

1 Table S2. Putative taxonomic affiliation of [FeFe]-hydrogenase sequences obtained from Prony metagenome P28.

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OTU	MG-RAST ID	Taxonomy (Phylum ; Class ; Order)	Highly similar sequence retrieved from Genbank % similarity (Genbank accession number) Species - clone
P28_hydA157	D4ZHLFP1:60:D2HDNACXX:2:2305:8886:3411:GGATGT	Bacteroidetes; Ignavibacterae; Ignavibacteria	85.9 (YP_006526890) Fe-only hydrogenase, catalytic subunit alpha [<i>Melioribacter roseus</i> P3M-2]
P28_hydA192	D4ZHLFP1:60:D2HDNACXX:2:1111:17909:53680:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	84.3 (WP_010803103) [FeFe] hydrogenase, group A [<i>Parabacteroides</i>]
P28_hydA236	D4ZHLFP1:60:D2HDNACXX:2:2302:10344:19825:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	75.9 (WP_010803103) [FeFe] hydrogenase, group A [<i>Parabacteroides</i>]
P28_hydA276	D4ZHLFP1:60:D2HDNACXX:2:1113:8675:13552:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	89.0 (WP_021928742) hydrogenase Fe-only [<i>Alistipes</i> sp. CAG:831]
P28_hydA342	D4ZHLFP1:60:D2HDNACXX:2:2107:20273:48824:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	81.6 (WP_021928742) hydrogenase Fe-only [<i>Alistipes</i> sp. CAG:831]
P28_hydA35	D4ZHLFP1:60:D2HDNACXX:2:2114:10078:90816:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	73.6 (WP_021928742) hydrogenase Fe-only [<i>Alistipes</i> sp. CAG:831]
P28_hydA357	D4ZHLFP1:60:D2HDNACXX:2:1313:16042:29537:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	63.9 (WP_021928742) hydrogenase Fe-only [<i>Alistipes</i> sp. CAG:831]
P28_hydA445	D4ZHLFP1:60:D2HDNACXX:2:2114:14460:89265:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	86.7 (WP_021928742) hydrogenase Fe-only [<i>Alistipes</i> sp. CAG:831]
P28_hydA96	D4ZHLFP1:60:D2HDNACXX:2:1302:11799:41654:GGATGT	Bacteroidetes; Bacteroidia; Bacteroidales	70.9 (WP_021928742) hydrogenase Fe-only [<i>Alistipes</i> sp. CAG:831]
P28_hydA282	D4ZHLFP1:60:D2HDNACXX:2:1306:12764:45449:GGATGT	Dictyoglomglom; Dictyoglomales	79.3 (YP_002352464) hydrogenase [<i>Dictyoglomus turgidum</i> DSM 6724]
P28_hydA20	D4ZHLFP1:60:D2HDNACXX:2:2309:18606:31980:GGATGT	Eukaryota; Viridiplantae; Chlorophyta	75.1 (XP_001693376) Fe hydrogenase [<i>Chlamydomonas reinhardtii</i>]
P28_hydA344	D4ZHLFP1:60:D2HDNACXX:2:2116:2593:55563:GGATGT	Firmicutes; Bacilli; Lactobacillales	66.6 (WP_010746116) [FeFe] hydrogenase, group A [<i>Enterococcus raffinosus</i>]
P28_hydA261	D4ZHLFP1:60:D2HDNACXX:2:1308:14293:75233:GGATGT	Firmicutes; Clostridia; Clostridiales	62.4 (WP_004629896) hydrogenase, Fe-only [<i>Ruminiclostridium</i>]
P28_hydA268	D4ZHLFP1:60:D2HDNACXX:2:1113:11668:83184:GGATGT	Firmicutes; Clostridia; Clostridiales	91.0 (YP_00113004) hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA171	D4ZHLFP1:60:D2HDNACXX:2:1109:1871:50152:GGATGT	Firmicutes	63.5 (WP_021856760) hydrogenase Fe only [<i>Firmicutes bacterium</i> CAG:555]
