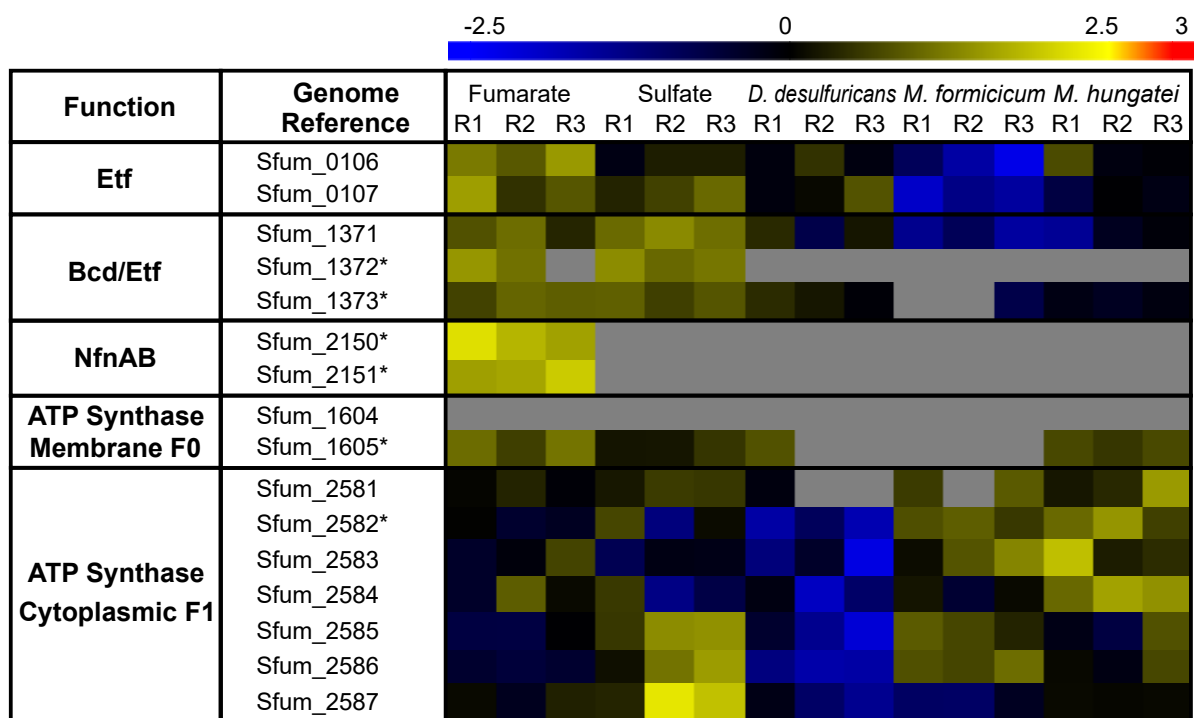
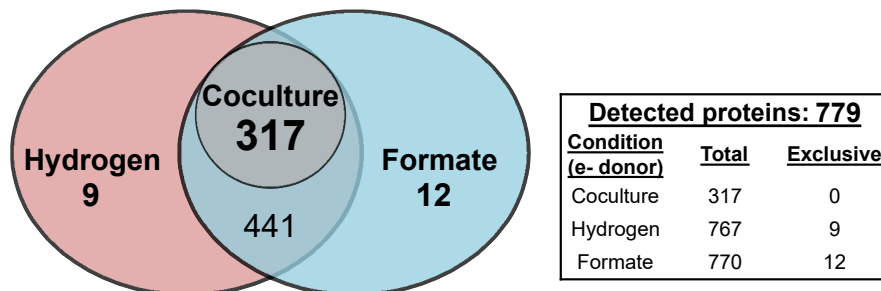


**Fig. S1. A.** Venn diagram of the 813 proteins detected in *Syntrophobacter fumaroxidans* growth on propionate with five different (biological or chemical) electron acceptors. **B.** Principal Component Analysis performed for *S. fumaroxidans* protein profiles obtained from each triplicate grown under five different conditions. Symbols: Orange diamonds, sulfate reducing; Red crosses, growth with fumarate; Grey squares, in coculture with *Desulfovibrio desulfuricans* in a sulfate rich environment; Green triangles, in syntrophy with *Methanospirillum hungatei*; Blue circles, in syntrophy with *Methanobacterium formicicum*.



**Fig. S2. Normalized expression matrix of energy conservation mechanisms predicted for *Syntrophobacter fumaroxidans*.** Proteins are shown for five different growth conditions, in triplicates; from left to right: fumarate, sulfate and interspecies compounds transferred to: *Desulfovibrio desulfuricans*, *Methanobacterium formicicum* and *Methanospirillum hungatei*. The colour scale illustrates the relative detection level of each protein across the 5 samples; blue (log ratio -2.5) and yellow (log ratio 2.5) indicate lower and higher levels compared to the average level value (in black), respectively. Not detected proteins in a specific condition appear in grey. (\*) indicates a statistical significant difference in at least one condition.

