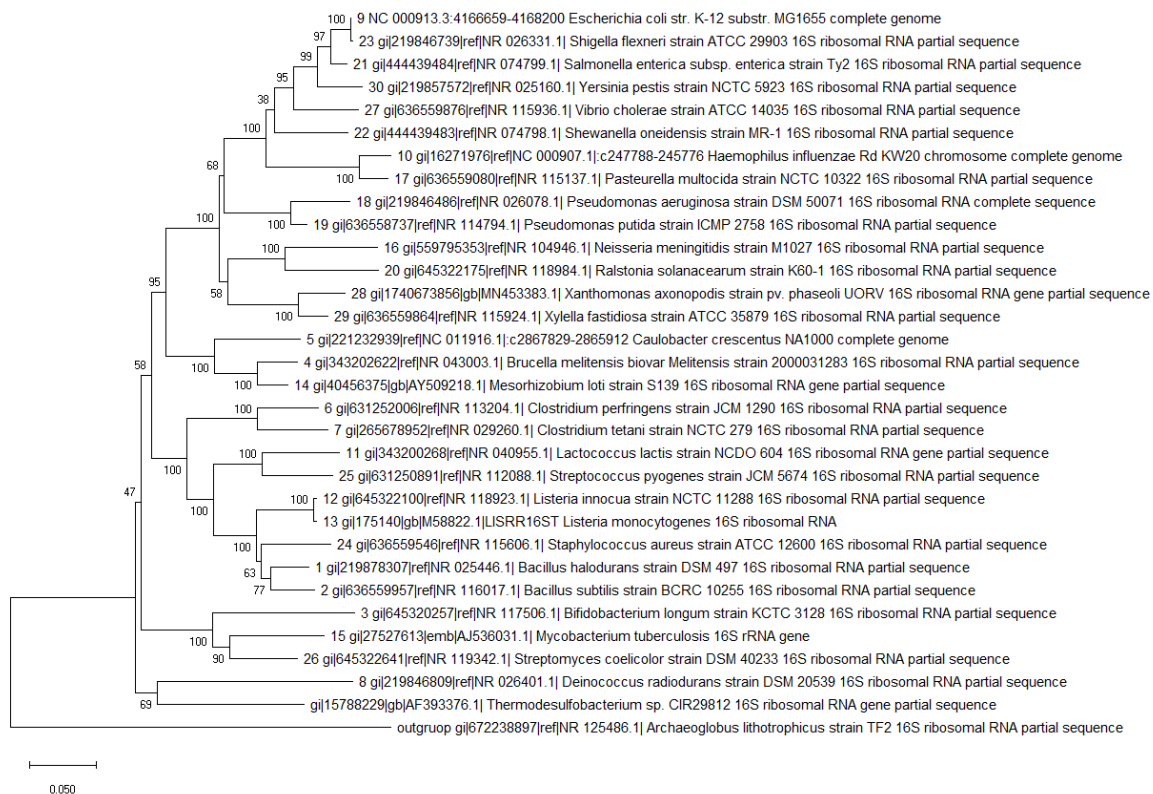


Figure S1.80: Phylogenetic tree of 16S rRNA gene sequences of *Thermodesulfatator indicus* DSM 15286 and microbial strains belonging to the training set of PhiSpy.

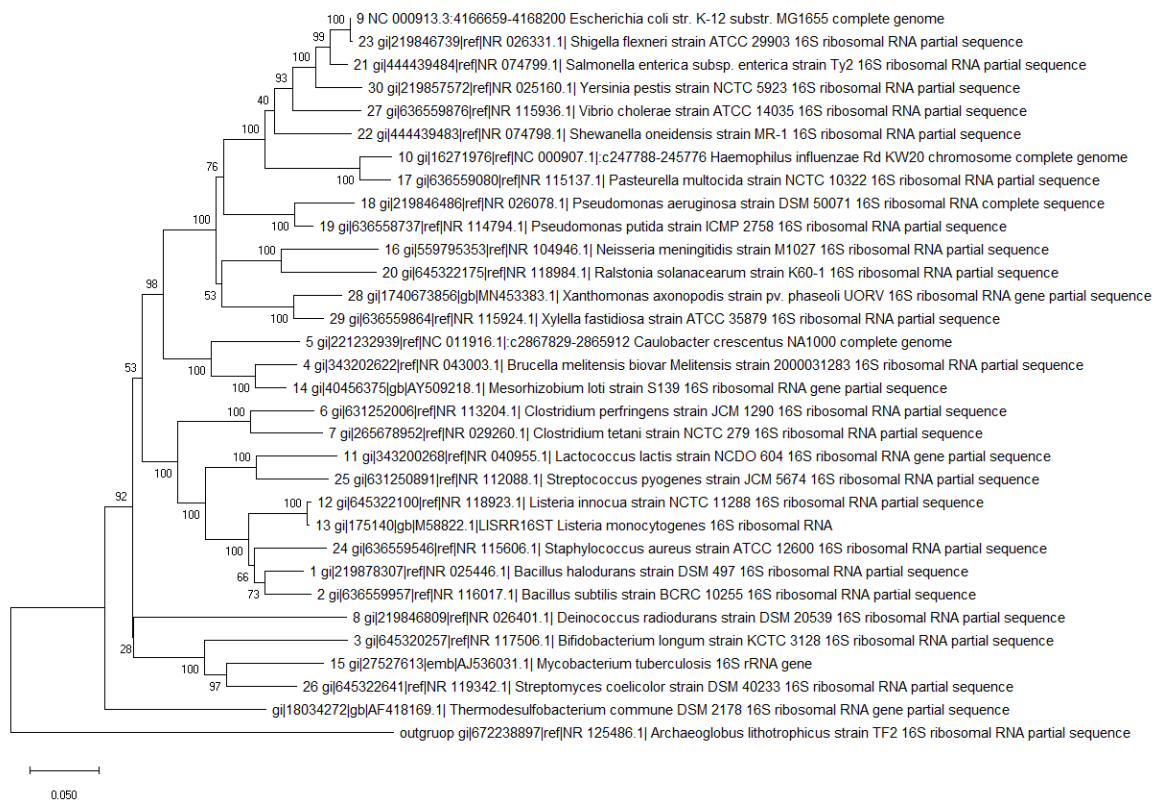


Figure S1.81: Phylogenetic tree of 16S rRNA gene sequences of *Thermodesulfobacterium commune* DSM 2178 and microbial strains belonging to the training set of PhiSpy.

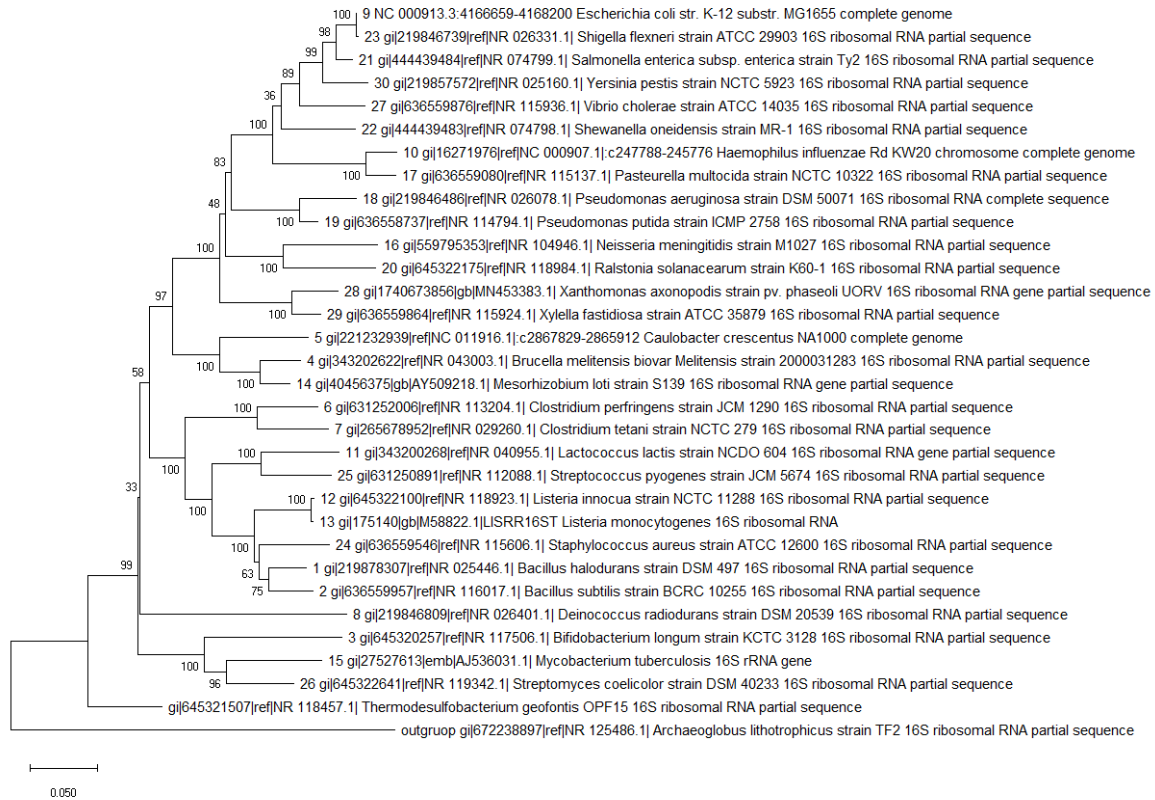


Figure S1.82: Phylogenetic tree of 16S rRNA gene sequences of *Thermodesulfobacterium geofontis* OPF15 and microbial strains belonging to the training set of PhiSpy.

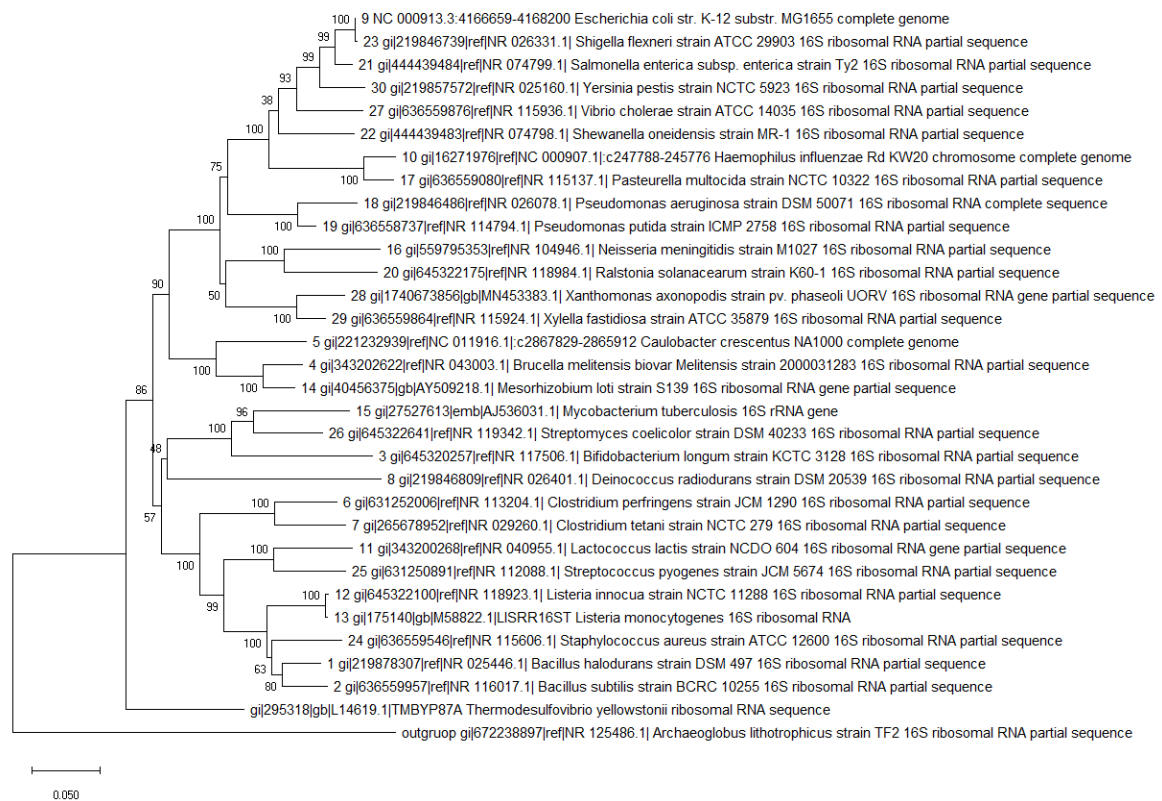


Figure S1.83: Phylogenetic tree of 16S rRNA gene sequences of *Thermodesulfovibrio yellowstonii* and microbial strains belonging to the training set of PhiSpy.

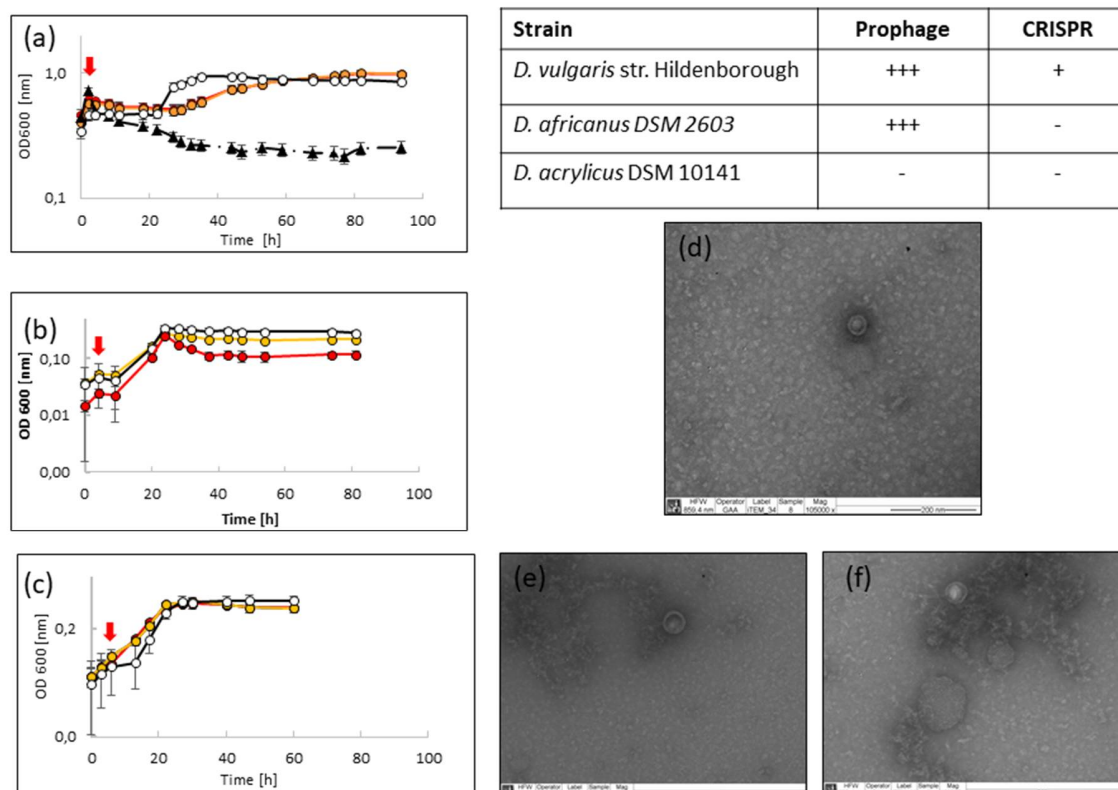


Figure S2: Effect of Mitomycin C on the growth of (a) *D. vulgaris* str. Hildenborough, (b) *D. africanus* 2603 and (c) *D. acrylicus* DSM 10141. White circles indicate cultures grown in the absence of Mitomycin C; orange circles, cultures grown in the presence of $1 \mu\text{g ml}^{-1}$ of Mitomycin C; red circles, cultures grown in the presence of $3.5 \mu\text{g ml}^{-1}$ of Mitomycin C. In (a), black triangles indicate cultures grown in the presence of $10 \mu\text{g ml}^{-1}$ of Mitomycin C. Data represent the mean \pm sd from three independent replicate cultures. Bars designate one standard deviation of the mean. The table in the upper right section indicate presence (+) or absence (-) of prophages and CRISPR. (d) TEM micrographs of viral-like particles with typical morphotype of *Podoviridae* were obtained from *D. vulgaris* str. Hildenborough batch cultures after induction with Mitomycin C. (e-f) TEM micrographs presents structures that resembles outer membrane vesicles previously observed in *D. alaskensis* DSM16109. Most of the micrographs obtained in this study contained low-resolution viral particles and structures, cell debris, and a noisy background as a result of the interactions of the compounds of the growth medium of SRP.