P28_hydA27	D4ZHLFP1:60:D2HDNACXX:2:1114:17042:69653:GGATGT	Firmicutes; Clostridia; Clostridiales	91.3 (YP_001111834) hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA269	D4ZHLFP1:60:D2HDNACXX:2:2106:11983:14451:GGATGT	Firmicutes; Clostridia; Clostridiales	70.9 (WP_018660435) Periplasmic [Fe] hydrogenase large subunit [<i>Thermobrachium celere</i>]
P28_hydA271	D4ZHLFP1:60:D2HDNACXX:2:1105:3061:43800:GGATGT	Firmicutes; Clostridia; Clostridiales	53.5 (WP_003640841) hydrogenase, Fe-only [<i>Thermicola potens</i> JR]
P28_hydA272	D4ZHLFP1:60:D2HDNACXX:2:2314:45734:35683:GGATGT	Firmicutes; Clostridia; Clostridiales	70.5 (WP_022278894) hydrogenase Fe-only [<i>Dorea</i> sp. AGR2135]
P28_hydA273	D4ZHLFP1:60:D2HDNACXX:2:2310:14510:53518:GGATGT	Firmicutes; Clostridia; Clostridiales	83.2 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA277	D4ZHLFP1:60:D2HDNACXX:2:2115:13480:35918:GGATGT	Firmicutes; Clostridia; Clostridiales	67.4 (WP_004518295) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA278	D4ZHLFP1:60:D2HDNACXX:2:2110:3525:23785:GGATGT	Firmicutes; Clostridia; Clostridiales	85.9 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA281	D4ZHLFP1:60:D2HDNACXX:2:2107:7774:19512:GGATGT	Firmicutes; Clostridia; Clostridiales	82.4 (WP_004518295) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA283	D4ZHLFP1:60:D2HDNACXX:2:1303:11048:87799:GGATGT	Firmicutes; Clostridia; Clostridiales	74.7 (WP_004969732) hydrogenase, Fe-only [<i>Desulfosporosinus orientis</i> DSM 765]
P28_hydA287	D4ZHLFP1:60:D2HDNACXX:2:1302:16282:18146:GGATGT	Firmicutes; Clostridia; Clostridiales	57.0 (WP_001113004) hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA294	D4ZHLFP1:60:D2HDNACXX:2:2316:11710:32579:GGATGT	Firmicutes; Clostridia; Clostridiales	79.3 (WP_008410064) Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA297	D4ZHLFP1:60:D2HDNACXX:2:1106:18479:88233:GGATGT	Firmicutes; Clostridia; Clostridiales	82.0 (WP_003640841) hydrogenase, Fe-only [<i>Thermicola potens</i> JR]
P28_hydA298	D4ZHLFP1:60:D2HDNACXX:2:2310:11693:54229:GGATGT	Firmicutes; Clostridia; Clostridiales	82.0 (WP_077035) Fe hydrogenase [<i>Symbiobacterium thermophilum</i> IAM 14863]
P28_hydA299	D4ZHLFP1:60:D2HDNACXX:2:2113:15551:3692:GGATGT	Firmicutes; Clostridia; Clostridiales	63.2 (WP_018660435) Periplasmic [Fe] hydrogenase large subunit [<i>Thermobrachium celere</i>]
P28_hydA30	D4ZHLFP1:60:D2HDNACXX:2:1303:3971:69538:GGATGT	Firmicutes; Clostridia; Clostridiales	73.6 (WP_021908252) hydrogenase Fe-only [<i>Eubacterium</i> sp. CAG:146]
P28_hydA301	D4ZHLFP1:60:D2HDNACXX:2:2309:14190:70653:GGATGT	Firmicutes; Clostridia; Clostridiales	80.1 (WP_001113007) hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA303	D4ZHLFP1:60:D2HDNACXX:2:2106:7935:41866:GGATGT	Firmicutes; Clostridia; Clostridiales	87.0 (WP_001212560) hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA304	D4ZHLFP1:60:D2HDNACXX:2:2315:4334:79513:GGATGT	Firmicutes; Clostridia; Clostridiales	84.7 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA305	D4ZHLFP1:60:D2HDNACXX:2:2309:12156:27025:GGATGT	Firmicutes; Clostridia; Clostridiales	90.9 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA306	D4ZHLFP1:60:D2HDNACXX:2:2313:10990:69037:GGATGT	Firmicutes; Clostridia; Clostridiales	95.5 (WP_004545921) hydrogenase Fe-only [<i>Desulfotomaculum ruminis</i> DSM 2154]