A



B

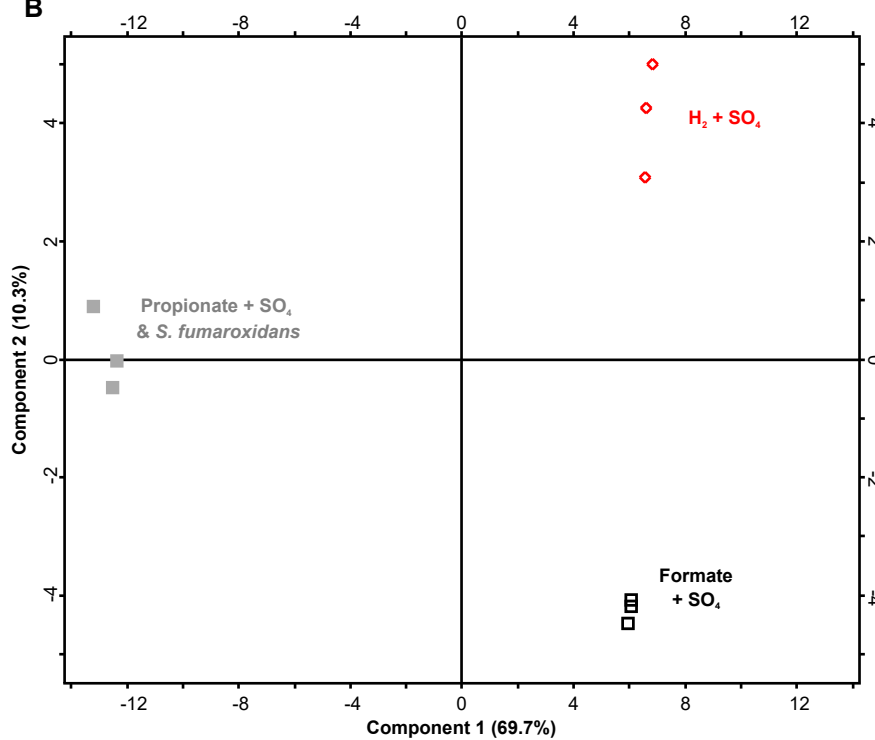
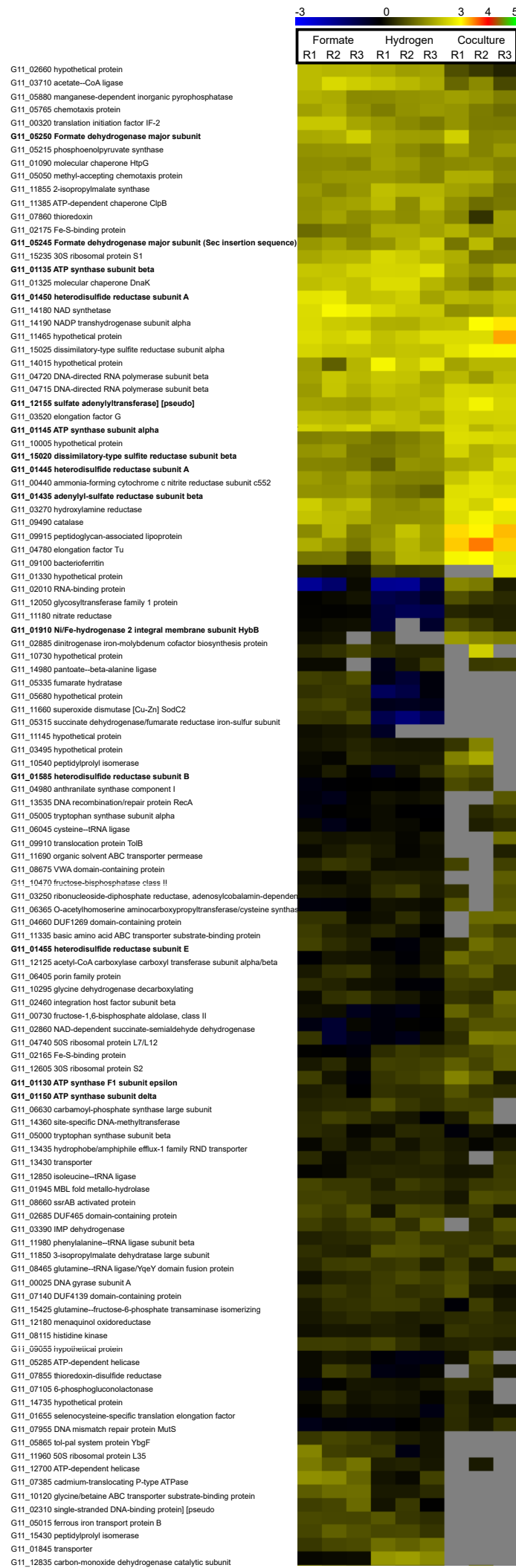
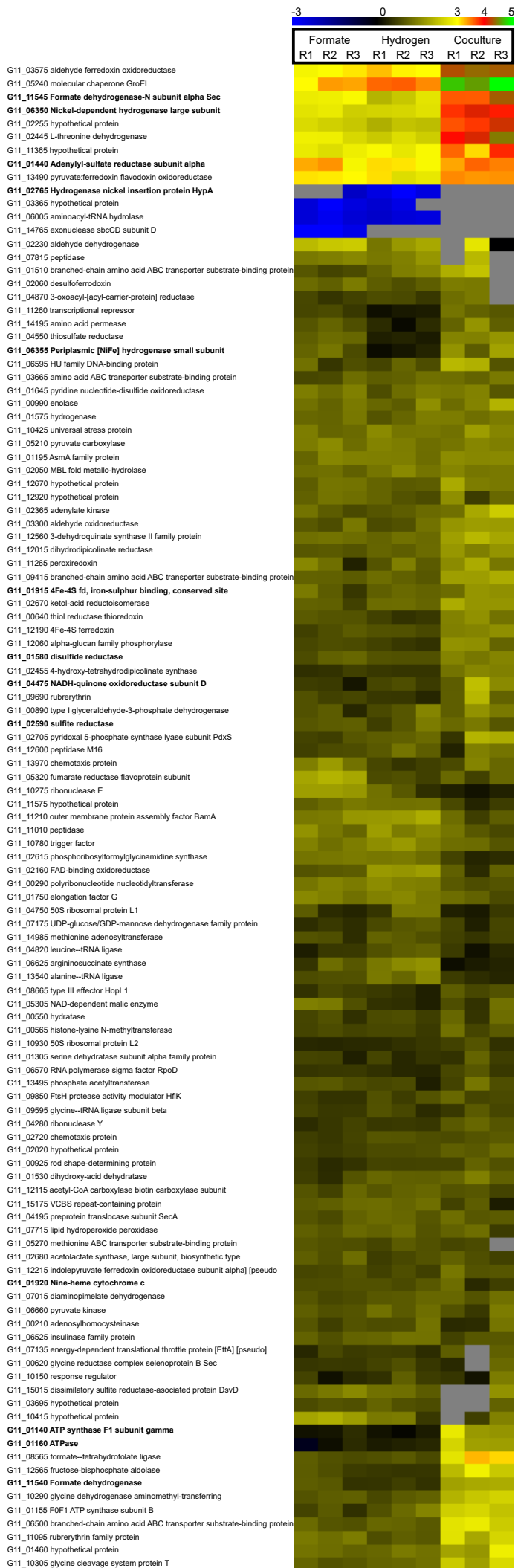
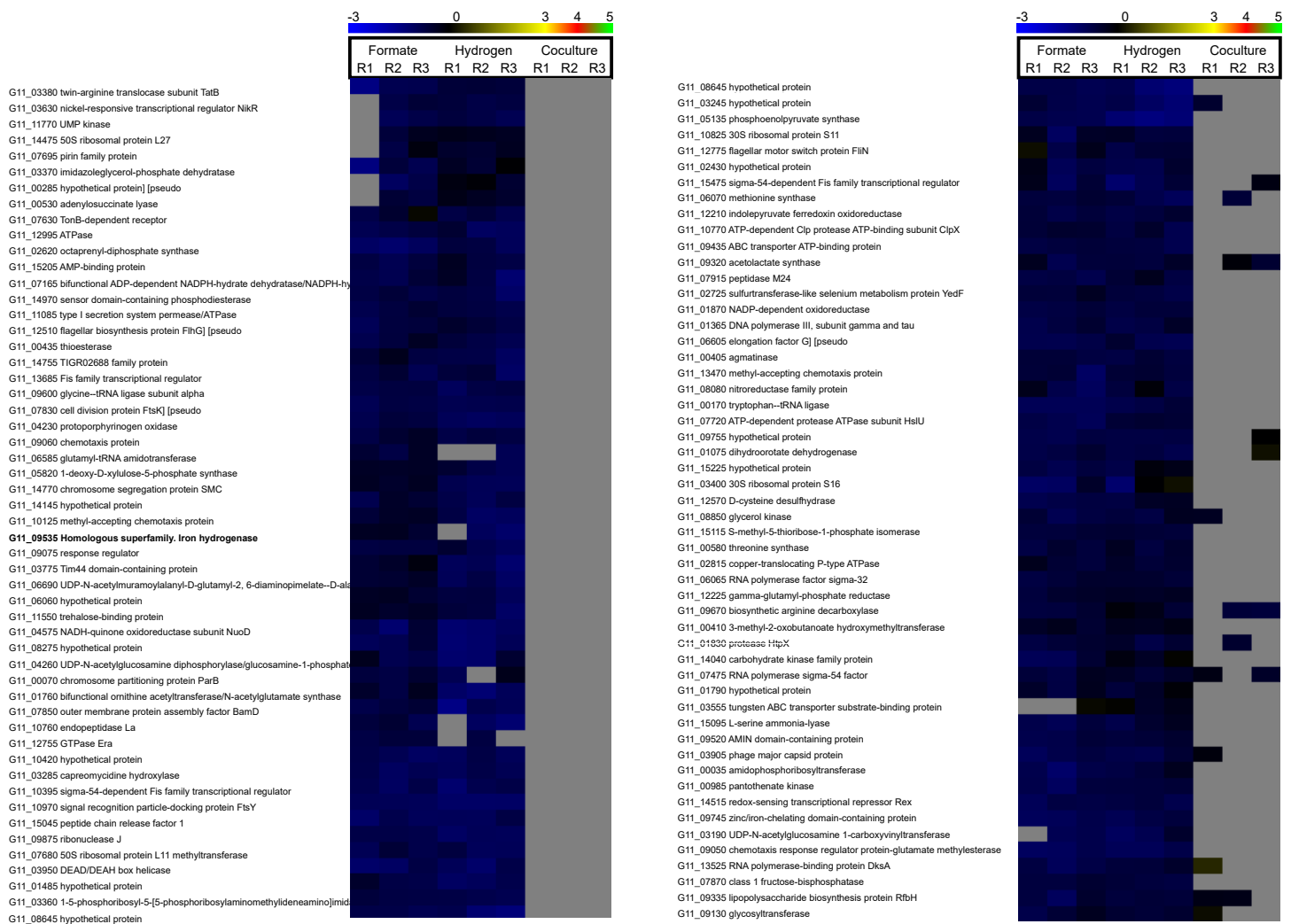


Fig. S3. A. Venn diagram of the 779 proteins detected in *Desulfovibrio desulfuricans* growing in sulfate rich medium in coculture with *Syntrophobacter fumaroxidans* or axenically on  $H_2/CO_2$  or formate. B. PCA performed for *D. desulfuricans* protein profiles. Symbols: red diamonds, hydrogenotrophic conditions; black squares, growth with formate and filled grey squares correspond to the cocultured partnership of *D. desulfuricans* with *S. fumaroxidans*.









**Fig. S4. Heat map of hierarchical clustered proteins produced by *Desulfovibrio desulfuricans*.