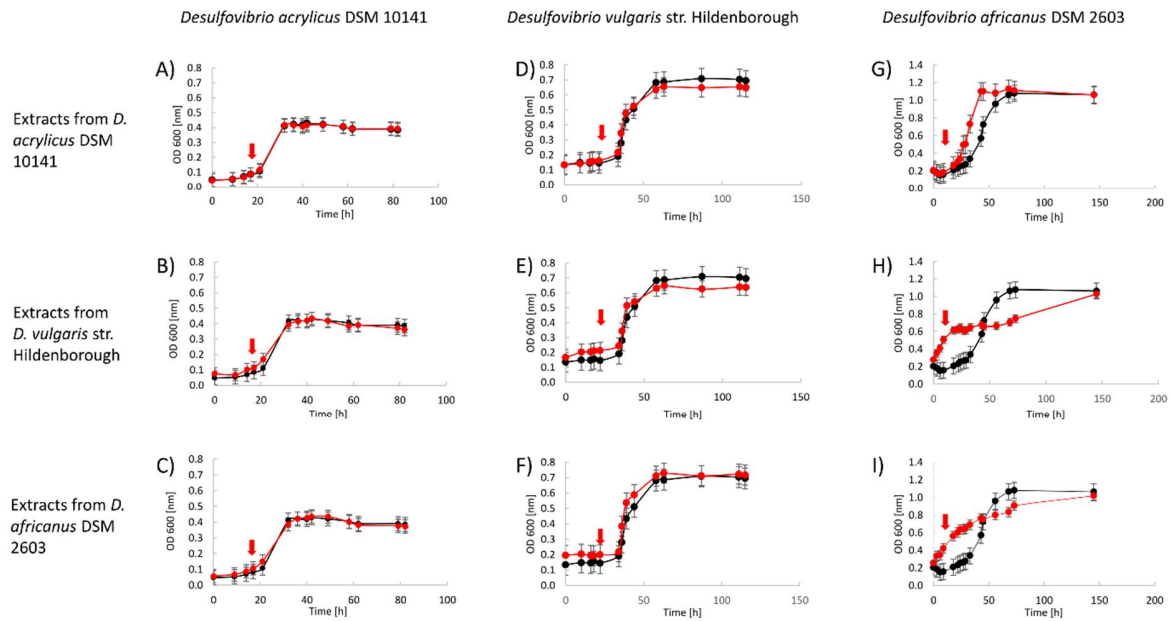


Figure S3A: Effect of filtrates from mitomycin induced SRB cultures added at early exponential phase on the growth of *Desulfovibrio acrylicus* DSM 10141 (A-C), *Desulfovibrio vulgaris* str. Hildenborough (D-F), and *Desulfovibrio africanus* DSM 2603 (G-I). Black and red circles indicate cultures grown in the absence and presence of filtrates. Data represent the mean \pm sd from three independent replicate cultures. Bars designate one standard deviation of the mean.

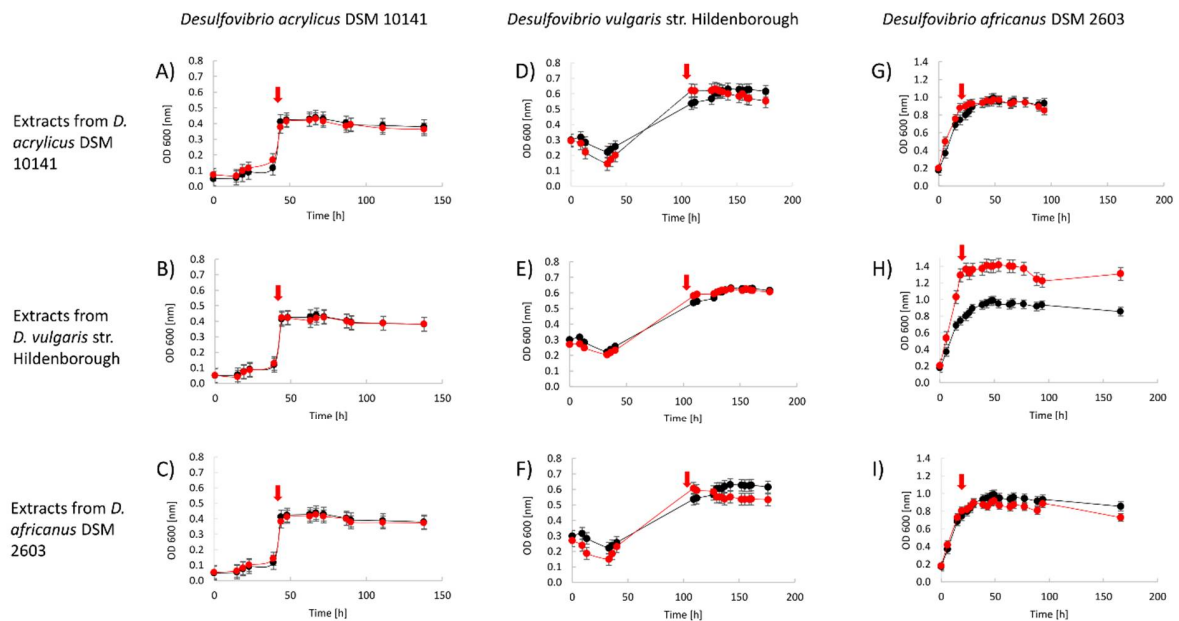


Figure S3B: Effect of filtrates from mitomycin induced SRB cultures added at early stationary phase on the growth of *Desulfovibrio acrylicus* DSM 10141 (A-C), *Desulfovibrio vulgaris* str. Hildenborough (D-F), and *Desulfovibrio africanus* DSM 2603 (G-I). Black and red circles indicate cultures grown in the absence and presence of filtrates. Data represent the mean \pm sd from three independent replicate cultures. Bars designate one standard deviation of the mean.

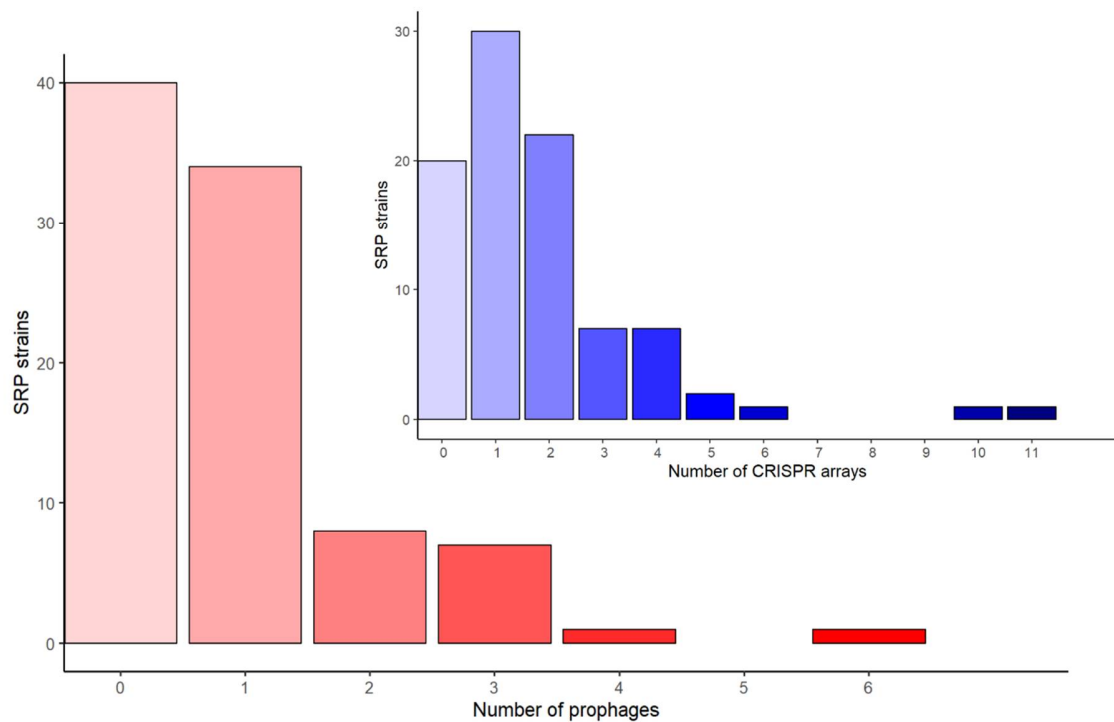


Figure S4: Frequencies of integrated prophages (light red) and CRISPR arrays (light blue) in the genomes of SRP strains.

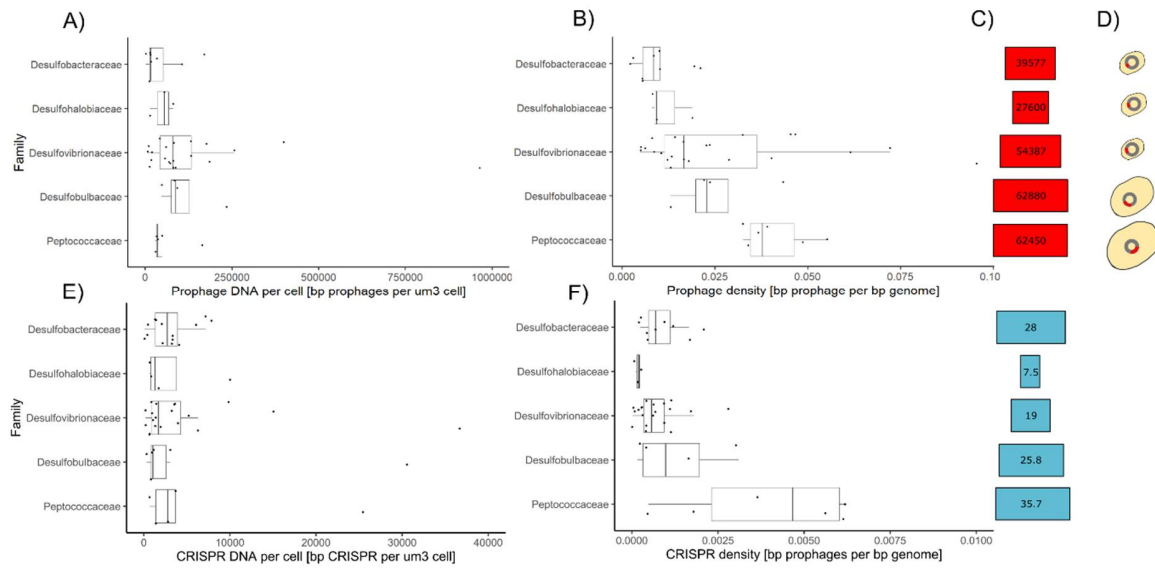


Figure S5: Box-plots of (A) DNA prophage per cell (volume) and (B) prophage density of lysogens belonging to five families of SRP; (C) red bars indicate the median of the length of prophages and (D) represents the median cellular volume and median genome size found in each family. Box-plots of (E) CRISPR DNA per cell and (F) CRISPR density of CRISPR-carrying strains belonging to five families of SRP; (G) light blue bars indicate the median of number of spacers belonging to strains of each family.

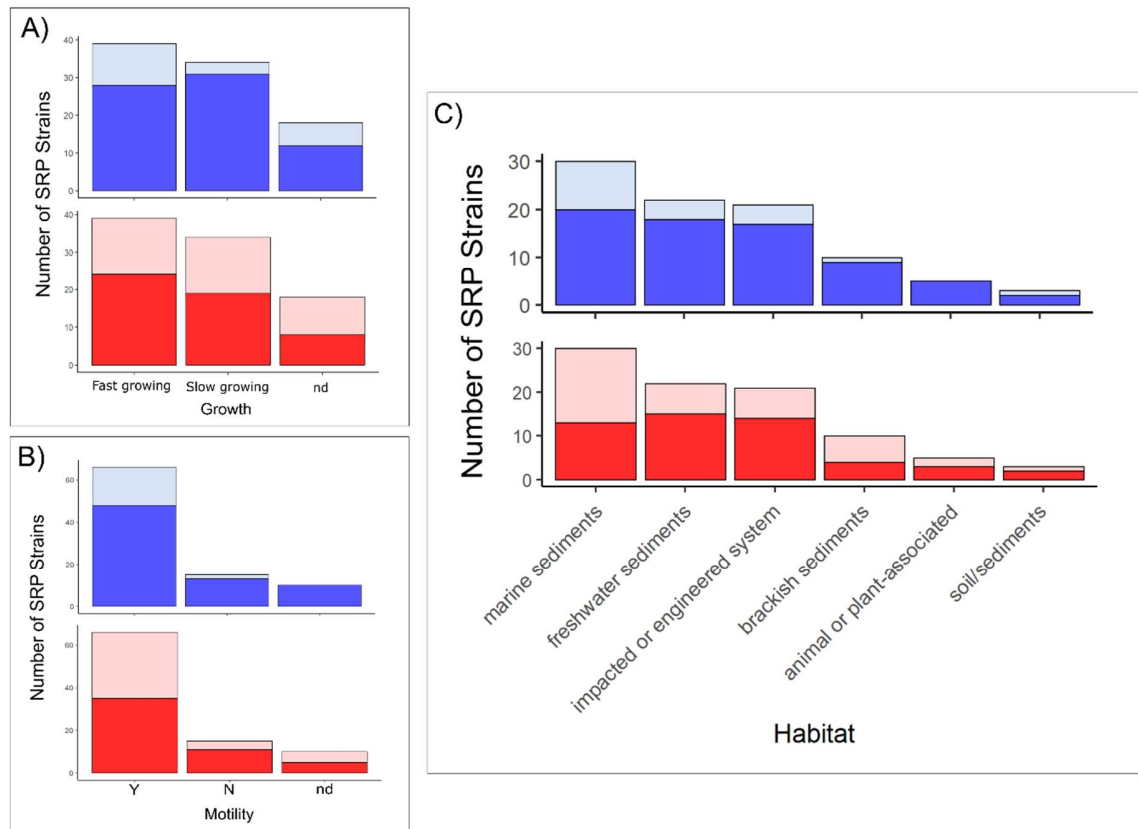
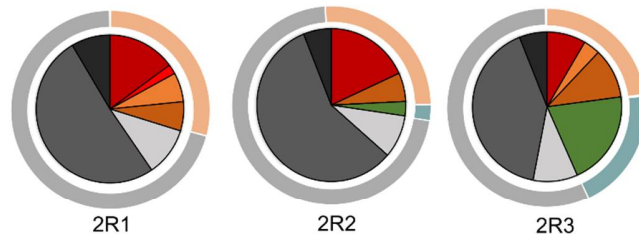
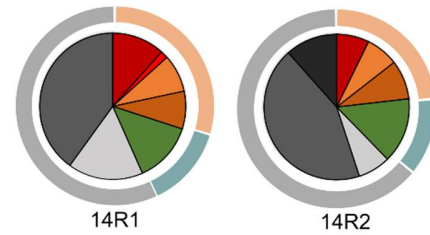


Figure S6: Distribution of prophages (red) and CRISPR (blue) according to different ecophysiological traits. In the left top (A), it is shown the distribution of prophages and CRISPR arrays according to the type of growth (doubling time ≤ 12 hours or > 12 hours, as fast-growing or slow-growing strains, respectively). In the left bottom (B), it is shown the distribution of prophages and CRISPR arrays according to the presence of flagellum, classified as strains with flagellum (Y), strains for which flagellum has not been observed (N) and strains with no information (nd). In the right (C), it is shown the distribution of prophages and CRISPR arrays according to type of environment in which strains were isolated or the source of material that allowed the reconstruction of the genomes.