P28_hydA307	D4ZHLFP1:60:D2HDNACXX:2:2308:16669:82442:GGATGT	Firmicutes; Clostridia; Clostridiales	89.4 (WP_008410059) Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA309	D4ZHLFP1:60:D2HDNACXX:2:1106:7395:56877:GGATGT	Firmicutes; Clostridia; Clostridiales	72.4 (GAE88237) hydrogenase [<i>Clostridium straminisolvens</i> JCM 21531]
P28_hydA310	D4ZHLFP1:60:D2HDNACXX:2:2306:18542:41819:GGATGT	Firmicutes; Clostridia; Clostridiales	51.2 (WP_003935869) Periplasmic [Fe] hydrogenase large subunit [<i>Clostridium sticklandii</i>]
P28_hydA311	D4ZHLFP1:60:D2HDNACXX:2:2306:18542:41819:GGATGT	Firmicutes; Clostridia; Clostridiales	59.3 (WP_022334732) hydrogenase Fe-only [<i>Clostridium</i> sp. CAG:452]
P28_hydA314	D4ZHLFP1:60:D2HDNACXX:2:2115:15661:25130:GGATGT	Firmicutes; Clostridia; Clostridiales	75.1 (WP_001212560) hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA321	D4ZHLFP1:60:D2HDNACXX:2:1314:6888:24210:GGATGT	Firmicutes; Clostridia; Clostridiales	69.3 (WP_004518295) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA323	D4ZHLFP1:60:D2HDNACXX:2:2311:18724:30480:GGATGT	Firmicutes; Clostridia; Clostridiales	70.9 (WP_004496996) hydrogenase, Fe-only [<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA324	D4ZHLFP1:60:D2HDNACXX:2:1106:14667:21673:GGATGT	Firmicutes; Clostridia; Clostridiales	84.7 (WP_003189750) hydrogenase, Fe-only [<i>Desulfotomaculum acetoxidans</i> DSM 771]
P28_hydA325	D4ZHLFP1:60:D2HDNACXX:2:2115:7933:6640:GGATGT	Firmicutes; Clostridia; Clostridiales	89.4 (WP_021944433) hydrogenase Fe-only [<i>Clostridium</i> sp. CAG:264]
P28_hydA329	D4ZHLFP1:60:D2HDNACXX:2:2306:5267:3583:GGATGT	Firmicutes; Clostridia; Clostridiales	68.9 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA330	D4ZHLFP1:60:D2HDNACXX:2:1108:10790:47267:GGATGT	Firmicutes; Clostridia; Clostridiales	98.0 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA333	D4ZHLFP1:60:D2HDNACXX:2:2304:19319:89346:GGATGT	Firmicutes; Clostridia; Clostridiales	75.9 (WP_023062885) hydrogenase, Fe-only [<i>Clostridium thermocellum</i>]
P28_hydA334	D4ZHLFP1:60:D2HDNACXX:2:2309:8979:10824:GGATGT	Firmicutes; Clostridia; Clostridiales	72.8 (WP_002575948) [FeFe] hydrogenase, group A [<i>LachnoClostridium</i>]
P28_hydA338	D4ZHLFP1:60:D2HDNACXX:2:1111:11445:80970:GGATGT	Firmicutes; Clostridia; Clostridiales	78.6 (WP_023055471) [FeFe] hydrogenase, group A [<i>Peptoniphilus</i> sp. BV3C26]
P28_hydA339	D4ZHLFP1:60:D2HDNACXX:2:1313:16269:20520:GGATGT	Firmicutes; Clostridia; Clostridiales	66.2 (WP_021631077) putative ferredoxin hydrogenase HydA1 [<i>Clostridium</i> sp. ATCC BAA-442]