** The proteins are shown in a clustered matrix after column Z-score normalization and automatic hierarchical columns clustering. Three growth conditions, in triplicates, are shown according to the electron donor used; from left to right: formate, hydrogen and compounds transferred from *Syntrophobacter fumaroxidans*. The colour scale represents the relative detection level of each protein across the samples; blue (log ratio -3), yellow (log ratio 3), red (log ratio 4) and green (log ratio 5) indicate lower and higher levels compared to the average level value 0 (in black), respectively. The colour intensity indicates the degree of protein up- or down regulation; the grey represents not detected.

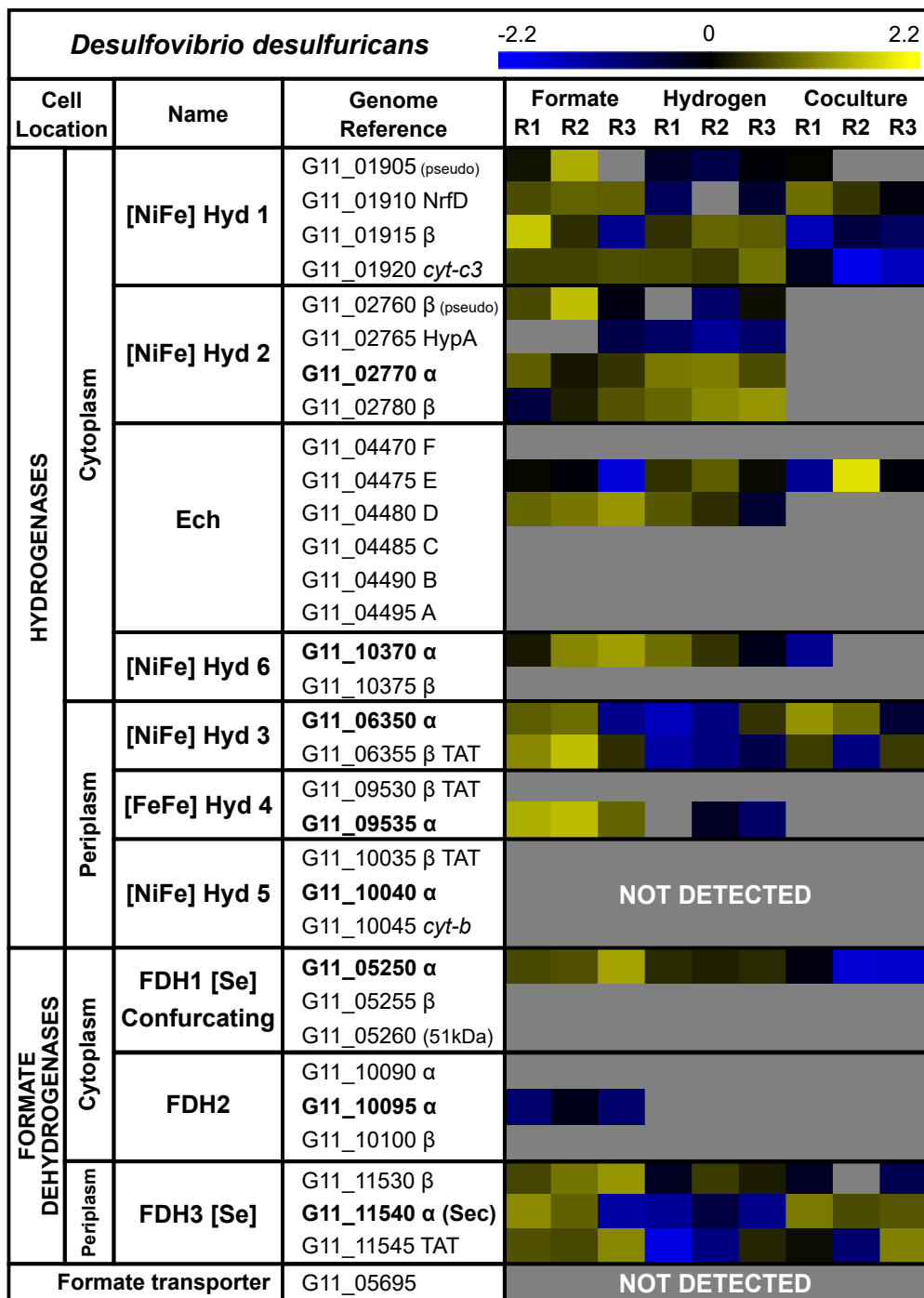


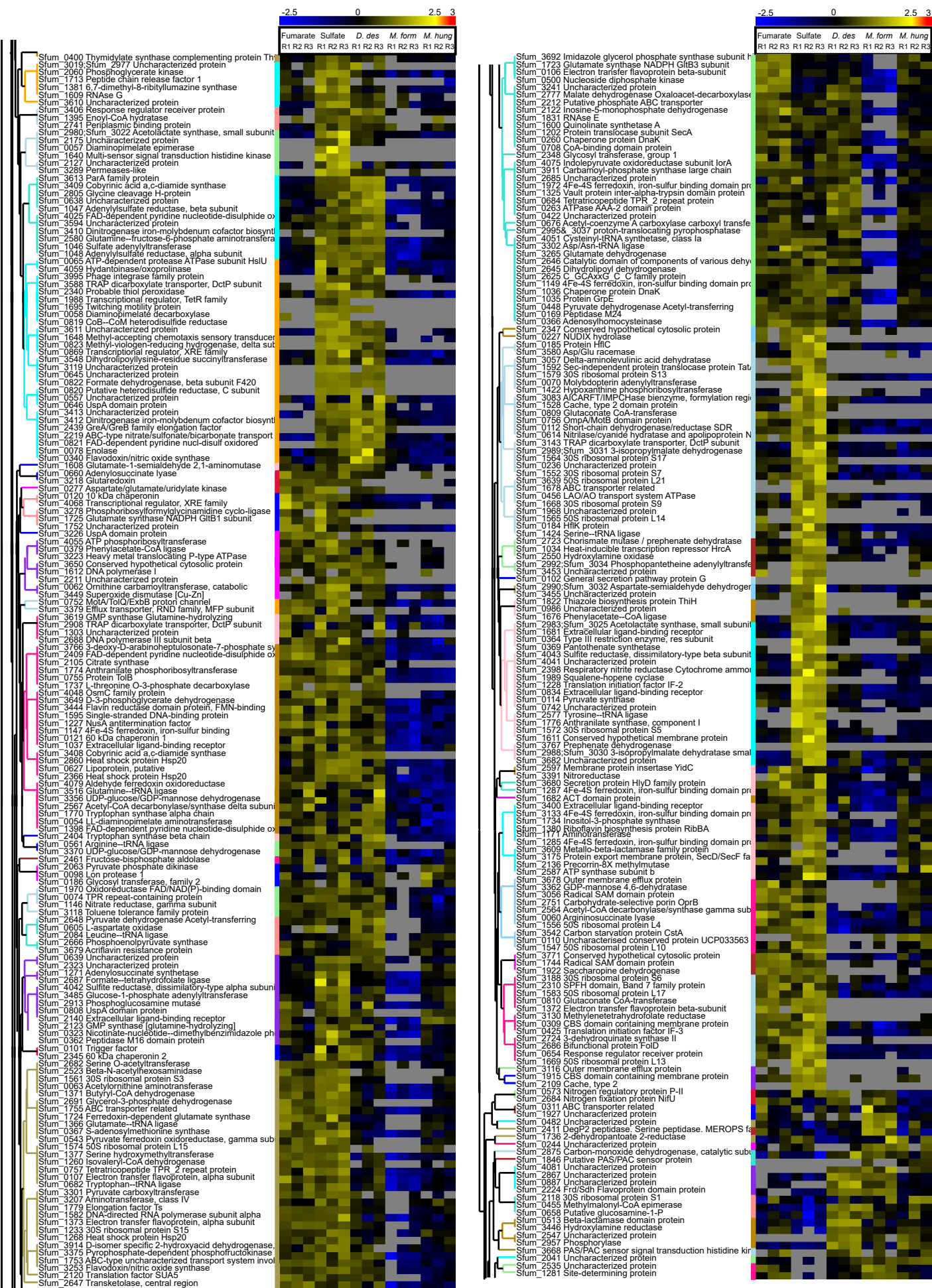
Fig. S5. Normalized expression matrix of hydrogenases and formate dehydrogenases of *Desulfovibrio desulfuricans*. The rows in the heat map show proteins levels after row Z-score standardization in three different growth conditions. The columns show from left to right, in triplicates, the electron donor used by *D. desulfuricans*: formate, hydrogen and interspecies compounds transferred from *Syntrophobacter fumaroxidans*. The colour scale indicates the degree of protein down- or up regulation ranging from blue (-2.2 log ratio), to yellow (2.2 log ratio). The colour intensities indicate lower and higher levels compared to the average level 0 value (in black); the grey colour represents not detected. Subunits, twin-arginine translocation (TAT) pathway signal and selenocysteine insertion (Sec) sequences are indicated after the locus tag.