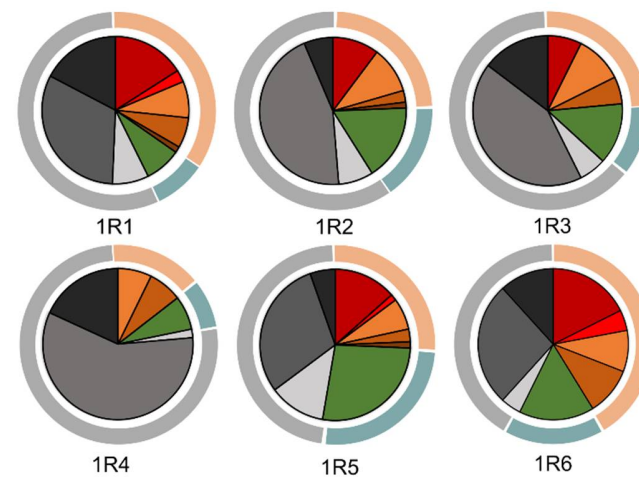
Desulfocurvibacter africanus DSM 2603



Desulfovibrio vulgaris str. Miyazaki



Desulfovibrio vulgaris str. Hildenborough



Desulfovibrio vulgaris DP4

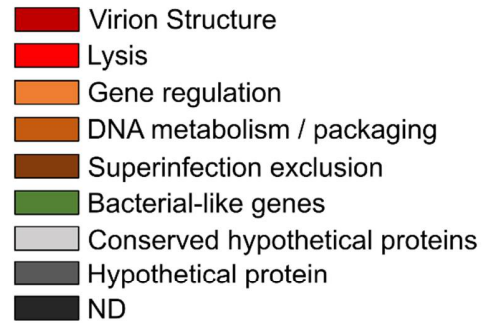
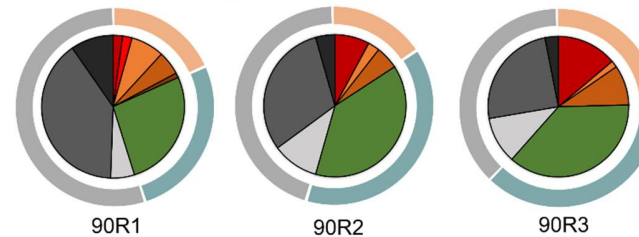


Figure S7: Comparison of genome annotations among SRP prophages. Pie charts indicate the annotation of prophages from *Desulfocurvibacter africanus* 2603, *Desulfovibrio vulgaris* str. Miyazaki, *Desulfovibrio vulgaris* str. Hildenborough and *Desulfovibrio vulgaris* DP4. The inner circle indicates functional classification (see color bar) and outer circle indicates the classification in the following categories; genes with bacterial origin (light green), genes with viral origin (light orange) and genes with unknown function (light gray).

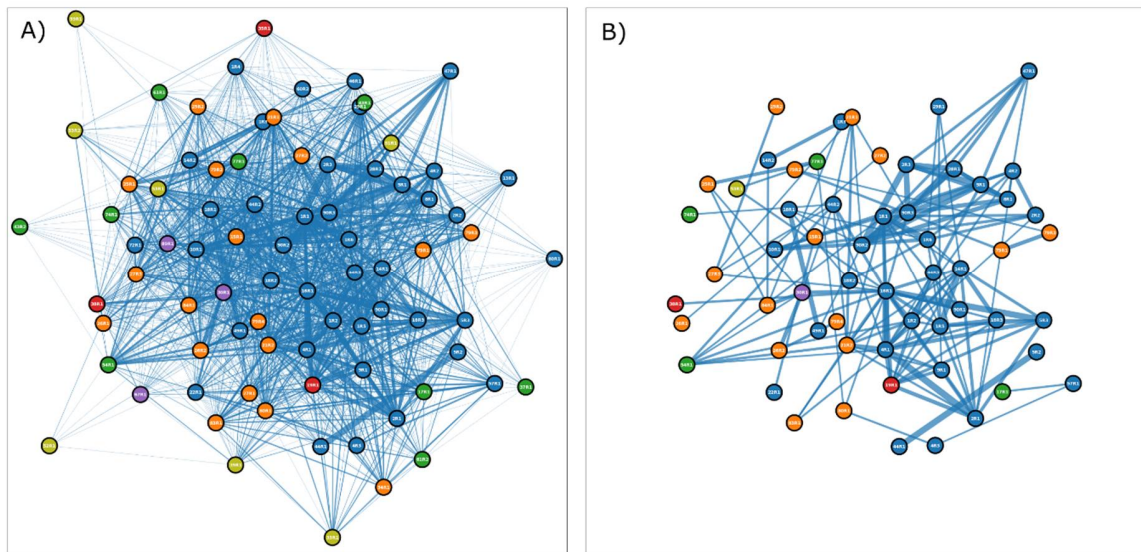


Figure S8: (A) Network shows the degree of homology among SRP prophages. Circles indicate each SRP, colored by the taxonomy of the host. Edges show the presence of homologous genes among prophages. (B) Network shows the degree of homology among SRP prophages that share more than 10 homologs. The width of edges indicates the number of homologous genes between two prophages.

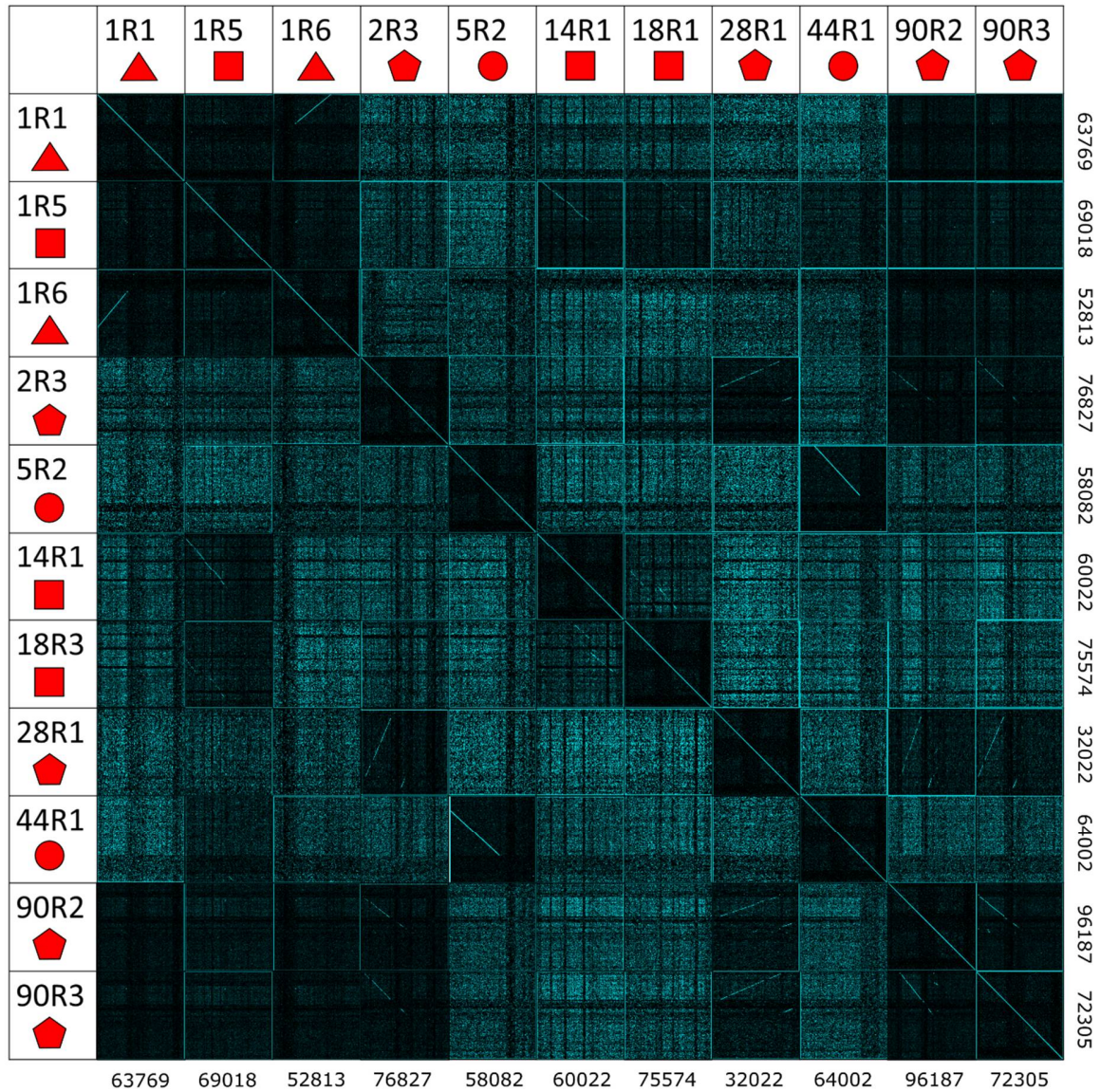


Figure S9: Whole-genome dot plot comparison of prophage nucleotides sequences of *Desulfovibrio* strains, prophages 1R1, 1R5 and 1R6 of *D. vulgaris* Hildenborough, 2R3 of *Desulfovibrio africanus* DSM 260, 5R2 of *Desulfovibrio aespoeensis* Aspo-2, 14R1 of *Desulfovibrio vulgaris* str. Miyazaki, 18R1 of *Desulfovibrio fructosivorans* JJ, 28R1 of *Desulfovibrio* sp. X2, 44R1 of *Desulfovibrio alaskensis* G20, and 90R2 and 90R3 of *Desulfovibrio vulgaris* DP4. Lack of grouping in dot plots are both reflection of the overall high degree of diversity and low level of synteny of the SRP prophages. The symbols indicate the classification of each prophage according to VIRFAM. The numbers in the right and bottom indicate the length of each prophage (in bp).

No	SRP Strain	Name	ID	CRISPR (2-4) found by CRISPRCasFinder	Putative CRISPR found by CRISPRCasFinder	Number of prophage like elements
1	<i>Desulfovibrio vulgaris</i> str. Hildenborough	plasmid pDV	NC_005863.1	1	0	0
7	<i>Desulfovibrio magneticus</i> RS-1	plasmid pDMC1	NC_012797.1	0	0	0
		plasmid pDMC2	NC_012795.1			
9	<i>Desulfovibrio gigas</i> DSM 1382	plasmid unnamed	NC_022436.1	0	0	0
24	<i>Desulfovibrio hydrothermalis</i> DSM 14728	plasmid DESAM_p	NC_019953.1	0	0	0
30	<i>Desulfosporosinus acidiphilus</i> SJ4	plasmid pDESACI.02	CP003641.1	0	0	0
		plasmid pDESACI.01	CP003640.1			
38	<i>Desulfohalobium retbaense</i>	plasmid pDRET01	NC_013224.1	0	0	0
40	<i>Desulfobacterium autotrophicum</i> HRM2	plasmid pHRM2a	NC_012109.1	0	0	0
43	<i>Desulfotalea psychrophila</i> LSv54	small plasmid	CR522872.1	0	2	0
		large plasmid	CR522871.1			
46	<i>Desulfovibrio</i> sp. FW1012B	plasmid pFW10102	NZ_CM001370.1	0	0	0
		plasmid pFW10101	NZ_CM001369_1			
67	<i>Desulfurella acetivorans</i> DSM 5264	plasmid unnamed	NZ_CP007052.1	0	0	0
76	<i>Desulfocapsa sulfexigens</i> DSM 10523	plasmid unnamed	NC_020305.1	0	0	0
86	<i>Archaeoglobus profundus</i> DSM 5631	plasmid pArcpr01	NC_013742.1	0	0	0
90	<i>Desulfovibrio vulgaris</i> DP4	plasmid pDVUL01	NC_008741.1	1	0	0

Table S1: CRISPR and putative CRISPR arrays identified in plasmids of SRP analyzed in this study.

Number	Strain name	Number of prophage	Prophage ID	Prophage Sequence ID	Start	End	length (bp)	Number of ORFs	Total prophage length (bp)	Avg prophage length (bp)	Genome Size (bp)	Prophage Density (%)	Total Prophages Density	Taxonomic classification according to VIRFAM
1	Desulfovibrio vulgaris str. Hildenborough	6	1R1	1R1 gi 46562128 ref NC_002937.3 Complete Genome 239651 303420	239651	303420	63769	75	360426	60071	3773160	1.69%	9.55%	Myoviridae of Type1 (Cluster 6)
			1R2	1R2 gi 46562128 ref NC_002937.3 Complete Genome 1205411 1277056	1205411	1277056	71645	78				1.90%		Myoviridae of Type1 (Cluster 8)
			1R3	1R3 gi 46562128 ref NC_002937.3 Complete Genome 1561263 1625178	1561263	1625178	63915	68				1.69%		Siphoviridae of Type1 (cluster 6)
			1R4	1R4 gi 46562128 ref NC_002937.3 Complete Genome 1783411 1822677	1783411	1822677	39266	55				1.04%		Podoviridae of Type3
			1R5	1R5 gi 46562128 ref NC_002937.3 Complete Genome 2801325 2870343	2801325	2870343	69018	74				1.83%		Myoviridae of Type1 (Cluster 8)
			1R6	1R6 gi 46562128 ref NC_002937.3 Complete Genome 2936361 2989174	2936361	2989174	52813	68				1.40%		Myoviridae of Type1 (Cluster 6)
2	Desulfocurvibacter africanus DSM 2603	3	2R1	2R1 gi 523389900 gb A_ULZ01000005.1 H585DRAFT_scaffold00004.4_C 86038 118974	86038	118974	32936	47	138181	46060	4400410	0.75%	3.14%	Myoviridae of Type1 (Cluster 8)
			2R2	2R2 gi 523389844 gb A_ULZ01000010.1 H585DRAFT_scaffold00008.8_C 45240 73658	45240	73658	28418	33				0.65%		Myoviridae of Type1 (Cluster 6)
			2R3	2R3 gi 523389782 gb A_ULZ01000012.1 H585DRAFT_scaffold0010.10_C 2130 78957	2130	78957	76827	83				1.75%		Myoviridae of Type1 (Cluster 9)

3	Desulfovibrio desulfuricans subsp. aestuarii ATCC 29578	0									3473760			
4	Desulfocurvibacter africanus str. Walvis Bay	3	4R1	4R1 gi 374298386 ref NC_016629.1 Complete Genome 727631 787504	727631	787504	59873	70	121145	40382	4200530	1.43%	2.88%	Myoviridae of Type1 (Cluster 8)
			4R2	4R2 gi 374298386 ref NC_016629.1 Complete Genome 2137665 21744 27	2137665	2174427	36762	51				0.88%		Myoviridae of Type1 (Cluster 6)
			4R3	4R3 gi 374298386 ref NC_016629.1 Complete Genome 3907176 39316 86	3907176	3931686	24510	26				0.58%		Myoviridae
5	Desulfovibrio aespocensis Asp- 2	3	5R1	5R1 gi 317151727 ref NC_014844.1 Complete Genome 460133 530699	460133	530699	70566	102	164722	54907	3629110	1.94%	4.54%	Myoviridae of Type1 (Cluster 9)
			5R2	5R2 gi 317151727 ref NC_014844.1 Complete Genome 1788329 18464 11	1788329	1846411	58082	55				1.60%		Myoviridae
			5R3	5R3 gi 317151727 ref NC_014844.1 Complete Genome 2595084 26311 58	2595084	2631158	36074	52				0.99%		Myoviridae of Type1 (Cluster 8)
6	Desulfovibrio acrylicus DSM 10141	0									3401710			
7	Desulfovibrio magneticus RS-1	0									4844650			
8	Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774	1	8R1	8R1 gi 220903286 ref NC_011883.1 Complete Genome 271014 318358	271014	318358	47344	55	47344	47344	2873437	1.65%	1.65%	Myoviridae of Type1 (Cluster 9)
9	Desulfovibrio gigas DSM 1382	1	9R1	9R1 gi 545640361 ref NC_022444.1 Complete Genome 992550 104693 7	992550	1046937	54387	69	54387	54387	3792120	1.43%	1.43%	Siphoviridae of Type1 (Cluster 8)
10	Desulfovibrio piger ATCC 29098	1	10R1	10R1 gi 209947761 gb A BXU01000026.1 1.0_Co nt4.1 16558 54731	16558	54731	38173	51	38173	38173	2867220	1.33%	1.33%	Myoviridae of Type1 (Cluster 6)