P28_hydA340	D4ZHLFP1:60:D2HDNACXX:2:1313:20645:57963:GGATGT	Firmicutes; Clostridia; Clostridiales	84.3 (WP_008410064) Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA348	D4ZHLFP1:60:D2HDNACXX:2:1308:18829:65204:GGATGT	Firmicutes; Clostridia; Clostridiales	99.8 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA352	D4ZHLFP1:60:D2HDNACXX:2:2312:20149:17973:GGATGT	Firmicutes; Clostridia; Clostridiales	58.2 (WP_001714748) hydrogenase, Fe-only [<i>Candidatus Desulfuricida audaxviator</i> MP104C]
P28_hydA355	D4ZHLFP1:60:D2HDNACXX:2:1108:1063:76207:GGATGT	Firmicutes; Clostridia; Clostridiales	92.0 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA358	D4ZHLFP1:60:D2HDNACXX:2:2313:12476:75649:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA362	D4ZHLFP1:60:D2HDNACXX:2:2104:11024:30939:GGATGT	Firmicutes; Clostridia; Clostridiales	91.3 (WP_004545925) hydrogenase Fe-only [<i>Desulfotomaculum ruminis</i> DSM 2154]
P28_hydA364	D4ZHLFP1:60:D2HDNACXX:2:2312:11597:12789:GGATGT	Firmicutes; Clostridia; Clostridiales	79.0 (WP_004092838) hydrogenase, Fe-only [<i>Ethanoligenens harbinense</i> YUAN-3]
P28_hydA365	D4ZHLFP1:60:D2HDNACXX:2:2308:6036:12495:GGATGT	Firmicutes; Clostridia; Clostridiales	80.1 (WP_001113007) hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA366	D4ZHLFP1:60:D2HDNACXX:2:2311:79720:97575:GGATGT	Firmicutes; Clostridia; Clostridiales	69.3 (WP_004517644) hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]

P28_hydA367	D4ZHLFP1:60:D2HDNACXX:2:2314:15145:33230:GGATGT	Firmicutes; Clostridia; Clostridiales	88.2	(WP_008410059)	Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA368	D4ZHLFP1:60:D2HDNACXX:2:2109:15313:70001:GGATGT	Firmicutes; Clostridia; Clostridiales	88.6	(WP_008410059)	Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA369	D4ZHLFP1:60:D2HDNACXX:2:1106:17580:24317:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5	(YP_001212560)	hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA370	D4ZHLFP1:60:D2HDNACXX:2:2116:20310:44187:GGATGT	Firmicutes; Clostridia; Clostridiales	94.7	(YP_001212560)	hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA375	D4ZHLFP1:60:D2HDNACXX:2:2107:16775:45547:GGATGT	Firmicutes; Clostridia; Clostridiales	78.2	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA378	D4ZHLFP1:60:D2HDNACXX:2:1313:18604:67031:GGATGT	Firmicutes; Clostridia; Clostridiales	54.7	(YP_00113004)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA379	D4ZHLFP1:60:D2HDNACXX:2:2310:9758:40457:GGATGT	Firmicutes; Clostridia; Clostridiales	72.4	(YP_004518295)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA38	D4ZHLFP1:60:D2HDNACXX:2:1310:3830:87646:GGATGT	Firmicutes; Clostridia; Clostridiales	90.5	(YP_004496996)	hydrogenase, Fe-only [<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA382	D4ZHLFP1:60:D2HDNACXX:2:1110:6113:88488:GGATGT	Firmicutes; Clostridia; Clostridiales	86.7	(YP_007946226)	hydrogenase, Fe-only [<i>Desulfotomaculum gibsoniae</i> DSM 7213]