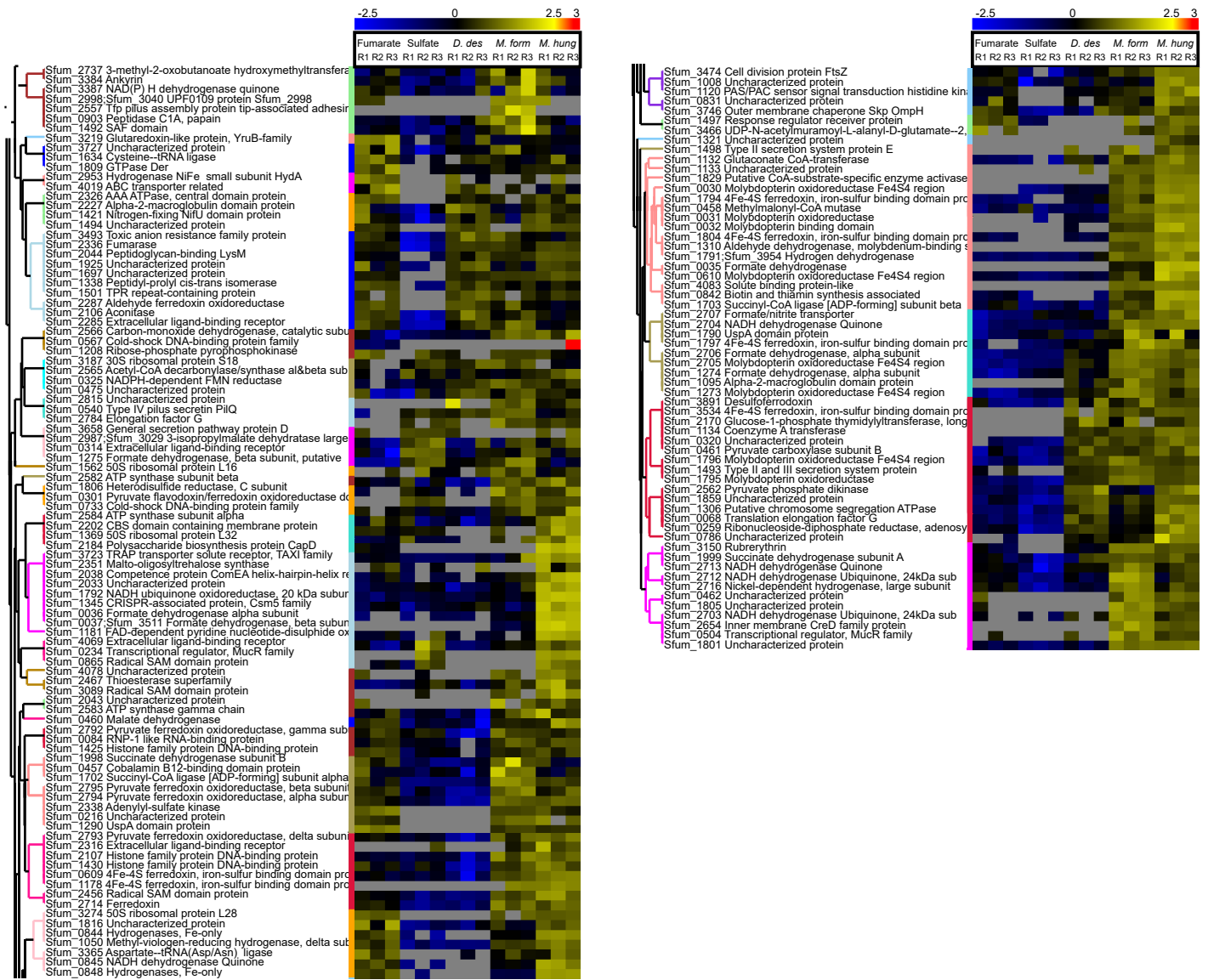




- Sfum\_2561 Citrate Pro-3S-lyase
- Sfum\_1302 Transketolase domain protein
- Sfum\_1198 Alpha-glucan phosphorylase
- Sfum\_1402 Acyl-CoA dehydrogenase domain protein
- Sfum\_2584 50S ribosomal protein L34
- Sfum\_1483 Heat shock protein DnaJ domain protein
- Sfum\_2000 Fumarate reductase respiratory complex, transmembrane
- Sfum\_1954 NADH-quinone oxidoreductase, chain G
- Sfum\_3489 ABC-type nitrate/sulfonate/bicarbonate transport
- Sfum\_1559 50S ribosomal protein L19
- Sfum\_0310 ABC transporter related
- Sfum\_1187 Uncharacterized protein
- Sfum\_3850 Helicase domain protein
- Sfum\_1418 1-deoxy-D-xylulose-5-phosphate synthase
- Sfum\_0268 Amidophosphoribosyltransferase
- Sfum\_0478 Cysteine synthase
- Sfum\_2081 Probable cytosol aminopeptidase
- Sfum\_1246 2,5-bisphosphate nucleotidase
- Sfum\_1746 Uncharacterized protein
- Sfum\_2947 Conserved hypothetical cytosolic protein
- Sfum\_4047 Cytochrome c class II
- Sfum\_4045 DsrC family protein
- Sfum\_3745 Outer membrane protein assembly factor BamA
- Sfum\_0739 Peptidase M1, membrane alanine aminopeptidase
- Sfum\_3697 Molybdenum ABC transporter, periplasmic molyb
- Sfum\_3903 Extracellular solute-binding protein, family 3
- Sfum\_0027 Extracellular solute-binding protein, family 1
- Sfum\_1347 CRISPR-associated protein, Csm3 family
- Sfum\_2350 Glycoside hydrolase, family 57
- Sfum\_1550 DNA-directed RNA polymerase subunit beta
- Sfum\_1351 Cupin 2, conserved barrel domain protein
- Sfum\_0511 Sulfurtransferase
- Sfum\_0429 Phenylalanine-tRNA ligase beta subunit
- Sfum\_0405 Bifunctional uridylyltransferase/uridylyl-removing
- Sfum\_0745 Acetyl-coenzyme A synthetase
- Sfum\_2466 CoA-binding domain protein
- Sfum\_3547 2-oxoglutarate dehydrogenase E1 component
- Sfum\_2445 Glycine-tRNA ligase beta subunit
- Sfum\_0870 AMP-dependent synthetase and ligase
- Sfum\_0020 ATP-dependent protease, putative
- Sfum\_0039 ABC-transporter, periplasmic substrate-binding p
- Sfum\_3510 Formate dehydrogenase alpha subunit
- Sfum\_0038 Protein involved in formate dehydrogenase form
- Sfum\_112 Uncharacterized protein
- Sfum\_1612 Signal transduction histidine kinase, nitrogen spe
- Sfum\_0530 Polysaccharide export protein
- Sfum\_1349 CRISPR-associated protein, Csm1 family
- Sfum\_3724 Prephenate dehydratase
- Sfum\_1771 Tryptophan synthase beta chain
- Sfum\_2982 Sfum\_3024 Acetolactate synthase
- Sfum\_2714 TonB-dependent receptor
- Sfum\_0192 Valine-tRNA ligase
- Sfum\_1549 DNA-directed RNA polymerase subunit beta
- Sfum\_3572 Uncharacterized protein
- Sfum\_0484 SPFH domain, band 7 family protein
- Sfum\_3201 Uroporphyrinogen-III synthase / uroporphyrinoge
- Sfum\_3495 Extracellular solute-binding protein, family 1
- Sfum\_3199 VacJ family lipoprotein
- Sfum\_2751 Cobalamin Vitamin B12 biosynthesis CblM protei
- Sfum\_2743 Uncharacterized protein
- Sfum\_1212 RNA polymerase sigma factor RpoD
- Sfum\_2208 Multi-sensor hybrid histidine kinase
- Sfum\_0417 Adenine deaminase
- Sfum\_3367 Asn/Gln-tRNA amidotransferase subunit B
- Sfum\_3105 Extracellular ligand-binding receptor
- Sfum\_1173 4Fe-4S ferredoxin, iron-sulfur binding domain pr
- Sfum\_1223 Carboxyl transferase
- Sfum\_3744 Lipoprotein-releasing system ATP-binding protein
- Sfum\_286 Cysteine synthase
- Sfum\_3285 Malonyl CoA-acyl carrier protein transacylase
- Sfum\_0481 Phosphomannomutase
- Sfum\_1788 Import inner membrane translocase, subunit Tim
- Sfum\_0197 Pyrolytic 5-carboxylate reductase
- Sfum\_1628 ATPase with chaperone activity
- Sfum\_0556 Peptidase C14, caspase catalytic subunit p20
- Sfum\_4011 Hydrogenase accessory protein HybB
- Sfum\_3252 Rubrethrin
- Sfum\_1742 Heat shock protein Hsp20
- Sfum\_2680 DNA gyrase subunit A
- Sfum\_3417 Superoxide dismutase
- Sfum\_1051 Uncharacterized protein
- Sfum\_0222 Peptidase C1A, papain
- Sfum\_0617 Pyruvate carboxyltransferase
- Sfum\_3549 Dihydrodipicolyl dehydrogenase
- Sfum\_1215 Phosphoribosyl carboxamide isomerase
- Sfum\_2681 DNA gyrase subunit B
- Sfum\_1712 50S ribosomal protein L31