11	Desulfovibrio cf. magneticus IFRC170	0									4844650			
12	Desulfovibrio oxycloinae DSM 11498	0									3324580			
13	Desulfovibrio cuneatus DSM 11391	1	13R1	13R1 gi 523621182 gb AUCY01000006.1 G497DRAFT_scaffold00003.3_C2 20537 76517	20537	76517	55980	50	55980	55980	3359130	1.67%	1.67%	Myoviridae
14	Desulfovibrio vulgaris str. Miyazaki	2	14R1	14R1 gi 218885109 ref NC_011769.1 Complete Genome 862570 922592	862570	922592	60022	60	121853	60927	3753760	1.60%	3.25%	Myoviridae of Type1 (Cluster 8)
			14R2	14R2 gi 218885109 ref NC_011769.1 Complete Genome 2016944 2078775	2016944	2078775	61831	69				1.65%		Siphoviridae of Type1 (Cluster 3)
15	Desulfobulbus elongatus DSM 2908	1	15R1	15R1 gi 607834641 gb JHZB01000015.1 Q362DRAFT_scaffold00014.14_C 78 51849	78	51849	51771	78	51771	51771	3961950	1.31%	1.31%	Myoviridae of Type1 (Cluster 6)
16	Desulfocurvus vexinensis DSM 17965	1	16R1	16R1 gi 573088796 gb JAEX01000002.1 WGS:JAEX01:G495DRAFT_scaffold00002.2_C 111939 257727	111939	257727	145788	142	145788	145788	3627180	4.02%	4.02%	Myoviridae of Type1 (Cluster 8)
17	Desulfovibrio alkalitolerans	1	17R1	17R1 gi 523463601 gb ATHI01000003.1 ctg12 31783 65856	31783	65856	34073	44	34073	34073	3202330	1.06%	1.06%	Myoviridae of Type1 (Cluster 8)
18	Desulfovibrio fructosivorans JJ	3	18R1	18R1 gi 302493090 gb AECZ01000001.1 ctg00049 320 75894	320	75894	75574	83	218120	72707	4673590	1.62%	4.67%	Siphoviridae of Type1 (No Cluster Assigned)
			18R2	18R2 gi 302493090 gb AECZ01000001.1 ctg00049 146136 239339	146136	239339	93203	95				1.99%		Siphoviridae of Type1 (Cluster 8)
			18R3	18R3 gi 302492071 gb AECZ01000006.1 ctg00055 46365 95708	46365	95708	49343	61				1.06%		Myoviridae of Type1 (Cluster 8)
19	Desulfonatronovibrio hydrogenovorans DSM 9292	1	19R1	19R1 gi 631913846 gb JMKT01000009.1 P771DRAFT_scaffold00002.2_C 55099 82699	55099	82699	27600	70	27600	27600	2939700	0.94%	0.94%	Myoviridae of Type1 (Cluster 8)

20	Desulfobulbaceae bacterium BRH_c16a	0									6515850			
21	Desulfobulbus propionicus type strain 1pr3	2	21R1	[21R1 gi 320352146 ref NC_014972.1 Complete Genome 179310 259153	179310	259153	79843	93	166855	83428	3851870	2.07%	4.33%	Siphoviridae of Type1 (Cluster 6)
			21R2	[21R2 gi 320352146 ref NC_014972.1 Complete Genome 2768665 2855677	2768665	2855677	87012	96				2.26%		Siphoviridae of Type1 (Cluster 8)
22	Desulfovibrio salexigens	1	22R1	[22R1 gi 242277482 ref NC_012881.1 Complete Genome 2324343 2361506	2324343	2361506	37163	51	37163	37163	4289850	0.87%	0.87%	Myoviridae of Type1 (Cluster 6)
23	Desulfovibrio frigidus DSM 17176	0									4185040			
24	Desulfovibrio hydrothermalis DSM 14728	0									3683790			
25	Desulfotomaculum hydrothermale Lam5	2	25R1	[25R1 gi 411455801 emb CAOS01000001.1 contig ABX_2590_1 30068 75464	30068	75464	45396	53	105398	52699	2695030	1.68%	3.91%	Siphoviridae of Type1 (Cluster 2)
			25R2	[25R2 gi 411454438 emb CAOS01000009.1 contig ABX_2590_1 77813 137815	77813	137815	60002	87				2.23%		Siphoviridae of Type1 (Cluster 2)
26	Desulfotomaculum ruminis DSM 2154	2	26R1	[26R1 gi 334089967 gb C_P002780.1 Complete Genome 1102652 1163694	1102652	1163694	61042	66	145572	72786	3969010	1.54%	3.67%	Podoviridae
			26R2	[26R2 gi 334089967 gb C_P002780.1 Complete Genome 3519929 3604459	3519929	3604459	84530	88				2.13%		Myoviridae of Type1 (Cluster 2)
27	Desulfotomaculum reducens MI-1	3	27R1	[27R1 gi 134050581 gb C_P000612.1 Complete Genome 532811 592446	532811	592446	59635	64	175852	58617	3608100	1.65%	4.87%	unclassified
			27R2	[27R2 gi 134050581 gb C_P000612.1 Complete	1258679	1310519	51840	69				1.44%		Myoviridae of Type1 (Cluster 6)

				Genome 1258679 1310519										
			27R3	[27R3 gi 134050581 gb C P000612.1 Complete Genome 2816410 2880787	2816410	2880787	64377	79				1.78%		Siphoviridae of Type1 (Cluster 2)
28	Desulfovibrio sp. X2	1	28R1	[28R1 gi 523471277 gb A THV01000018.1 ctg26 48753 80775	48753	80775	32022	49	32022	32022	3966570	0.81%	0.81%	Myoviridae of Type1 (Cluster 9)
29	Desulfovibrio sp. A2	1	29R1	[29R1 gi 347519856 gb A GFG01000018.1 contig.17 24810	2	24810	24808	26	24808	24808	3966570	0.63%	0.63%	Myoviridae
30	Desulfosporosinus acidiphilus SJ4	1	30R1	[30R1 gi 391353422 gb C P003639.1 1337287 1506880	1337287	1506880	169593	207	169593	169593	4991180	3.40%	3.40%	Myoviridae of Type1 (Cluster 6)
31	Desulfovibrio aminophilus DSM 12254	0									3419060			
32	Desulfobacter curvatus DSM 3379	0									5644280			
33	Desulfobacter vibrioformis DSM 8776	1	33R1	[33R1 gi 675284508 gb J QKJ01000011.1 Q366D RAFT_scaffold00010.10 C 137688 162790	137688	162790	25102	35	25102	25102	4466780	0.56%	0.56%	Siphoviridae of Type1 (Cluster 8)
34	Desulfobacterium anilini DSM 4660	1	34R1	[34R1 gi 523385977 gb A ULM01000002.1 H567D RAFT_scaffold00002.2_ C 335738 382795	335738	382795	47057	49	47057	47057	4667340	1.01%	1.01%	Siphoviridae of Type1 (Cluster 8)
35	Desulfovermiculus halophilus DSM 18834	1	35R1	[35R1 gi 607833964 gb J AK01000030.1 N902DR AFT_scaffold00028.28_ C 221 26613	221	26613	26392	32	26392	26392	3242090	0.81%	0.81%	unclassified
36	Desulfovibrio piezophilus C1TLV30	0									3646100			
37	Desulfomicrobium baculatum DSM 4028	1	37R1	[37R1 gi 256827818 ref NC_013173.1 Complete Genome 1362708 1399475	1362708	1399475	36767	42	36767	36767	3942660	0.93%	0.93%	unclassified

38	Desulfohalobium retbaense	1	38R1	[38R1 gi 258404138 ref NC_013223.1 Complete Genome 1646202 1701330	1646202	1701330	55128	61	55128	55128	2909570	1.89%	1.89%	unclassified
39	Desulfatibacillum alkenivorans AK-01	1	39R1	[39R1 gi 218777860 ref NC_011768.1 Complete Genome 4517116 4553239	4517116	4553239	36123	30	36123	36123	6517070	0.55%	0.55%	unclassified
40	Desulfobacterium autotrophicum HRM2	0									5657780			
41	Desulfobacula sp. TS	0									2803910			
42	Desulfobacula toluolica Tol2	0									5197910			
43	Desulfotalea psychrophila LSv54	2	43R1	[43R1 gi 51243852 ref NC_006138.1 Complete Genome 1742755 1794946	1742755	1794946	52191	55	81001	40501	3659630	1.43%	2.21%	Siphoviridae
			43R2	[43R2 gi 51243852 ref NC_006138.1 Complete Genome 2277660 2306470	2277660	2306470	28810	33				0.79%		Podoviridae of Type3
44	Desulfovibrio alaskensis G20	3	44R1	[44R1 gi 78355047 ref NC_007519.1 Complete Genome 940169 1004171	940169	1004171	64002	65	224308	74769	3642100	1.76%	6.16%	Myoviridae
			44R2	[44R2 gi 78355047 ref NC_007519.1 Complete Genome 2753210 2863858	2753210	2863858	110648	98				3.04%		unclassified
			44R3	[44R3 gi 78355047 ref NC_007519.1 Complete Genome 3322987 3372645	3322987	3372645	49658	65				1.36%		Myoviridae of Type1 (Cluster 8)
45	Desulforegula conservatrix Mb1Pa	0									4469040			
46	Desulfovibrio sp. FW1012B	1	46R1	[46R1 gi 357632130 ref NZ_CM001368.1 Complete Genome 3969968 4041255	3969968	4041255	71287	107	71287	71287	3966570	1.80%	1.80%	Siphoviridae of Type1 (Cluster 3)

				Genome 3969968 4041255										
47	Desulfovibrio bastinii DSM 16055	1	47R1	47R1 gi 523620924 gb AUCX01000031.1 G496DRAFT_scaffold00028.28C 734 21301	734	21301	20567	30	20567	20567	3909170	0.53%	0.53%	Myoviridae
48	Desulfonatronospira thiodismutans	0									4107390			
49	Desulfovibrio alcoholivorans DSM 5433	1	49R1	49R1 gi 651606221 gb JNJA01000003.1 Q368DRAFT_scaffold00003.3_C 13924 135240	13924	135240	121316	125	121316	121316	5128910	2.37%	2.37%	Siphoviridae of Type1 (Cluster 5)
50	Desulfovibrio desulfuricans 642	0									3132560			
51	Desulfobacter postgatei 2ac9	1	51R1	51R1 gi 387144466 gb AGJR02000005.1 Desposcaffold_1_Cont5 217845 258576	217845	258576	40731	36	40731	40731	3974660	1.02%	1.02%	unclassified
52	Desulfotignum phosphitoxidans DSM 13687	1	52R2	52R1 gi 474489389 gb APJX01000002.1 Dpo_2c 129284 145082	129284	145082	15798	18	15798	15798	4998760	0.32%	0.32%	unclassified
53	Desulfotignum balticum DSM 7044	2	53R1	53R1 gi 522811039 gb ATWO01000001.1 K365DRAFT_scaffold00001.1_C 1713792 1767040	1713792	1767040	53248	55	108373	54187	5118760	1.04%	2.12%	unclassified
			53R2	53R2 gi 522811039 gb ATWO01000001.1 K365DRAFT_scaffold00001.1_C 3158452 3213577	3158452	3213577	55125	68				1.08%		unclassified
54	Desulfatirhabdium butyrivorans DSM 18734	1	54R1	54R1 gi 523620761 gb AUCU01000021.1 G492DRAFT_scaffold00016.16_C 22017 60400	22017	60400	38383	39	38383	38383	4481980	0.86%	0.86%	unclassified
55	Desulfobulbus japonicus DSM 18378	0									5800570			
56	Desulfovibrio zosterae DSM 11974	0									4092650			

57	Desulfovibrio putealis DSM 16056	1	57R1	[57R1 gi 523618705 gb AUBQ01000004.1 G453DRAFT_scaffold00003.3_C 295731 319243	295731	319243	23512	33	23512	23512	4705740	0.50%	0.50%	Myoviridae of Type1 (Cluster 8)
58	Desulfospira joergensenii DSM 10085	0									6119470			
59	Desulfatitalea sp. BRH_c12	1	59R1	[59R1 gi 780825309 gb LADR01000084.1 BRHa_1003299 256 13379	256	13379	13123	9	13123	13123	5997610	0.22%	0.22%	unclassified
60	Desulfovibrio inopinatus DSM 10711	2	60R1	[60R1 gi 523618871 gb AUBP01000017.1 G451DRAFT_scaffold00012.12_C 67194 100067	67194	100067	32873	33	70945	35473	5767550	0.57%	1.23%	Podoviridae of Type3
			60R2	[60R2 gi 523618858 gb AUBP01000024.1 G451DRAFT_scaffold00017.17_C 80515 118587	80515	118587	38072	49				0.66%		Podoviridae of Type3
61	Desulfobacca acetoxidans DSM 11109	2	61R1	[61R1 gi 328951746 ref NC_015388.1 Complete Genome 629290 671508	629290	671508	42218	58	75188	37594	3282540	1.29%	2.29%	unclassified
			61R2	[61R2 gi 328951746 ref NC_015388.1 Complete Genome 1673469 1706439	1673469	1706439	32970	33				1.00%		Siphoviridae of Type1 (Cluster 8)
62	Desulfobulbus mediterraneus DSM 13871	0									4796810			
63	Desulfomicrobium escambiense DSM 10707	0									3782110			
64	Desulfonatronum lacustre DSM 10312	0									3761450			
65	Desulfosarcina sp. BuS5	0									3600570			
66	Desulfovibrio longus DSM 6739	0									3701830			
67	Desulfurella acetivorans DSM 5264	1	67R1	[67R1 gi 754092674 ref NZ_CP007051.1 Complete	1671975	1693619	21644	24	21644	21644	1819990	1.19%	1.19%	unclassified

				Genome 1671975 1693619										
68	Desulfonauticus sp. A7A	0									2014890			
69	Desulfonatronovibrio magnus	0									4809660			
70	Desulfonatronum thioautotrophicum ASO4-1	0									4634600			
71	Desulfonatronum thiodismutans	0									3923650			
72	Desulfovibrio desulfuricans ND132	1	72R1	72R1 gi 376294792 ref NC_016803.1 Complete Genome 1652158 1703138	1652158	1703138	50980	42	50980	50980	3858580	1.32%	1.32%	unclassified
73	Desulfococcus multivorans DSM 2059	0									4403010			
74	Desulfococcus oleovorans Hxd3	1	74R1	74R1 gi 158520017 ref NC_009943.1 Complete Genome 3444657 3521470	3444657	3521470	76813	75	76813	76813	3944170	1.95%	1.95%	unclassified
75	Desulfobulbus sp. Dsb1 (Tol1)	0									4211780			
76	Desulfocapsa sulfexigens DSM 10523	0									4023510			
77	Desulfurivibrio alkaliphilus AHT 2	1	77R1	77R1 gi 297567992 ref NC_014216.1 Complete Genome 2336043 2409612	2336043	2409612	73569	71	73569	73569	3097760	2.37%	2.37%	unclassified
78	Thermodesulfatator indicus DSM 15286	0									2322220			
79	Desulfotomaculum acetoxidans DSM 771	4	79R1	79R1 gi 257777071 gb CP001720.1 Complete Genome 1925642 1989115	1925642	1989115	63473	59	251019	62755	4545620	1.40%	5.52%	unclassified
			79R2	79R2 gi 257777071 gb CP001720.1 Complete	3847376	3910858	63482	91				1.40%		unclassified