P28_hydA390	D4ZHLFP1:60:D2HDNACXX:2:1303:16851:39485:GGATGT	Firmicutes; Clostridia; Clostridiales	84.0	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA392	D4ZHLFP1:60:D2HDNACXX:2:2105:4564:41998:GGATGT	Firmicutes; Clostridia; Clostridiales	91.0	(YP_001717478)	hydrogenase, Fe-only [<i>Candidatus Desulfurodus audaxviator</i> MP104C]
P28_hydA394	D4ZHLFP1:60:D2HDNACXX:2:1311:9862:93498:GGATGT	Firmicutes; Clostridia; Clostridiales	94.4	(YP_007946226)	hydrogenase, Fe-only [<i>Desulfotomaculum gibsoniae</i> DSM 7213]
P28_hydA395	D4ZHLFP1:60:D2HDNACXX:2:1315:19794:29264:GGATGT	Firmicutes; Clostridia; Clostridiales	72.4	(YP_004497002)	hydrogenase, Fe-only [<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA399	D4ZHLFP1:60:D2HDNACXX:2:2314:6545:58167:GGATGT	Firmicutes; Clostridia; Clostridiales	67.8	(YP_001036861)	hydrogenase, Fe-only [<i>Clostridium thermoaceticum</i> ATCC 27405]
P28_hydA4	D4ZHLFP1:60:D2HDNACXX:2:1303:7759:53542:GGATGT	Firmicutes; Clostridia; Clostridiales	91.3	(YP_001111834)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA40	D4ZHLFP1:60:D2HDNACXX:2:1306:1645:61729:GGATGT	Firmicutes; Clostridia; Clostridiales	87.8	(WP_008410059)	Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA400	D4ZHLFP1:60:D2HDNACXX:2:1309:6420:91463:GGATGT	Firmicutes; Clostridia; Clostridiales	82.8	(YP_001212560)	hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA404	D4ZHLFP1:60:D2HDNACXX:2:2102:9403:88261:GGATGT	Firmicutes; Clostridia; Clostridiales	61.2	(YP_004518238)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA405	D4ZHLFP1:60:D2HDNACXX:2:2112:4472:70529:GGATGT	Firmicutes; Clostridia; Clostridiales	66.6	(WP_023055471)	[FeFe] hydrogenase, group A [<i>Peptoniphilus</i> sp. BV3C26]
P28_hydA406	D4ZHLFP1:60:D2HDNACXX:2:2105:5939:33002:GGATGT	Firmicutes; Clostridia; Clostridiales	92.4	(YP_001113007)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA408	D4ZHLFP1:60:D2HDNACXX:2:2314:12785:56856:GGATGT	Firmicutes; Clostridia; Clostridiales	73.9	(YP_004496996)	hydrogenase, Fe-only [<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA41	D4ZHLFP1:60:D2HDNACXX:2:1115:4212:75038:GGATGT	Firmicutes; Clostridia; Clostridiales	80.5	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA413	D4ZHLFP1:60:D2HDNACXX:2:1315:19383:15464:GGATGT	Firmicutes; Clostridia; Clostridiales	86.7	(YP_004518238)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA42	D4ZHLFP1:60:D2HDNACXX:2:1303:12690:67984:GGATGT	Firmicutes; Clostridia; Clostridiales	74.7	(YP_00113004)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA423	D4ZHLFP1:60:D2HDNACXX:2:2302:5669:10810:GGATGT	Firmicutes; Clostridia; Clostridiales	83.2	(WP_021908252)	hydrogenase Fe-only [<i>Eubacterium</i> sp. CAG:146]
P28_hydA427	D4ZHLFP1:60:D2HDNACXX:2:2304:15003:48833:GGATGT	Firmicutes; Clostridia; Clostridiales	98.6	(YP_001716352)	hydrogenase, Fe-only [<i>Candidatus Desulfurodus audaxviator</i> MP104C]
P28_hydA429	D4ZHLFP1:60:D2HDNACXX:2:2110:8435:29603:GGATGT	Firmicutes; Clostridia; Clostridiales	78.6	(YP_004518238)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA43	D4ZHLFP1:60:D2HDNACXX:2:1116:16600:90499:GGATGT	Firmicutes; Clostridia; Clostridiales	81.6	(YP_007946226)	hydrogenase, Fe-only [<i>Desulfotomaculum gibsoniae</i> DSM 7213]