- Sfum\_3539 Uncharacterized protein
- Sfum\_2806 ParB-like partition proteins
- Sfum\_0849 NADH dehydrogenase Ubiquinone,24kDasubuni
- Sfum\_1605 ATP synthase subunit a
- Sfum\_3492 ABC-type nitrate/sulfonate/bicarbonate transport
- Sfum\_0210 Uncharacterized protein
- Sfum\_2611 Transcriptional regulator, TraR/DksA family
- Sfum\_3074 Molybdopterin-guanine dinucleotide biosynthesis
- Sfum\_2583 Aminotransferase, class V
- Sfum\_0281 Chaperone DnaJ domain protein
- Sfum\_1375 3-oxoacyl-[acyl-carrier-protein] synthase 2
- Sfum\_2929 Radical SAM domain protein
- Sfum\_1236 Nucleoside-reducing hydrogenase, delta sub
- Sfum\_1918 Uncharacterized protein
- Sfum\_3184 Primary replicative DNA helicase
- Sfum\_1305 Penicillin-binding protein 6, Serine peptidase, ME
- Sfum\_0497 Protoporphyrin IX magnesium chelatase
- Sfum\_0568 Pp1c-type peptidyl-prolyl cis-trans isomerase
- Sfum\_1545 50S ribosomal protein L11
- Sfum\_1049 Heterodisulfide reductase, subunit A
- Sfum\_1374 3-oxoacyl-[acyl-carrier-protein] reductase
- Sfum\_2578 Ribonuclease Y
- Sfum\_0492 TonB-dependent receptor
- Sfum\_2183 Lipopolysaccharide biosynthesis
- Sfum\_2058 Protein translocase subunit secC
- Sfum\_0938 5-carboxymethyl-2-hydroxymuconate delta-iso
- Sfum\_1546 50S ribosomal protein L1
- Sfum\_3653 50S ribosomal protein L25
- Sfum\_0055 4-hydroxy-tetrahydrodipicolinate reductase
- Sfum\_2192 UDP-sulfoglucosamine-N-acetylmutamuramyl
- Sfum\_2856 DNA methylase N-6/9 domain protein
- Sfum\_2776 Phosphomethylpyrimidine synthase
- Sfum\_0356 Dihydroxy-acid dehydratase
- Sfum\_2091 Dihydrodipicolyl dehydrogenase
- Sfum\_2188 Glycosyl transferase, group 1
- Sfum\_0449 Transketolase domain protein
- Sfum\_1781 Ribosome-recycling factor
- Sfum\_2997 Sfum\_3039 30S ribosomal protein S16
- Sfum\_2745 Sirohydrochlorin cobaltochelatase
- Sfum\_1683 Phenylacetate-CoA ligase
- Sfum\_1571 50S ribosomal protein L18
- Sfum\_0624 Universal stress protein
- Sfum\_1218 Homoserine dehydrogenase
- Sfum\_2984 Sfum\_3026 Ketol-acid reductoisomerase
- Sfum\_0424 Threonine-tRNA ligase
- Sfum\_2135 Precorrin-2 C20-methyltransferase / cobalt-factor
- Sfum\_3742 Lysine-tRNA ligase
- Sfum\_1352 CRISPR-associated protein, Csx2 family
- Sfum\_1544 Transcription termination/antitermination protein I
- Sfum\_2756 UDP-N-acetylglucosamine-N-acetylmuramyl
- Sfum\_0561 Sfum\_3191 ATP-dependent zinc metalloprotease
- Sfum\_2460 Signal recognition particle receptor FtsY
- Sfum\_4095 Fumarate reductase/succinate dehydrogenase fl
- Sfum\_4058 Sporulation domain protein
- Sfum\_3220 Rubrethrin
- Sfum\_2952 Nickel-dependent hydrogenase, large subunit
- Sfum\_2527 Alanine-tRNA ligase
- Sfum\_2410 Phosphoglycerate mutase
- Sfum\_1220 Selenocysteine-specific translation elongation fac
- Sfum\_1576 Adenylylase kinase
- Sfum\_1651 Presp peptidase, Metallo peptidase, MEROPS fam
- Sfum\_2409 Heat shock regulator
- Sfum\_1239 Protein translocase subunit SecD
- Sfum\_0122 Isoleucine-tRNA ligase
- Sfum\_0715 Lon protease
- Sfum\_1762 Aldolketo reductase
- Sfum\_3159 Nitrite and sulphite reductase 4Fe-4S region
- Sfum\_3184 Conserved hypothetical cytosolic protein
- Sfum\_0024 Periplasmic solute binding protein
- Sfum\_2678 UspA domain protein
- Sfum\_4093 Uncharacterized protein
- Sfum\_2290 3-oxoacyl-CoA transferase, A subunit
- Sfum\_2083 Phosphoserine aminotransferase
- Sfum\_0160 Pp1c-type peptidyl-prolyl cis-trans isomerase
- Sfum\_0298 Aldolketo reductase
- Sfum\_2385 Heat shock protein Hsp20
- Sfum\_0576 Glutamine synthetase
- Sfum\_1767 Superoxide dismutase
- Sfum\_3438 ATP-dependent zinc metalloprotease FtsH

- Sfum\_4094 4Fe-4S ferredoxin, iron-sulfur binding domain pr
- Sfum\_1971 4Fe-4S ferredoxin, iron-sulfur binding domain pr
- Sfum\_1721 Catalase
- Sfum\_1357 Uncharacterized protein
- Sfum\_1629 Uncharacterized protein
- Sfum\_2468 Rubrethrin
- Sfum\_3648 Molybdopterin oxidoreductase subunit A
- Sfum\_3287 Molybdopterin oxidoreductase
- Sfum\_1468 Glyceroldehyde-3-phosphate dehydrogenase
- Sfum\_0387 Indolepyruvate oxidoreductase subunit IorA