				Genome 3847376 3910858										
			79R3	[79R3 gi 257777071 gb C P001720.1 Complete Genome 4060951 4122610	4060951	4122610	61659	65				1.36%		unclassified
			79R4	[79R4 gi 257777071 gb C P001720.1 Complete Genome 4396496 4458901	4396496	4458901	62405	64				1.37%		Myoviridae of Type1 (No Cluster Assigned)
80	Thermodesulfobacterium commune DSM 2178	1	80R1	[80R1 gi 668351138 gb C P008796.1 Complete Genome 1308664 1372825	1308664	1372825	64161	73	64161	64161	1559460	4.11%	4.11%	Myoviridae of Type1 (Cluster 9)
81	Thermodesulfobacterium geofontis OPF15	0									1634380			
82	Desulfocurvibacter africanus PCS	0									3929487			
83	Syntrophobacter fumaroxidans MPOB	1	83R1	[83R1 gi 116696516 gb C P000478.1 Complete Genome 2290794 2350190	2290794	2350190	59396	55	59396	59396	4990250	1.19%	1.19%	Siphoviridae of Type1 (Cluster 8)
84	Desulfarculus baarsii DSM 2075	1	84R1	[84R1 gi 301638057 gb C P002085.1 Complete Genome 2838573 2921972	2838573	2921972	83399	81	83399	83399	3655730	2.28%	2.28%	unclassified
85	Archaeoglobus sulfatocaldus PM70-1	0									2076930			
86	Archaeoglobus profundus DSM 5631	0									1563420			
87	Archaeoglobus fulgidus DSM 4304	0									2107990			
88	Thermodesulfovibrio yellowstonii DSM 11347	0									2003800			
89	Candidatus Desulforudis audaxviator MP104C	1	89R1	[89R1 gi 169637063 gb C P000860.1 Complete Genome 773247 849934	773247	849934	76687	74	76687	76687	2349480	3.26%	3.26%	unclassified

90	Desulfovibrio vulgaris DP4	3	90R1	[90R1 gi CP000527.1 gb NC_008751.1 Complete Genome 1273249 1354897	1273249	1354897	81648	93	250140	83380	3462887	2.36%	7.22%	Siphoviridae of Type1 (Cluster 6)
			90R2	[90R2 gi CP000527.1 gb NC_008751.1 Complete Genome 1731933 1828120	1731933	1828120	96187	114				2.78%		Myoviridae of Type1 (Cluster 9)
			90R3	[90R3 gi CP000527.1 gb NC_008751.1 Complete Genome 3196647 3268952	3196647	3268952	72305	65				2.09%		Myoviridae of Type1 (Cluster 9)
91	Desulfatibacillum alkenivorans DSM 16219	0									6464641			

Table S2. List of prophages predicted by Phaster and PhiSpy. Columns indicate the following; total number of predicted prophages per host, prophage ID, prophage sequence ID, the start and end of the prophage in the genome, the length of the prophage (bp), the number of ORF, total prophage length (bp), average of the length, genome size of the host, prophage density, total prophage density, and taxonomic classification according to Virfam. Prophage density represents the portion of the host genome that contain each prophage ($\text{bp prophage} * \text{bp}^{-1}\text{host} * 100$).

N	Strain	Range pH	Range T (°C)	Classification	Gram	Motility	Morphology	Type of habitat	Type of growth under optimum conditions	Oxidation	Size (µm ²)	Cell Volume (µm ³)	Volume category	Surface cell area (µm ²)	Reference
1	<i>Desulfovibrio vulgaris</i> str. Hildenborough	7	25 - 40	Mesophile	Neg.	Y	Rod	soil/sediments	fast-growing	I	0.8-1.2*2.2-3	2.042	middle-size	9.739	[1,2]
2	<i>Desulfocurvibacter africanus</i> DSM 2603	6.6 to 7.65	20 to 40	Mesophile	Neg.	Y	vibrio-shaped	freshwater sediments	fast-growing	I	0.5*5-10	1.472	middle-size	12.173	[3]
3	<i>Desulfovibrio desulfuricans</i> subsp. aestuarii ATCC 29578	6.5 to 8.5	10 to 40	Mesophile	Neg.	Y	vibrio-shaped	soil/sediments	fast-growing	I	0.5-0.8*1.5-4	0.885	small	6.172	[4,5]
4	<i>Desulfocurvibacter africanus</i> subsp. africanus str. Walvis Bay	7	28 to 40	Mesophile	Neg.	Y	sigmoid rods	freshwater/brackish	fast-growing ¹	I	0.5*5-10	1.475	middle-size	12.173	[3]
5	<i>Desulfovibrio aespoeensis</i>	nd	4 to 35	Mesophile	Neg.	Y	Vibrioid-shaped cells	freshwater sediments	fast-growing	I	0.5*1.7-2.5	0.412	small	3.691	[6,7]
6	<i>Desulfovibrio acrylicus</i> DSM 10141	nd	nd	Mesophile	Neg.	Y	Small rods to vibrios	marine sediments	fast-growing	I	0.8*2-4	1.508	middle-size	3.691	[8]
7	<i>Desulfovibrio magneticus</i> RS-1	nd	nd	Mesophile	Neg.	Y	Vibrio-shaped	freshwater sediments	fast-growing	I	1*3-5	3.142	big	14.137	[9]
8	<i>Desulfovibrio desulfuricans</i> subsp. desulfuricans str. ATCC 27774	nd	28 to 44	Mesophile	Neg.	N	Vibrios	animal or plant-associated	fast-growing	I	1*0,25	0.0491	small	0.883	[10-13]
9	<i>Desulfovibrio gigas</i> DSM 1382	nd	nd	Mesophile	Neg.	Y	Large curved rods	freshwater sediments	fast-growing	I	1*5-6	4.320	big	18.849	[14,15]
10	<i>Desulfovibrio piger</i> ATCC 29098	nd	nd	Mesophile	Neg.	N	rods	animal or plant-associated	fast-growing	I	0.8-1.0*2.5-10	3.976	big	18.943	[16,17]

1 1	<i>Desulfovibrio cf. magneticus</i> IFRC170	nd	nd	Mesophile	Neg.	Y	Vibrio-shaped	freshwater sediments	nd	nd	nd	nd	nd	nd	[9]
1 2	<i>Desulfovibrio oxycliniae</i> DSM 11498	7 to 7.5	nd	Mesophile	Neg.	Y	Straight or curved rods	marine sediments	slow-growing	I	0.5*2-3	0.491	small	4.3196	[18]
1 3	<i>Desulfovibrio cuneatus</i> DSM 11391	7.2 to 7.4	0 to 33	Mesophile	Neg.	Y	Slightly curved rods	marine sediments	slow-growing	I	0.4-0.6*1.6-2.7	0.422	small	3.770	[19]
1 4	<i>Desulfovibrio vulgaris</i> str. Miyazaki F	nd	nd	Mesophile	Neg.	Y	vibrios	freshwater sediments	fast-growing	I	0.8-1.2*2.2-3 ²	2.042	middle-size	9.739	[20,21]
1 5	<i>Desulfobulbus elongatus</i> DSM 2908	6.0 to 7.8	20 to 40	Mesophile	Neg.	Y	Straight to slightly curved rod with pointed ends	impacted or engineered system	fast-growing	I	0.5-0.7*1.5-2.5	0.565	small	4.335	[22]
1 6	<i>Desulfocurvus vexinensis</i> DSM 17965	5.0 to 9.0	20 to 50	Mesophile	Neg.	Y	rods or vibrios	freshwater sediments	fast-growing	I	0.5*3-5	0.785	small	6.676	[23]
1 7	<i>Desulfovibrio alkalitolerans</i>	6.9 to 9.9	16 to 47	Mesophile	Neg.	Y	vibrio-shaped	impacted or engineered system	fast-growing	I	0.5–0.86*1.4–1.9	0.599	small	4.251	[24]
1 8	<i>Desulfovibrio fructosivorans</i> JJ	6.5 - 7	nd	Mesophile	Neg.	Y	curved rods	brackish sediments	fast-growing	I	0.5-0.7*2-4	0.848	small	6.220	[25]
1 9	<i>Desulfonatronovibrio hydrogenovorans</i> DSM 9292	7.0 to 10.2	15 to 43	Mesophile	Neg.	Y	vibrio	brackish sediments	slow-growing	C	0.5*1.5-2	0.344	small	3.141	[26]
2 0	<i>Desulfobulbaceae bacterium</i> BRH_c16a	nd	nd	Mesophile	nd	nd	nd	freshwater sediments	nd	nd	nd	nd	nd	nd	[27]
2 1	<i>Desulfobulbus propionicus</i> type strain (1pr3)	6.0 to 8.6	10 to 43	Mesophile	Neg.	N	Ellipsoidal to lemon-shaped	freshwater/brackish	fast-growing	I	1-1.3*1.8-2	1.973	middle-size	8.941	[28,29]
2 2	<i>Desulfovibrio salexigens</i>	nd	nd	Mesophile	Neg.	Y	Vibrio	marine sediments	nd	I	0.7-2*1-2	2.115	middle-size	9.135	[30,31]
2 3	<i>Desulfovibrio frigidus</i> DSM 17176	6.9 to 7.5	22 to 25	Mesophile	Neg.	Y	rod-shaped or vibrioid	marine sediments	nd	I	2.5-5*0.7	1.443	middle-size	9.016	[32]

24	<i>Desulfovibrio hydrothermalis</i> DSM 14728	6.7 to 8.2	20 to 40	Mesophile	Neg.	Y	vibrio-shaped or sigmoid	marine sediments	fast-growing	I	0.5-1*1-2	0.663	small	4.418	[33]
25	<i>Desulfotomaculum hydrothermale</i> Lam5	5.8 to 8.2	40 to 60	Thermophiles	Pos.	Y	slightly curved rods	freshwater sediments	nd	I	1*3-6	3.534	big	15.707	[34]
26	<i>Desulfotomaculum ruminis</i> DSM 2154	6 to 8.5	30 to 48	Mesophile	Neg.	Y	Rods	animal or plant-associated	fast-growing	I	0.5*3-6	0.883	small	7.461	[35]
27	<i>Desulfotomaculum reducens</i> MI-1	7.0 to 7.2	37	Mesophile	Pos.	Y	slightly curved rods	marine sediments	slow-growing	I	0.8-1*5-10	4.771	big	22.477	[36-38]
28	<i>Desulfovibrio</i> sp. X2	nd	nd	Mesophile	Neg.	nd	nd	freshwater sediments	nd	nd	nd	nd	nd	nd	[39]
29	<i>Desulfovibrio</i> sp. A2	7.2 to 7.4	nd	Mesophile	Neg.	nd	rods	freshwater sediments	fast-growing	nd	0.5-1.5 * 0.4-0.8	0.283	small	2.450	[40,41]
30	<i>Desulfosporosinus acidiphilus</i> SJ4	3.6 to 5.5	25 to 40	Mesophile	Neg.	N	curved rods	impacted or engineered system	fast-growing	I	4-7*0.8-1	3.499	big	16.823	[42]
31	<i>Desulfovibrio aminophilus</i> DSM 12254	6.7 to 8.0	25 to 40	Mesophile	Neg.	Y	Vibrios	impacted or engineered system	nd	I	0.2*3-4	0.110	small	2.262	[43]
32	<i>Desulfobacter curvatus</i> DSM 3379	6.8 to 7.2	28-31	Mesophile	Neg.	Y	vibrio-shaped coils	marine sediments	slow-growing	C	0.5-1*1.7-3.5	1.149	middle-size	7.009	[44]
33	<i>Desulfobacter vibrioformis</i> DSM 8776	6.8 to 7.0	5 to 38	Mesophile	Neg.	Y	Vibrio-shaped	impacted or engineered system	slow-growing	C	1.9-2.3*4.5-8	21.647	big	48.159	[45]
34	<i>Desulfobacterium anilini</i> DSM 4660	nd	nd	Mesophile	Neg.	N	rod-shaped	marine sediments	slow-growing	C	1.25*1.5-3	2.761	big	11.290	[46]
35	<i>Desulfovermiculus halophilus</i> DSM 18834	6.4 to 8.2	25 to 47	Mesophile	Neg.	Y	vibrios or spirilla	impacted or engineered system	slow-growing	I	0.5-0.6*1-15	1.901	middle-size	14.298	[47]
36	<i>Desulfovibrio piezophilus</i> C1TLV30	5.4 to 8.6	15 to 45	Mesophile	Neg.	Y	nonspore-forming vibrios	marine sediments	fast-growing	I	2-4*0.5	0.589	small	5.105	[48]

37	<i>Desulfomicrobium baculatum</i> DSM 4028	nd	2 to 41	Mesophile	Neg.	Y	rods	marine sediments	nd	I	1.4-2.9*0.7-0.9	1.081	middle-size	6.409	[49]
38	<i>Desulfohalobium retbaense</i>	5.5 to 8.0	nd	Mesophile	Neg.	Y	Straight to slightly curved rods	marine sediments	fast-growing	I	1-3*0.7-0.9	1.005	middle-size	6.032	[50]
39	<i>Desulfatibacillum aliphaticivorans</i> DSM 15576	6.6 to 7.8	15 to 40	Mesophile	Neg.	N	slightly curved rods	marine sediments	slow-growing	C	0.6*2.2-5.5	1.088	middle-size	7.822	[51]
40	<i>Desulfobacterium autotrophicum</i> HRM2	nd	nd	Mesophile	Neg.	Y	Oval	marine sediments	fast-growing	C	1.2-2.5*1	0.968	small	5.0367	[52]
41	<i>Desulfobacula</i> sp. TS	nd	nd	Mesophile	Neg.	nd	nd	impacted or engineered system	nd	nd	nd	nd	nd	nd	[53,54]
42	<i>Desulfobacula toluolica</i> Tol2	7 to 7.1	nd	Mesophile	Neg.	Y	coccoid	impacted or engineered system	slow-growing	C	nd	nd	nd	nd	[55]
43	<i>Desulfotalea psychrophila</i> LSv54	nd	1,8 to 19	Psychrotrophs	Neg.	Y	Rods	marine sediments	slow-growing	I	0.6*4.5-7.4	1.682	middle-size	11.781	[56]
44	<i>Desulfovibrio alaskensis</i> G20 ³	6.5 to 8.5	10 to 45	Mesophile	Neg.	Y	vibrio-shaped cells	impacted or engineered system	fast-growing	I	1-5*0.5-1.2	1.702	middle-size	9.146	[57]
45	<i>Desulforegula conservatrix</i> Mb1Pa	nd	25 - 30	Mesophile	Neg.	Y	rod-shaped	freshwater sediments	nd	I	1-1.3*2.6-3	2.908	big	12.193	[58]
46	<i>Desulfovibrio</i> sp. FW1012B	nd	nd	Mesophile	Neg.	Y	nd	impacted or engineered system	nd	nd	nd	nd	nd	nd	[59]
47	<i>Desulfovibrio bastinii</i> DSM 16055	5.2 to 7.4	20 to 50	Mesophile	Neg.	Y	vibrioid	impacted or engineered system	slow-growing	I	0.5*2-3	0.491	small	4.3196	[60]
48	<i>Desulfonatronospira thiodismutans</i>	8.3 to 10.5	28 to 43	Mesophile	Neg.	Y	vibrio-shaped	brackish sediments	slow-growing	I	0.6-0.8*2-3	0.962	small	6.267	[61]
49	<i>Desulfovibrio alcoholivorans</i> DSM 5433	5.5 to 8.5	20 to 42	Mesophile	Neg.	Y	curved rods	impacted or engineered system	nd	I	0.7-0.9*2.8-3.2	1.508	middle-size	8.545	[62]

50	<i>Desulfovibrio desulfuricans</i> 642 ⁴	nd	nd	Mesophile	Neg.	Y	Vibrios	impacted or engineered system	nd	I	1*0.25	0.049	small	0.883	[10-12,63]
51	<i>Desulfobacter postgatei</i> 2ac9	6.2 to 8.5	10 to 37	Mesophile	Neg.	Y	Rod-shaped to ellipsoidal	marine sediments	slow-growing	C	1-1.5*1.7-2.5	2.577	big	10.701	[45,64]
52	<i>Desulfotignum phosphitoxidans</i> DSM 13687	5.0 to 8.0	15 to 30	Mesophile	Neg.	N	Rod-shaped	marine sediments	slow-growing	I	0.6-0.8*2-4	1.154	middle-size	7.367	[65]
53	<i>Desulfotignum balticum</i> DSM 7044	6.5 to 8.2	10 to 32	Mesophile	Neg.	Y	short rods	marine sediments	slow-growing	C	0.5-0.7*1.5-3	0.636	small	4.806	[66,67]
54	<i>Desulfatirhabdium butyrativorans</i> DSM 18734	6.5 to 8.0	15 to 37	Mesophile	Neg.	nd	lens-shaped	impacted or engineered system	slow-growing	C	1-1.3*2.6-3.5	3.168	big	13.096	[68]
55	<i>Desulfobulbus japonicus</i> DSM 18378	6.1 to 7.5	15 to 35	Mesophile	Neg.	Y	rod-shaped	brackish/marine	fast-growing	C	0.8-1.6*1.4-2.9	2.431	middle-size	10.367	[69]
56	<i>Desulfovibrio zosterae</i> DSM 11974	nd	nd	Mesophile	Neg.	Y	Curved rods to sigmoid-shaped cells	animal or plant-associated	fast-growing	I	0.5*3	0.589	small	5.105	[70]
57	<i>Desulfovibrio putealis</i> DSM 16056	nd	nd	Mesophile	Neg.	Y	Vibrioid	freshwater sediments	fast-growing	I	2.3-4.1*0.7	1.231	middle-size	7.807	[71]
58	<i>Desulfospira joergensenii</i> DSM 10085	nd	nd	Mesophile	Neg.	N	curved	marine sediments	nd	C	0.7-0.8*1-2	0.663	small	4.418	[72]
59	<i>Desulfatitalea</i> sp. BRH_c12	nd	nd	Mesophile	nd	nd	nd	freshwater sediments	nd	nd	nd	nd	nd	nd	[27]
60	<i>Desulfovibrio inopinatus</i> DSM 10711	5.0 to 8.0	15 to 42	Mesophile	Neg.	Y	Vibrioid	marine sediments	slow-growing	I	1-1.5*4-12	9.817	big	33.869	[73]
61	<i>Desulfobacca acetoxidans</i> DSM 11109	6.5 to 8.3	27 to 47	Mesophile	Neg.	N	oval to rod-shaped	impacted or engineered system	slow-growing	C	1.3*1.9-2.2	2.721	big	11.027	[74]
62	<i>Desulfobulbus mediterraneus</i> DSM 13871	6.3 to 8.0	10 to 35	Mesophile	Neg.	Y	Ovoid	marine sediments	slow-growing	I	1.2-1.7*1.4-3.2	2.496	middle-size	9.211	[75]

63	<i>Desulfomicrobium escambiense</i> DSM 10707	nd	nd	Mesophile	Neg.	Y	short rod	freshwater sediments	fast-growing	I	1.7-2.2*0.5	0.382	small	3.456	[76]
64	<i>Desulfonatronum lacustre</i> DSM 10312	8.0 to 10.0	22 to 45	Mesophile	Neg.	Y	Vibrio	freshwater sediments	slow-growing	C	0.7-0.9*2.5-3	1.382	middle-size	7.916	[77,78]
65	<i>Desulfosarcina</i> sp. BuS5	6.0 to 7.4	10 to 33	Mesophile	Neg.	nd	Rod shape	marine sediments	slow-growing	nd	1-2*1-1.5	1.870	middle-size	8.431	[79]
66	<i>Desulfovibrio longus</i> DSM 6739	6.5 to 8.5	10 to 40	Mesophile	Neg.	Y	Long, thin, straight, rod-shaped	impacted or engineered system	fast-growing	I	0.4-0.5*5-10	1.192	middle-size	10.921	[80]
67	<i>Desulfurella acetivorans</i> DSM 5264	4.3 to 7.5	44 to 70	Thermophiles	Neg.	Y	short rods with oval ends	freshwater sediments	fast-growing	C	0.5-0.7*1-2	0.424	small	3.393	[81]
68	<i>Desulfonauticus</i> sp. A7A	6.2 to 8.6	40 to 64	Thermophiles	Neg.	Y	straight to slightly curved rods	impacted or engineered system	fast-growing	I	0.6*1.2-4	0.735	small	5.466	[82]
69	<i>Desulfonatronovibrio magnus</i>	8.5 to 10.5	max. 41	Mesophile	Neg.	Y	vibrio-shaped	brackish sediments	slow-growing	C	0.8-1*2-3	1.590	middle-size	8.341	[77]
70	<i>Desulfonatronum thioautotrophicum</i> ASO4-1	8.3 to 10.5	max. 40 – 41	Mesophile	Neg.	Y	vibrio-shaped	brackish sediments	slow-growing	I	0.5-0.6*2-4	0.687	small	5.547	[77]
71	<i>Desulfonatronum thiodismutans</i>	8.0 to 10.0	15 to 48	Mesophile	Neg.	Y	vibrio-shaped	brackish sediments	slow-growing	nd	0.6-0.7*1.2-2.7	0.647	small	4.645	[78]
72	<i>Desulfovibrio desulfuricans</i> ND132	6.8 to 8.2	30 to 37	Mesophile	Neg.	Y	vibrio-shaped	freshwater sediments	fast-growing	I	0.5-0.7*2-3	0.707	small	5.278	[83]
73	<i>Desulfococcus multivorans</i> DSM 2059			Mesophile	Neg.	Y	Coccus	marine sediments	slow-growing	C	1.3-2.5	3.590	big	11.341	[84]
74	<i>Desulfococcus oleovorans</i> Hxd3	nd	nd	Mesophile	Neg.	nd	Rod	impacted or engineered system	slow-growing	C	0.4-0.5*0.8-2	0.721	small	4.593	[85]
75	<i>Desulfobulbus</i> sp. Dsb1 (Tol1)	nd	nd	Mesophile	nd	nd	nd	animal or plant-associated	nd	nd	nd	nd	nd	nd	[86]

76	<i>Desulfocapsa sulfexigens</i> DSM 10523	6.0 to 8.2	4 to 35	Mesophile	Neg.	Y	elongated with slightly pointed ends	marine sediments	slow-growing	nd	0.5*2-4	0.589	small	5.105	[87]
77	<i>Desulfurivibrio alkaliphilus</i> AHT 2	8.5 to 10.5	nd	Mesophile	Neg.	N	rod-shaped	brackish sediments	slow-growing	nd	0.4*2.5	0.314	small	3.393	[88]
78	<i>Thermodesulfatator indicus</i> DSM 15286	6.0 to 6.7	55 to 80	Thermophiles	Neg.	Y	rods	marine sediments	fast-growing	nd	0.8-1*0.4-0.5	0.143	small	1.590	[89]
79	<i>Desulfotomaculum acetoxidans</i> DSM 771	6.6 to 7.6	20 to 40	Mesophile	Neg.	Y	Straight or slightly curved rods	brackish/marine / animal or plant-associated	fast-growing	C	1-1.5*3.5-9	7.670	big	26.997	[90]
80	<i>Thermodesulfobacterium commune</i> DSM 2178	6.0 to 8.0	45 to 85	Thermophiles	Neg.	N	Tiny rods	freshwater sediments	fast-growing	I	0.3*0.9	0.064	small	0.989	[91]
81	<i>Thermodesulfobacterium geofontis</i> OPF15	5.5 to 8.5	60 to 90	Thermophiles	Neg.	N	short, straight rods	freshwater sediments	fast-growing	nd	2*0.3	0.141	small	2.026	[92]
82	<i>Desulfocurvibacter africanus</i> PCS	5.5 to 8	25 to 45	Mesophile	Neg.	Y	curved rods	marine sediments	slow-growing	I	0.3*5-10	0.530	small	7.210	[93]
83	<i>Syntrophobacter fumaroxidans</i> MPOB	6.0 to 8.0	20 to 40	Mesophile	Neg.	N	rod- to eye-shaped	impacted or engineered system	slow-growing	I	1.1-1.6*1.8-2.5	3.077	big	11.981	[94]
84	<i>Desulfarculus baarsii</i> DSM 2075	6.5 to 8.2	20 to 39	Mesophile	Neg.	Y	vibrio-shaped	freshwater sediments	slow-growing	C	0.5-0.7*1.5-4	0.777	small	5.749	[95,96]
85	<i>Archaeoglobus sulfaticallidus</i> PM70-1	6.3 to 7.6	60 to 80	Thermophiles	nd	N	irregular lobes or triangles	marine sediments	nd	I	0.4*2.2	0.184	small	2.188	[97]
86	<i>Archaeoglobus profundus</i> DSM 5631	4.5 to 7.5	65 to 90	Thermophiles	Neg.	N	triangular-shaped	marine sediments	fast-growing	nd	1.3*0.75	0.574	small	3.946	[98]
87	<i>Archaeoglobus fulgidus</i> DSM 4304	5.5 to 7.5	60 to 95	Thermophiles	nd	Y	Regular to irregular coccoid	marine sediments	fast-growing	I	0.4-1	0.179	small	1.539	[99,100]
88	<i>Thermodesulfovibrio yellowstonii</i> DSM 11347	6.5 to 7.7	40 to 70	Thermophiles	Neg.	Y	Curved rods or vibrios	brackish sediments	slow-growing	I	0.3*1.5	0.106	small	1.555	[101]

89	<i>Candidatus Desulforudis audaxviator</i> MP104C	nd	nd	Mesophile	Pos.	Y	nd	impacted or engineered system	nd	nd	nd	nd	nd	nd	[102]
90	<i>Desulfovibrio vulgaris</i> DP4 ⁵	nd	nd	Mesophile	Neg.	Y	rods	soil/sediments	fast-growing	nd	0.8-1.5*2-4	3.116	big	12.915	[103]
91	<i>Desulfatibacillum alkenivorans</i> DSM 16219	6.2 to 8.0	22 to 38	Mesophile	Neg.	Y	slightly curved rods	impacted or engineered system	slow-growing	C	0.68*1.2-4.5	1.035	middle-size	6.814	[104]

¹Similar value as *Desulfocurvibacter africanus* DSM 2603. ²Size was assumed to be the same as *Desulfovibrio vulgaris* str. Hildenborough. ³Based on info from *Desulfovibrio alaskensis* DSM 16109. ⁴Some aspects were assumed to be same as *Desulfocurvibacter desulfuricans* ATCC 27774. ⁵Some physiological aspects were assumed to be the same as *Desulfovibrio vulgaris* str. Miyazaki F.

Table S3: Ecophysiological traits of SRP. The columns show the different SRP in this study, pH range, temperature range, classification with respect to temperature, cell wall type (gram), motility (denoted with Y for those for which the flagellum has been observed and N for which it has not been observed), habitat type, growth type under optimal conditions, oxidation (complete or incomplete), size (μm²), cell volume (μm³) and cell surface area.

N o	Strain	n	CRISPR Sequence ID	CRISPR Id	CRISPR Start	CRISPR End	Consensus Repeat	Repeat Length	Spacers	Evidence Level	Total CRISPR Size
7	Desulfovibrio magneticus RS-1	2	gi 239904639 ref NC_012796.1	NC_012796_1	1589785	1591828	gtcgccccctgcgcggggcgctg gattgaaac	32	30	4	3272
			gi 239904639 ref NC_012796.1	NC_012796_3	4725356	4726585	tttctgagctgcctatgcggcagtg aac	29	20	4	
8	Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774	1	gi 220903286 ref NC_011883.1	NC_011883_1	1083779	1085579	gtgttccccacggcggtgggatg aaccg	29	29	4	1800
9	Desulfovibrio gigas DSM 1382	1	gi 545640361 ref NC_022444.1	NC_022444_7	2555284	2555600	cacccgactattgaatcgggcctc attgaag	32	4	3	316
10	Desulfovibrio piger ATCC 29098	2	gi 209947786 gb ABXU01000001.1	ABXU01000001_1	28213	29888	cggttcatccccacgcgtgtgggg aatac	29	27	4	2375
			gi 209947778 gb ABXU01000009.1	ABXU01000009_1	17863	18563	gtattccccacgcacgtgggatg aaccg	29	11	4	
11	Desulfovibrio cf. magneticus IFRC170	2	gi 573972682 gb JAGC01000009.1	JAGC01000009_1	628799	633388	gtcgccccctgcgcggggcgctg gattgaagc	32	69	4	6203
			gi 573972682 gb JAGC01000009.1	JAGC01000009_5	1931181	1932795	gtgttccccgtagcgcgggatg aaccg	29	26	4	
12	Desulfovibrio oxycloinae DSM 11498	2	gi 481039505 gb AQXE01000003.1	AQXE01000003_1	8	878	gttcactgccgcgtaggcagctca gaaa	28	14	4	1496
			gi 481039489 gb AQXE01000010.1	AQXE01000010_1	166675	167301	tttctgagctgcctacgcggcagtg aac	28	10	4	
14	Desulfovibrio vulgaris str. Miyazaki F	1	gi 218885109 ref NC_011769.1	NC_011769_4	2444693	2448088	gtcgccccctcacgcggggcgctg gatagaaac	32	51	4	3395
15	Desulfobulbus elongatus DSM 2908	1	gi 607834666 gb JHZB01000008.1	JHZB01000008_1	130150	130441	gtcgccccctcacggggcggtgga ttgaaac	31	4	3	291
16	Desulfocurvus vexinensis DSM 17965	2	gi 573088800 gb JAEX01000001.1	JAEX01000001_3	26779	27260	gccccggcgccccggccaagg gc	24	8	2	752
			gi 573088793 gb JAEX01000003.1	JAEX01000003_1	211016	211287	cccgcgtgctgcgcgccggag ataagg	29	4	2	
17	Desulfovibrio alkalitolerans	4	gi 523462140 gb ATHI01000015.1	ATHI01000015_1	52	3897	gtttcaatccacgccccgtcgg ggggcgac	32	58	4	9023
			gi 523462085 gb ATHI01000018.1	ATHI01000018_1	51	1870	gtcgcccccgacggggcgctg gattgaaac	32	27	4	

			gi 523462062 gb ATHI01000019.1	ATHI01000019_1	52	1862	gtcgcccccgacggggcggtg gattgaaac	32	27	4	
			gi 523461280 gb ATHI01000024.1	ATHI01000024_1	12	1561	gtcgcccccgacggggcggtg gattgaaac	32	23	4	
18	Desulfovibrio fructosivorans JJ	2	gi 302493090 gb AECZ01000001.1	AECZ01000001_1	41517	42405	gtcgcaactcgcgctgtgcggg gatgaagg	32	13	4	2563
			gi 302490808 gb AECZ01000016.1	AECZ01000016_1	1246	2921	gggactaccccgcgcgagcggg gaagac	29	27	4	
19	Desulfonatronovibrio hydrogenovorans DSM 9292	1	gi 631913834 gb JMKT01000012.1	JMKT01000012_1	4	391	gtgaaccgcccgcataggcggtta gaaa	28	6	4	387
20	Desulfobulbaceae bacterium BRH_c16a	2	gi 780797249 gb LADS01000002.1	LADS01000002_1	651	2597	gtcactccccgcgcgggagtgtgg attgaaac	32	29	4	14917
			gi 780792556 gb LADS01000049.1	LADS01000049_1	319036	332007	gtcactccccgcgcgggagtgtgg attgaaac	32	196	4	
21	Desulfobulbus propionicus type strain (1pr3)	1	gi 320352146 ref NC_014972.1	NC_014972_1	1701541	1707620	gtcgccccccacgcggggcggtg gattgaaac	32	91	4	6079
24	Desulfovibrio hydrothermalis DSM 14728	2	gi 436839709 ref NC_020055.1	NC_020055_4	118127	118736	gtcaaaaccataccgatatggata cctcttttgag	36	8	4	1716
			gi 436839709 ref NC_020055.1	NC_020055_6	2574826	2575933	gttcactgccgataggcagcttag aaa	28	18	4	
25	Desulfotomaculum hydrothermale Lam5	4	gi 411455086 emb CAOS01000004.1	CAOS01000004_1	71022	75642	gttacaaccattgccgataaaca ggggactgaaat	37	62	4	9527
			gi 411455050 emb CAOS01000006.1	CAOS01000006_1	1348	5087	gtttcaattccttataggtaggcta aac	30	56	4	
			gi 411455050 emb CAOS01000006.1	CAOS01000006_2	6735	7552	gtttcaattccttataggtaggcta aac	30	12	4	
			gi 411454671 emb CAOS01000008.1	CAOS01000008_1	43280	43631	gtttcaattccttataggtaggcta aac	30	5	4	
26	Desulfotomaculum ruminis DSM 2154	10	gi 334089967 gb CP002780.1	CP002780_1	1100345	1102451	gtttcaaatccttataggtaggcta aaac	30	31	4	22298
			gi 334089967 gb CP002780.1	CP002780_2	1143003	1143369	gtttcaaatccttataggtaggcta aaac	30	5	4	
			gi 334089967 gb CP002780.1	CP002780_4	1421835	1423727	gtcgctctctaggtgagagcgtgg attgaaat	32	28	4	
			gi 334089967 gb CP002780.1	CP002780_5	1424987	1427147	gtcgctctctaggtgagagcgtgg attgaaat	32	32	4	