- Sfum\_0862 Extracellular ligand-binding receptor
- Sfum\_2110 Antibiotic biosynthesis moXoxoygenase
- Sfum\_3648 DNA oxidoreductase
- Sfum\_3243 PAS/PAC sensor signal transduction histidine kin
- Sfum\_2401 Multi-sensor hybrid histidine kinase
- Sfum\_1512 Redoxin domain protein
- Sfum\_1470 Phosphorylase
- Sfum\_0833 Delta-1-pyrroline-5-carboxylate dehydrogenase
- Sfum\_0443 Uncharacterized protein
- Sfum\_0008 Carbamoyl-phosphate synthase large subunit
- Sfum\_0191 Uncharacterized protein
- Sfum\_3932 4-hydroxyphenylacetate 3-hydroxylase
- Sfum\_3451 1,4-alpha-glucan branching enzyme GlgB
- Sfum\_2441 Uncharacterized protein
- Sfum\_1950 Putative signal transduction protein with EFhand
- Sfum\_0644 Uncharacterized protein
- Sfum\_0564 Uncharacterized protein
- Sfum\_2075 CTP synthase
- Sfum\_1119 ATPase, P-type Transporting, HAD superfamily, s
- Sfum\_0744 Phosphoglucomutase, alpha-D-glucose phospho
- Sfum\_0828 PAS/PAC sensor hybrid histidine kinase
- Sfum\_0901 Phosphoenolpyruvate carboxykinase [GTP]
- Sfum\_3185 50S ribosomal protein L9
- Sfum\_1717 Transcription termination factor Rho
- Sfum\_1821 Thiazole synthase
- Sfum\_3063 Carboxyl-terminal protease
- Sfum\_3100 D-3-phosphoglycerate dehydrogenase
- Sfum\_0651 Thioester-disulfide reductase
- Sfum\_2061 Glyceroldehyde-3-phosphate dehydrogenase
- Sfum\_2059 Triosephosphate isomerase
- Sfum\_1563 50S ribosomal protein L29
- Sfum\_1958 Beta-lactamase domain protein
- Sfum\_0893 NADPH-dependent FMN reductase
- Sfum\_1743 Heat shock protein Hsp20
- Sfum\_0984 Phospho D0
- Sfum\_1219 Aminotransferase
- Sfum\_0780 Uncharacterized protein
- Sfum\_2592 Rod shape-determining protein MreB
- Sfum\_1777 3-deoxy-D-arabinoheptulosonate-7-phosphate sy
- Sfum\_3380 Acriflavin resistance protein
- Sfum\_0113 3-oxoacyl-[acyl-carrier-protein] synthase 3
- Sfum\_0214 CsmJ family protein
- Sfum\_2112 4-hydroxy-3-methylbut-2-en-1-yl diphosphate syr
- Sfum\_4049 Cold-shock protein, DNA-binding
- Sfum\_2151 Sulfide dehydrogenase Flavoprotein subunit Suc
- Sfum\_2972 Sfum\_3014 Methyl-viologen-reducing hydrogena
- Sfum\_3950 Extracellular solute-binding protein, family 3
- Sfum\_3256 Hydroxyglutaryl-CoA dehydratase, D-compone
- Sfum\_0663 Extracellular solute-binding protein, family 1
- Sfum\_2494 3-dehydroquininate synthase
- Sfum\_2150 Sulfide dehydrogenase Flavoprotein subunit Suc
- Sfum\_2493 Ferrrous iron transport protein B
- Sfum\_3402 SirA family protein
- Sfum\_2146 Uncharacterized protein
- Sfum\_2592 Molybdopterin oxidoreductase
- Sfum\_3181 Hydroxyglutaryl-CoA dehydratase, D-compone
- Sfum\_0286 Phosphate binding protein
- Sfum\_2971 Sfum\_3013 4Fe-4S ferredoxin, iron-sulfur bindin
- Sfum\_2173 50S ribosomal protein L30
- Sfum\_1708 Thioredoxin
- Sfum\_1655 DsrE family protein
- Sfum\_1555 50S ribosomal protein L3
- Sfum\_2583 Uncharacterized protein
- Sfum\_0418 Uncharacterized protein
- Sfum\_1558 50S ribosomal protein L2
- Sfum\_0004 Uncharacterized protein
- Sfum\_2563 Dihydroterpate synthase, DHPS
- Sfum\_2464 Deoxyribose-phosphate aldolase/phospho-2-deh
- Sfum\_1778 30S ribosomal protein S2
- Sfum\_2116 Histidinol-phosphate aminotransferase
- Sfum\_3098 Branched-chain-amino-acid aminotransferase
- Sfum\_2115 RNA polymerase sigma factor
- Sfum\_1773 3-glycerol phosphate synthase
- Sfum\_1513 Cyclic nucleotide-binding protein
- Sfum\_0059 Fibronectin, type III domain protein
- Sfum\_0470 Nitroreductase
- Sfum\_0061 Argininosuccinate synthase
- Sfum\_0447 Transcriptional regulator, Fis family
- Sfum\_1569 30S ribosomal protein S8
- Sfum\_0288 Protein RecA
- Sfum\_2986 Sfum\_3028 CDP-diacylglycerol-serine O-phosp
- Sfum\_1917 Rod shape-determining protein MreB
- Sfum\_2870 Cystathionine gamma-synthase
- Sfum\_0180 Universal stress protein
- Sfum\_2009 Uncharacterized protein
- Sfum\_0778 Sulfotransferase
- Sfum\_0174 Protein ClnA4 Amidotransferase subunit B
- Sfum\_0484 Imidazole glycerol phosphate synthase subunit I
- Sfum\_0427 50S ribosomal protein L20
- Sfum\_0056 4-hydroxy-tetrahydrodipicolinate synthase
- Sfum\_0467 Phosphopantothenate-cysteine ligase / Phospho
- Sfum\_1570 50S ribosomal protein L6
- Sfum\_3556 NAD-dependent epimerase/dehydratase
- Sfum\_0426 Phosphoribosylaminoimidazolecarboxamide form
- Sfum\_0426 50S ribosomal protein L35
- Sfum\_1581 30S ribosomal protein S4
- Sfum\_2093 Sigma 54 modulator protein / SSU ribosomal pr
- Sfum\_0465 Nucleation efficiency protein NfeD
- Sfum\_1560 50S ribosomal protein L22
- Sfum\_2087 30S ribosomal protein S20
- Sfum\_0100 ATP-dependent Clp protease proteolytic subunit
- Sfum\_1603 Redox-sensing transcriptional repressor Rex
- Sfum\_1423 MJ042 family finger-like protein
- Sfum\_3102 Hydrogenase
- Sfum\_1554 30S ribosomal protein S10
- Sfum\_2581 ATP synthase epsilon chain
- Sfum\_2585 ATP synthase subunit delta
- Sfum\_1665 L-aspartate aminotransferase
- Sfum\_0811 Coenzyme A transferase
- Sfum\_1553 Elongation factor Tu
- Sfum\_1687 N-acetyl-gamma-glutamyl-phosphate reductase
- Sfum\_2586 ATP synthase subunit b
- Sfum\_0428 Phenylalanine-tRNA ligase alpha subunit
- Sfum\_0789 Lipopolysaccharide biosynthesis
- Sfum\_2672 TRAP dicarboxylate transporter-DctP subunit
- Sfum\_1567 50S ribosomal protein L5
- Sfum\_2346 10 kDa chaperonin
- Sfum\_1238 Protein-export membrane protein SecF
- Sfum\_2446 Glycine-tRNA ligase alpha subunit
- Sfum\_1166 2-oxoglutarate ferredoxin oxidoreductase, alpha
- Sfum\_4076 Pyruvate ferredoxin/flavodoxin oxidoreductase
- Sfum\_1467 Putative GAF sensor protein
- Sfum\_2018 Beta-lactamase domain protein
- Sfum\_0920 O-methyltransferase, family 2
- Sfum\_1537 50S ribosomal protein L23
- Sfum\_2174 2-isopropylmalate synthase
- Sfum\_0306 2-isopropylmalate synthase
- Sfum\_2062 Glyceroldehyde-3-phosphate dehydrogenase Ph
- Sfum\_0378 Extracellular ligand-binding receptor
- Sfum\_2377 Imidazolonepropionase
- Sfum\_1709 Thioredoxin reductase
- Sfum\_1923 Short-chain dehydrogenase/reductase SDR
- Sfum\_2173 Aspartokinase
- Sfum\_1240 Protein translocase subunit yajC
- Sfum\_1551 30S ribosomal protein S12
- Sfum\_1548 50S ribosomal protein L7/L12
- Sfum\_0615 Molybdenum cofactor synthesis domain
- Sfum\_2912 Glucosamine-6-phosphate deaminase
- Sfum\_1966 4Fe-4S ferredoxin, iron-sulfur binding domain pr
- Sfum\_1966 CoA-binding domain protein
- Sfum\_1234 Polyribonucleotide nucleotidyltransferase
- Sfum\_1404 3-hydroxyacyl-CoA dehydrogenase / short chain
- Sfum\_0574 Bifunctional uridylyltransferase/uridylyl-removing
- Sfum\_1195 Putative PAS/PAC sensor protein
- Sfum\_1087 Aldehyde dehydrogenase
- Sfum\_1684 Major facilitator superfamily MFS\_1
- Sfum\_3591 Glucose-6-phosphate isomerase
- Sfum\_3097 Glycerol-3-phosphate acyltransferase
- Sfum\_0432 Phosphoribosylglycylaminoimidazole synthase sul
- Sfum\_0108 AMP-dependent synthetase and ligase
- Sfum\_0154 Methionine-tRNA ligase
- Sfum\_2951 Sfum\_3023 Acetolactate synthase
- Sfum\_1745 Uncharacterized protein
- Sfum\_0935 CBS domain containing membrane protein
- Sfum\_3411 Nitrogen-fixing NifU domain protein
- Sfum\_0824 FAD-dependent pyridine nucleotide-disulphide o
- Sfum\_1975 Uncharacterized protein
- Sfum\_0213 DNA topoisomerase 1





**Fig. S6. Heat map of hierarchical clustered proteins produced by *Syntrophobacter fumaroxidans* for propionate degradation.** The proteins are shown in a clustered matrix after automatic hierarchical cluster of rows from row Z-score normalization values. Proteins appear from left to right, in triplicates, according to the growth conditions defined by the electron acceptor used by *S. fumaroxidans* to oxidize propionate: fumarate, sulfate and interspecies compounds transferred to: *Desulfovibrio desulfuricans*, *Methanobacterium formicicum* and *Methanospirillum hungatei*. The colour scale illustrates the relative detection level of each protein across the samples; blue (log ratio -2.5), yellow (log ratio 2.5) and red (log ratio 3) indicate lower and higher levels compared to the average level value 0 (in black). The colour intensity indicates the degree of protein up- or down regulation; the grey colour represents not detected.