			gi 334089967 gb CP002780.1	CP002780_6	1435556	1439454	gtcgctctctgtacgagcgtgga tttaaac	32	58	4	
			gi 334089967 gb CP002780.1	CP002780_7	1800074	1803706	gttactagcctacctataaggattg aaac	30	54	4	
			gi 334089967 gb CP002780.1	CP002780_8	2490237	2491527	gttttagcctacctataaggattga aac	30	19	4	
			gi 334089967 gb CP002780.1	CP002780_10	3057773	3061057	gtttcaaatccttataggtagactag aac	30	49	4	
			gi 334089967 gb CP002780.1	CP002780_11	3091332	3093024	gttttagcctacctataagggttg aaac	30	25	4	
			gi 334089967 gb CP002780.1	CP002780_12	3099787	3101765	gtttctagcctacctataaggattga aac	30	29	4	
27	Desulfotomaculum reducens MI-1	4	gi 134050581 gb CP000612.1	CP000612_1	586379	587743	gttatcagcctacctataaggaattg aaac	30	20	4	6608
			gi 134050581 gb CP000612.1	CP000612_2	1079904	1083390	gtcgccctcacgcagggcgtg gattgaaac	32	52	4	
			gi 134050581 gb CP000612.1	CP000612_4	1764821	1766001	gtcaaaacacaaaataattcccttg ggaattgaaac	37	15	4	
			gi 134050581 gb CP000612.1	CP000612_5	1768139	1768717	gtcaaaacacaaaataattcccttg ggaattgaaac	37	7	4	
28	Desulfovibrio sp. X2	1	gi 523471633 gb ATHV01000015.1	ATHV01000015_1	54654	58637	gtcgccctcgcacagggcgtg gattgaaac	32	60	4	3983
29	Desulfovibrio sp. A2	1	gi 347517814 gb AGFG01000055.1	AGFG01000055_1	37	554	ggcctatccccgcaggcgcgggg ggaac	28	8	4	517
30	Desulfosporosinus acidiphilus SJ4	1	gi 391353422 gb CP003639.1	CP003639_1	1538047	1540340	gtcgctccctacgtgggagcgtgg attgaaat	32	34	4	2293
32	Desulfobacter curvatus DSM 3379	2	gi 480985097 gb AREY01000003.1	AREY01000003_1	129598	131150	gtttcaatccacgctcccgcatggg gagcgac	32	23	4	2173
			gi 480985033 gb AREY01000024.1	AREY01000024_1	7348	7969	gtttcaatccacgttggtctgattaa aag	30	9	4	
33	Desulfobacter vibrioformis DSM 8776	1	gi 675284502 gb JQKJ01000013.1	JQKJ01000013_1	70505	72652	ttcacaatccctcatgggtagat aac	28	33	4	2147
34	Desulfobacterium anilini DSM 4660	1	gi 523385901 gb AULM01000007.1	AULM01000007_1	158972	159548	gtttccccgcgcgcatcggggatc gacc	28	9	4	576
38	Desulfohalobium retbaense	1	gi 258404138 ref NC_013223.1	NC_013223_1	1876848	1877552	gcttcaatggggccacattgcag tgtggttgagac	37	9	4	704
39	Desulfatibacillum aliphaticivorans DSM 15576	1	gi 218777860 ref NC_011768.1	NC_011768_4	6093236	6097299	gtcttccccacgcccggtggggtgt ttct	29	66	4	4063

40	Desulfobacterium autotrophicum HRM2	1	gi 224367124 ref NC_012108.1	NC_012108_1	629857	636222	cctggaatgcctgatccacgacaa caaggattgaaac	37	87	4	6365
41	Desulfobacula sp. TS	2	gi 667676329 gb JIBV01000103.1	JIBV01000103_1	2052	3985	gtctgaacaccatatccagaagaa caaggattgaaac	37	26	4	2624
			gi 667676328 gb JIBV01000104.1	JIBV01000104_1	67	758	gtctgaacaccatatccagaagaa caaggattgaaac	37	9	4	
42	Desulfobacula toluolica Tol2	3	gi 408417460 ref NC_018645.1	NC_018645_1	1120959	1125463	ctttaatcagaccagtggtgaattg aaac	30	68	4	5418
			gi 408417460 ref NC_018645.1	NC_018645_2	1127872	1128164	ctttaatcagaccagtggtgaattg aaac	30	4	4	
			gi 408417460 ref NC_018645.1	NC_018645_4	3489798	3490420	gtctgaacggcatatccagaagaa caaggattgaaac	37	8	4	
43	Desulfotalea psychrophila LSv54	1	gi 51243852 ref NC_006138.1	NC_006138_2	198142	199100	gcttcaatgtagtcaccccttcgag gtgattgatac	37	13	4	958
44	Desulfovibrio alaskensis DSM 16109	1	gi 78355047 ref NC_007519.1	NC_007519_1	885036	886223	cgggtcatccccgcgggtgcgggg aacac	29	19	4	1187
45	Desulforegula conservatrix Mb1Pa	1	gi 523394517 gb AUEY01000013.1	AUEY01000013_1	58842	62107	gtttcaatcacgctccgcgcgg ggagcgac	32	49	4	3265
46	Desulfovibrio sp. FW1012B	1	gi 357632130 ref NZ_CM001368.1	NZ_CM001368_4	1487613	1491182	gtgttccccgcaggcgcgggatg atccg	29	58	4	3569
47	Desulfovibrio bastinii DSM 16055	5	gi 523620996 gb AUCX01000005.1	AUCX01000005_1	70064	70392	tttctaagctgcctatccggcagtga ac	28	5	4	1793
			gi 523620975 gb AUCX01000012.1	AUCX01000012_1	2	270	tttctaagctgcctatccggcagtga ac	28	4	3	
			gi 523620975 gb AUCX01000012.1	AUCX01000012_2	7887	8205	ctcaaaagagggtttccgatctggat cgggttttgaca	37	4	3	
			gi 523620975 gb AUCX01000012.1	AUCX01000012_3	11471	11788	ctcaaaagagggtttccgatctggat cgggttttgaca	37	4	4	
			gi 523620944 gb AUCX01000024.1	AUCX01000024_1	562	1124	tttctaagctgcctatccggcagtga ac	28	9	4	
48	Desulfonatronospira thiodismutans	5	gi 298510264 gb ACJN02000002.1	ACJN02000002_1	277891	280378	gtgatccaccgcataggtggctaa gaaa	28	41	4	8502
			gi 298510264 gb ACJN02000002.1	ACJN02000002_2	729341	730304	gtccgaaggactggcagggttag aaccattgcgac	36	13	4	
			gi 298510264 gb ACJN02000002.1	ACJN02000002_3	736657	737407	gtccgaaggactggctgggttag aaccattgcggc	36	10	4	
			gi 298510264 gb ACJN02000002.1	ACJN02000002_4	1140480	1143097	gtcgccccctgcgcggggcgtg gattgaaac	32	39	4	

			gi 298509225 gb ACJN02000003.1	ACJN02000003_5	1042604	1044289	gcttcaatggagccacatttttaatgtggaatgagac	37	23	4	
49	Desulfovibrio alcoholivorans DSM 5433	1	gi 651606202 gb JNJA01000008.1	JNJA01000008_1	61423	62524	gtgctcaacgcttttcagcatcgaa gatggaatcac	36	15	4	1101
51	Desulfobacter postgatei 2ac9	3	gi 387144458 gb AGJR02000013.1	AGJR02000013_1	325928	326468	gtctcaatcctctctaatecaggcaatcttcggac	36	7	4	8661
			gi 387144458 gb AGJR02000013.1	AGJR02000013_2	336571	337833	gtctcaatcctctctaatecaggcaatcttcggac	36	12	4	
			gi 387144457 gb AGJR02000014.1	AGJR02000014_1	27231	34090	cggatcatccccacgggggtggggaaaag	29	112	4	
52	Desulfotignum phosphitoxidans DSM 13687	2	gi 474488791 gb APJX01000003.1	APJX01000003_1	373490	374536	gtctcaatcctctctaatecaggcgtgattcggac	36	14	4	2008
			gi 474487091 gb APJX01000007.1	APJX01000007_1	11184	12146	gtcgtccccatgcgggagcgtggattgaaac	32	14	4	
53	Desulfotignum balticum DSM 7044	2	gi 522811039 gb ATW001000001.1	ATW001000001_1	2611973	2614198	gcttcaatggggccggagctgatatgctccgaaaac	37	30	4	4692
			gi 522811039 gb ATW001000001.1	ATW001000001_4	3498968	3501435	ggaacacccccacaggcgtggggaagat	28	40	4	
54	Desulfatirhabdium butyrivorans DSM 18734	1	gi 523620767 gb AUCU01000018.1	AUCU01000018_1	21190	21949	ggatcatccccgcgtgtgcgggggagcc	28	12	4	759
56	Desulfovibrio zosteriae DSM 11974	1	gi 523389953 gb AUDC01000019.1	AUDC01000019_1	85377	85757	gttgatgattctgcgtaatgacagcagattgaaac	36	5	4	380
59	Desulfatitalea sp. BRH_c12	1	gi 780826867 gb LADR01000053.1	LADR01000053_1	38009	47735	cgggtcatccccgcgtctgcgggggaacac	29	159	4	9726
60	Desulfovibrio inopinatus DSM 10711	2	gi 523618915 gb AUBP01000007.1	AUBP01000007_1	172429	173377	gtttcaatccacgcacccgcgtgggggtgcgac	32	14	4	1289
			gi 523618538 gb AUBP01000078.1	AUBP01000078_1	64	405	tcgtctcctcgcgggtattgat	23	5	2	
61	Desulfobacca acetoxidans DSM 11109	4	gi 328951746 ref NC_015388.1	NC_015388_1	87673	94203	gtttcaatcctgttttagtggaatgatacgccaaaag	37	89	4	9397
			gi 328951746 ref NC_015388.1	NC_015388_9	1488840	1490146	cttacaacgataagaagagtcttcggacgattgcgac	37	17	4	
			gi 328951746 ref NC_015388.1	NC_015388_11	1934754	1935816	ctcagaacattgacctgattagaa gggattgcgac	36	14	4	
			gi 328951746 ref NC_015388.1	NC_015388_14	3066547	3067046	gtcgcgaatcccttctaatacaggtcaatgaagcagag	37	6	4	

62	Desulfobulbus mediterraneus DSM 13871	1	gi 523620997 gb AUCW01000012.1	AUCW01000012_1	164045	164508	gcttcaatgtagccacctctccga ggtggttggtac	37	6	4	463
64	Desulfonatronum lacustre DSM 10312	2	gi 573089367 gb JAFE0100001.1	JAFE01000001_1	387972	389525	cgggttatccccacgtgtgtgggga acgc	29	25	4	2859
			gi 573089362 gb JAFE0100002.1	JAFE01000002_1	313754	315060	gtttcaatccacgccccgcgcg gggggcgac	33	19	4	
65	Desulfosarcina sp. BuS5	2	gi 548693802 gb AXAM01000095.1	AXAM010000095_1	3835	4858	cttttaatcagaccagaatggaattg aaac	30	15	4	1913
			gi 548693795 gb AXAM01000096.1	AXAM010000096_1	4	894	cttttaatcagaccagaatggaattg aaac	30	13	4	
66	Desulfovibrio longus DSM 6739	2	gi 522808638 gb ATVA01000003.1	ATVA010000003_2	75640	75909	ttcatccccgcgcacgcggggaac ac	26	4	3	1455
			gi 522808608 gb ATVA01000015.1	ATVA010000015_1	364054	365240	attacactgcatacccgctagaaa ggggattgcgac	37	15	4	
67	Desulfurella acetivorans DSM 5264	3	gi 754092674 ref NZ_CP007051.1	NZ_CP007051_1	545525	549853	gttttagcccccaattgtgggattta aag	29	66	4	5839
			gi 754092674 ref NZ_CP007051.1	NZ_CP007051_2	659173	659971	gtcgaattccctcaaacgggaa agaatgcaac	35	10	4	
			gi 754092674 ref NZ_CP007051.1	NZ_CP007051_3	1684621	1685334	gttgcatctttcccgtttgaaggga attacgac	35	9	4	
69	Desulfonatronovibrio magnus	2	gi 761631872 gb JYNP01000039.1	JYNP010000039_1	57578	57903	gtctcaatccctcaagtcggggca atgtttctgac	36	4	4	576
			gi 761631790 gb JYNP01000074.1	JYNP010000074_1	287	538	cagtttggtcctgaaaggttggt cc	27	5	2	
70	Desulfonatronum thioautotrophicum ASO4-1	1	gi 761631699 gb JYNO01000016.1	JYNO010000016_1	18293	18690	agtccgaaagcgggttgcgatttg ggggcttgagatc	38	5	2	397
71	Desulfonatronum thiodismutans	3	gi 665768126 gb JPIK01000006.1	JPIK010000006_1	89016	89346	gtctcggcaagcttggtcagtggtg ggtgattggcac	37	4	4	3477
			gi 665768112 gb JPIK01000020.1	JPIK010000002_1	72797	73705	gtcgcccccgcggggggcgt ggattgaaac	33	13	4	
			gi 665768104 gb JPIK01000028.1	JPIK010000008_1	10844	13083	gttttcggggcattcctccccgg cctcattgaagc	37	30	4	
72	Desulfovibrio desulfuricans ND132	1	gi 376294792 ref NC_016803.1	NC_016803_5	3491653	3498191	gtcgccccacgcggggcggtg gattgaaac	32	98	4	6538
73	Desulfococcus multivorans DSM 2059	6	gi 523473342 gb ATHJ01000001.1	ATHJ010000001_1	56	533	gtctgaaccactgccccgattcgag gggattgagac	36	6	4	11090

			gi 523473333 gb ATHJ01000003.1	ATHJ01000003_2	5694	7043	gtctgaaccactgccccgattcgaggggattgagac	36	18	4	
			gi 523473330 gb ATHJ01000004.1	ATHJ01000004_1	52	1813	gtctcaatccctcggaatcggggcatgtgttcagac	36	23	4	
			gi 523468025 gb ATHJ01000087.1	ATHJ01000087_1	51699	57633	ccgcaccgatctccgatccgaaaaggcgttgagcac	36	83	4	
			gi 523461284 gb ATHJ01000127.1	ATHJ01000127_1	46953	47499	gtctgaaccactgccccgattcgaggggattgagac	36	7	4	
			gi 523459347 gb ATHJ01000145.1	ATHJ01000145_1	3273	4296	gtctgaaccattgcccgattcgaggggattgagac	36	13	4	
74	Desulfococcus oleovorans Hxd3	2	gi 158520017 ref NC_009943.1	NC_009943_1	860153	861365	gtcgcgaatccctctaacagcgggtctctccttc	35	16	4	3680
			gi 158520017 ref NC_009943.1	NC_009943_8	3590108	3592576	atgtccccacacgtgtggggatgaaccg	29	40	4	
75	Desulfobulbus sp. Dsb1 (Tol1)	4	gi 700403941 gb JROS01000049.1	JROS01000049_1	7	2520	cccggaaacgaatgccccgatcagaggggattgagac	36	34	4	10165
			gi 700403923 gb JROS01000050.1	JROS01000050_1	25099	26732	cccggaaacgaatgccccgatcagaggggattgagac	36	22	4	
			gi 700403522 gb JROS01000061.1	JROS01000061_1	51	1039	cttcactgccgcacaggcagctga gaaa	28	16	4	
			gi 700403118 gb JROS01000084.1	JROS01000084_1	10259	15290	ccgttccccgcacccgcggggatg aaccg	29	82	4	
76	Desulfocapsa sulfexigens DSM 10523	1	gi 451945650 ref NC_020304.1	NC_020304_1	3932262	3932826	gtttcaatccacgccccgcattgga gggcgac	32	8	4	564
77	Desulfurivibrio alkaliphilus AHT 2	2	gi 297567992 ref NC_014216.1	NC_014216_2	1780099	1782570	cggttcatccccgcgagtgcgggg aacat	29	40	4	9413
			gi 297567992 ref NC_014216.1	NC_014216_3	1785014	1791956	tttctgagctgcctgtgcggcagtg aac	28	115	4	
78	Thermodesulfatator indicus DSM 15286	3	gi 335358205 gb CP002683.1	CP002683_1	238340	242182	gttcacagcctaactaaaaggaatg gaaac	30	57	4	9249
			gi 335358205 gb CP002683.1	CP002683_4	918034	919769	gtgagaaaaacctgcctgattaaga aggcattacgac	37	22	4	
			gi 335358205 gb CP002683.1	CP002683_5	1410352	1414024	gtgagaaaaacctgcctgattaaga aggcattacgac	37	47	4	
79	Desulfotomaculum acetoxidans DSM 771	11	gi 257777071 gb CP001720.1	CP001720_1	933526	937981	gatctaatttagccatagtggaaatg aaat	30	67	4	28109
			gi 257777071 gb CP001720.1	CP001720_2	940048	943825	gatctaatttagccatagtggaaatg aaat	30	57	4	

			gi 257777071 gb CP001720.1	CP001720_3	2198816	2202288	gttttagcctac tataaggaattga aat	30	52	4	
			gi 257777071 gb CP001720.1	CP001720_4	2203726	2204020	gttttagcctac tataaggaattga aat	30	4	3	
			gi 257777071 gb CP001720.1	CP001720_5	2217925	2219152	gttttagcctac tatgaggattg aaat	30	18	4	
			gi 257777071 gb CP001720.1	CP001720_6	3161588	3162074	agtttcaattccctatgggaattat gtttcagac	38	6	4	
			gi 257777071 gb CP001720.1	CP001720_7	3171662	3171997	gtttcaattccctacgggaattat gtttcagat	37	4	3	
			gi 257777071 gb CP001720.1	CP001720_8	3189932	3199658	atttcaatacatcaaatgtgacggt ccc	30	147	4	
			gi 257777071 gb CP001720.1	CP001720_9	3748348	3749510	gttttagtctac tatgaggaattga aac	30	17	4	
			gi 257777071 gb CP001720.1	CP001720_10	3834582	3836462	atttcaatccacgccccgtgtagg gagcgac	32	28	4	
			gi 257777071 gb CP001720.1	CP001720_13	4451140	4452435	atttcaattcctcatagataggctaa aaac	30	19	4	
80	Thermodesulfobacterium commune DSM 2178	2	gi 668351138 gb CP008796.1	CP008796_1	1356859	1357792	gtagaaacctgccctacttcaaaag ggattgcgac	35	12	4	2365
			gi 668351138 gb CP008796.1	CP008796_2	1461789	1463221	gttttgagcctac tacaaggaattg aaac	30	21	4	
81	Thermodesulfobacterium geofontis OPF15	2	gi 334901311 gb CP002829.1	CP002829_1	1115343	1118449	gttgaaacctgccctggattaaaag ggattgcgaa	35	41	4	6662
			gi 334901311 gb CP002829.1	CP002829_2	1221572	1225128	gtttcaatccaccaaagaggaattta aac	29	54	4	
83	Syntrophobacter fumaroxidans MPOB	2	gi 116696516 gb CP000478.1	CP000478_10	1684126	1689168	gacggagacagagccccgattga ggggattgagac	36	69	4	9893
			gi 116696516 gb CP000478.1	CP000478_17	3489022	3493873	gtgtccccacgcggtggggatg aaccg	29	79	4	
84	Desulfarculus baarsii DSM 2075	4	gi 301638057 gb CP002085.1	CP002085_2	1844781	1865928	gtcgccctcacgcaggggcgtg gattgaac	32	318	4	23168
			gi 301638057 gb CP002085.1	CP002085_3	1894474	1895008	gtttcaatccgttctctagcggca tcctcaatag	37	7	4	
			gi 301638057 gb CP002085.1	CP002085_4	1902297	1902763	gtttcaatccgttctctagcggca tcctcaatag	37	6	4	
			gi 301638057 gb CP002085.1	CP002085_10	3332441	3333462	ggcgcggggtccagcggcgcg gcaacatcctctacaactacggctc ggt	50	10	2	

85	Archaeoglobus sulfaticallidus PM70-1	1	gi 484591393 gb CP005290.1	CP005290_2	1137912	1142191	ctttcaatcctacaatagtctgattttac	30	62	4	4279
87	Archaeoglobus fulgidus DSM 4304	3	gi 6626247 gb AE000782.1	AE000782_1	148	4213	gttgaaatcagacaaaatgggattgaaag	30	59	4	10537
			gi 6626247 gb AE000782.1	AE000782_2	398369	401590	ctttcaatcccattttggtctgatttcaac	30	47	4	
			gi 6626247 gb AE000782.1	AE000782_3	1690930	1694181	gtaagaaaggagggtcctgaaaaaggagattgaaag	37	43	4	
88	Thermodesulfovibrio yellowstonii DSM 11347	3	gi 206741110 gb CP001147.1	CP001147_2	632030	633918	gtaggaaacaagacctcatttaaaagggattgacgac	36	26	4	11897
			gi 206741110 gb CP001147.1	CP001147_3	1074817	1076909	gttttgagcctacatatgaggaattgaaac	30	31	4	
			gi 206741110 gb CP001147.1	CP001147_5	1929305	1937222	ctttatatcccacatggttcagatgaac	29	120	4	
89	Candidatus Desulforudis audaxviator MP104C	4	gi 169637063 gb CP000860.1	CP000860_2	1355523	1359324	ctttcagtccccttttcgtcgggtcgtcgctgaaac	37	51	4	14257
			gi 169637063 gb CP000860.1	CP000860_4	1898301	1900891	gtttcaatccctcgtaggtaggctggaaac	30	38	4	
			gi 169637063 gb CP000860.1	CP000860_5	1902525	1904408	gtttcaatccctcgtaggtaggctggaaac	30	28	4	
			gi 169637063 gb CP000860.1	CP000860_6	1906089	1912072	gtttcaatccctcgtaggtaggctggaaac	30	90	4	
91	Desulfatibacillum alkenivorans DSM 16219	1	NZ_FQZU01000026.1	NZ_FQZU01000026_1	46146	48681	ctcataaccctcatggggatggataac	28	39	4	2535

Table S4: List of CRISPR elements found by CRISPRCas-Finder. The columns indicate the following: The number assigned to each strain in this study, strain name, CRISPR sequence ID, CRISPR ID (named by CRISPRCas-Finder), beginning and end of each CRISPR array, consensus repeat, repeat length, number of spacers, level of evidence and the total size of each CRISPR found.

Strain name	Prophage Sequence ID	Start	End	CRISPR Sequence ID	Start	End
Desulfovibrio fructosivorans JJ	18R1 gi 302493090 gb AECZ01000001.1 ctg00049 320 75894	320	75894	gi 302493090 gb AECZ01000001.1	41517	42405
Desulfotomaculum ruminis DSM 2154	26R1 gi 334089967 gb CP002780.1 Complete Genome 1102652 1163694	1102652	1163694	gi 334089967 gb CP002780.1	1143003	1143369
Desulfotomaculum reducens MI-1	27R1 gi 134050581 gb CP000612.1 Complete Genome 532811 592446	532811	592446	gi 134050581 gb CP000612.1	586379	587743
Desulfurella acetivorans DSM 5264	67R1 gi 754092674 ref NZ_CP007051.1 Complete Genome 1671975 1693619	1671975	1693619	gi 754092674 ref NZ_CP007051.1	545525	549853
Desulfotomaculum acetoxidans DSM 771	79R4 gi 257777071 gb CP001720.1 Complete Genome 4396496 4458901	4396496	4458901	gi 257777071 gb CP001720.1	4451140	4452435

Table S5: List of CRISPR elements found inside prophages. The columns indicate the strain name, the prophage sequence ID, the beginning and end of the prophage in the genome, CRISPR sequence ID and the beginning and end of CRISPR in the nucleotide sequence.

Prophage ID	Classification by Head-neck-tail module genes	bp	Strain name
1R1	Myoviridae of Type1 (Cluster 6)	63769	Desulfovibrio vulgaris str. Hildenborough
1R2	Myoviridae of Type1 (Cluster 8)	71645	
1R3	Siphoviridae of Type1 (cluster 6)	63915	
1R4	Podoviridae of Type3	39266	
1R5	Myoviridae of Type1 (Cluster 8)	69018	
1R6	Myoviridae of Type1 (Cluster 6)	52813	
2R1	Myoviridae of Type1 (Cluster 8)	32936	Desulfocurvibacter africanus DSM 2603
2R2	Myoviridae of Type1 (Cluster 6)	28418	
2R3	Myoviridae of Type1 (Cluster 9)	38770	
4R1	Myoviridae of Type1 (Cluster 8)	59873	Desulfocurvibacter africanus str. Walvis Bay
4R2	Myoviridae of Type1 (Cluster 6)	36762	
4R3	Myoviridae	24510	
5R1	Myoviridae of Type1 (Cluster 9)	70566	Desulfovibrio aespoensis Aspo-2
5R2	Myoviridae	58082	
5R3	Myoviridae of Type1 (Cluster 8)	36074	
8R1	Myoviridae of Type1 (Cluster 9)	47344	Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774
9R1	Siphoviridae of Type1 (Cluster 8)	54387	Desulfovibrio gigas DSM 1382
10R1	Myoviridae of Type1 (Cluster 6)	38173	Desulfovibrio piger ATCC 29098
13R1	Myoviridae	55980	Desulfovibrio cuneatus DSM 11391
14R1	Myoviridae of Type1 (Cluster 8)	60022	Desulfovibrio vulgaris str. Miyazaki
14R2	Siphoviridae of Type1 (Cluster 3)	61831	
15R1	Myoviridae of Type1 (Cluster 6)	51771	Desulfobulbus elongatus DSM 2908
16R1	Myoviridae of Type1 (Cluster 8)	145788	Desulfocurvus vexinensis DSM 17965
17R1	Myoviridae of Type1 (Cluster 8)	34073	Desulfovibrio alkalitolerans

18R1	Siphoviridae of Type1 (No Cluster Assigned)	75574	Desulfovibrio fructosivorans JJ
18R2	Siphoviridae of Type1 (Cluster 8)	93203	
18R3	Myoviridae of Type1 (Cluster 8)	49343	
19R1	Myoviridae of Type1 (Cluster 8)	27600	Desulfonatronovibrio hydrogenovorans DSM 9292
21R1	Siphoviridae of Type1 (Cluster 6)	79843	Desulfobulbus propionicus type strain 1pr3
21R2	Siphoviridae of Type1 (Cluster 8)	87012	
22R1	Myoviridae of Type1 (Cluster 6)	37163	Desulfovibrio salexigens
25R1	Siphoviridae of Type1 (Cluster 2)	45396	Desulfotomaculum hydrothermale Lam5
25R2	Siphoviridae of Type1 (Cluster 2)	60002	
26R1	Podoviridae	61042	Desulfotomaculum ruminis DSM 2154
26R2	Myoviridae of Type1 (Cluster 2)	84530	
27R1	unclassified	59635	Desulfotomaculum reducens MI-1
27R2	Myoviridae of Type1 (Cluster 6)	51840	
27R3	Siphoviridae of Type1 (Cluster 2)	64377	
28R1	Myoviridae of Type1 (Cluster 9)	32022	Desulfovibrio sp. X2
29R1	Myoviridae	24808	Desulfovibrio sp. A2
30R1	Myoviridae of Type1 (Cluster 6)	169593	Desulfosporosinus acidiphilus SJ4
33R1	Siphoviridae of Type1 (Cluster 8)	25102	Desulfobacter vibrioformis DSM 8776
34R1	Siphoviridae of Type1 (Cluster 8)	47057	Desulfobacterium anilini DSM 4660
35R1	unclassified	26392	Desulfovermiculus halophilus DSM 18834
37R1	unclassified	36767	Desulfomicrobium baculatum DSM 4028
38R1	unclassified	55128	Desulfohalobium retbaense
39R1	unclassified	36123	Desulfatibacillum alkenivorans AK-01
43R1	Siphoviridae	52191	Desulfotalea psychrophila LSv54
43R2	Podoviridae of Type3	28810	
44R1	Myoviridae	64002	Desulfovibrio alaskensis G20
44R2	unclassified	110648	
44R3	Myoviridae of Type1 (Cluster 8)	49658	

46R1	Siphoviridae of Type1 (Cluster 3)	71287	Desulfovibrio sp. FW1012B
47R1	Myoviridae	20567	Desulfovibrio bastinii DSM 16055
49R1	Siphoviridae of Type1 (Cluster 5)	121316	Desulfovibrio alcoholivorans DSM 5433
51R1	unclassified	40731	Desulfobacter postgatei 2ac9
52R1	unclassified	15798	Desulfotignum phosphitoxidans DSM 13687
53R1	unclassified	53248	Desulfotignum balticum DSM 7044
53R2	unclassified	55125	
54R1	unclassified	38383	Desulfatirhabdium butyrativorans DSM 18734
57R1	Myoviridae of Type1 (Cluster 8)	23512	Desulfovibrio putealis DSM 16056
59R1	unclassified	13123	Desulfatitalea sp. BRH_c12
60R1	Podoviridae of Type3	32873	Desulfovibrio inopinatus DSM 10711
60R2	Podoviridae of Type3	38072	
61R1	unclassified	42218	Desulfobacca acetoxidans DSM 11109
61R2	Siphoviridae of Type1 (Cluster 8)	32970	
67R1	unclassified	21644	Desulfurella acetivorans DSM 5264
72R1	unclassified	50980	Desulfovibrio desulfuricans ND132
74R1	unclassified	76813	Desulfococcus oleovorans Hxd3
77R1	unclassified	73569	Desulfurivibrio alkaliphilus AHT 2
79R1	unclassified	63473	Desulfotomaculum acetoxidans DSM 771
79R2	unclassified	63482	
79R3	unclassified	61659	
79R4	Myoviridae of Type1 (No Cluster Assigned)	62405	
80R1	Myoviridae of Type1 (Cluster 9)	64161	Thermodesulfobacterium commune DSM 2178
83R1	Siphoviridae of Type1 (Cluster 8)	59396	Syntrophobacter fumaroxidans MPOB
84R1	unclassified	83399	Desulfarculus baarsii DSM 2075
89R1	unclassified	76687	Candidatus Desulforudis audaxviator MP104C

90R1	Siphoviridae of Type1 (Cluster 6)	81648	Desulfovibrio vulgaris DP4
90R2	Myoviridae of Type1 (Cluster 9)	96187	
90R3	Myoviridae of Type1 (Cluster 9)	72305	

Table S6: Classification of prophages according to Virfam. Columns indicate the following: Prophage ID, classification assigned by Virfam using head-neck-tail module genes, the length of the prophage (bp) and the name of the host.

This table is available at https://github.com/robertoorellanar/Prophages_in_SRP.git

Table S7: Pairwise amino acid comparison of all predicted open reading frames (ORFs) from the SRP prophages. The abbreviation used is the following: p1 and p2, correspond to orfs for each prophage, pident, percentage of identical matches, length, alignment length, mismatch, number of mismatches, gaopen, number of gap openings, qstart, start of alignment in query, qend, end of alignment in query, sstart, start of alignment in subject, send, end of alignment in subject, and eval, expected value.