P28_hydA432	D4ZHLFP1:60:D2HDNACXX:2:1113:6864:54911:GGATGT	Firmicutes; Clostridia; Clostridiales	79.3	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA435	D4ZHLFP1:60:D2HDNACXX:2:2308:11447:88223:GGATGT	Firmicutes; Clostridia; Clostridiales	52.4	(YP_005045889)	hydrogenase, Fe-only [<i>Clostridium clariflavum</i> DSM 19732]
P28_hydA437	D4ZHLFP1:60:D2HDNACXX:2:2316:19962:48015:GGATGT	Firmicutes; Clostridia; Clostridiales	69.3	(YP_004549525)	hydrogenase Fe-only [<i>Desulfotomaculum ruminis</i> DSM 2154]
P28_hydA442	D4ZHLFP1:60:D2HDNACXX:2:1301:9253:62978:GGATGT	Firmicutes; Clostridia; Clostridiales	77.4	(YP_001113007)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA449	D4ZHLFP1:60:D2HDNACXX:2:1314:2209:70843:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5	(YP_007946226)	hydrogenase, Fe-only [<i>Desulfotomaculum gibsoniae</i> DSM 7213]
P28_hydA450	D4ZHLFP1:60:D2HDNACXX:2:1309:2955:95343:GGATGT	Firmicutes; Clostridia; Clostridiales	73.2	(WP_025056620)	hydrogenase, Fe-only [<i>Clostridium cellulolyticum</i> H10]
P28_hydA453	D4ZHLFP1:60:D2HDNACXX:2:2301:13500:63367:GGATGT	Firmicutes; Clostridia; Clostridiales	65.1	(WP_008373638)	hydrogenase [<i>Coprococcus comes</i>]
P28_hydA454	D4ZHLFP1:60:D2HDNACXX:2:2310:12419:73074:GGATGT	Firmicutes; Clostridia; Clostridiales	82.8	(YP_007946226)	hydrogenase, Fe-only [<i>Desulfotomaculum gibsoniae</i> DSM 7213]
P28_hydA459	D4ZHLFP1:60:D2HDNACXX:2:1314:17708:39938:GGATGT	Firmicutes; Clostridia; Clostridiales	80.9	(YP_004518238)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA46	D4ZHLFP1:60:D2HDNACXX:2:1101:16067:94997:GGATGT	Firmicutes; Clostridia; Clostridiales	92.4	(WP_008410064)	Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA461	D4ZHLFP1:60:D2HDNACXX:2:2306:11974:33002:GGATGT	Firmicutes; Clostridia; Clostridiales	87.8	(YP_004545921)	hydrogenase Fe-only [<i>Desulfotomaculum ruminis</i> DSM 2154]
P28_hydA462	D4ZHLFP1:60:D2HDNACXX:2:1315:2857:77555:GGATGT	Firmicutes; Clostridia; Clostridiales	72.0	(YP_008699055)	hydrogenase, Fe-only [<i>Clostridium autoethanogenum</i> DSM 10061]
P28_hydA463	D4ZHLFP1:60:D2HDNACXX:2:2109:17068:70952:GGATGT	Firmicutes; Clostridia; Clostridiales	53.9	(WP_010244148)	hydrogenase [<i>Acetivibrio cellulolyticus</i>]
P28_hydA464	D4ZHLFP1:60:D2HDNACXX:2:2308:9561:58911:GGATGT	Firmicutes; Clostridia; Clostridiales	74.3	(YP_004518238)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA465	D4ZHLFP1:60:D2HDNACXX:2:2303:8752:77532:GGATGT	Firmicutes; Clostridia; Clostridiales	93.2	(WP_003189750)	hydrogenase, Fe-only [<i>Desulfotomaculum acetoxidans</i> DSM 771]
P28_hydA467	D4ZHLFP1:60:D2HDNACXX:2:2108:12294:80384:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5	(YP_077035)	iron hydrogenase [<i>Symbiobacterium thermophilum</i> IAM 14863]
P28_hydA468	D4ZHLFP1:60:D2HDNACXX:2:1309:18520:11621:GGATGT	Firmicutes; Clostridia; Clostridiales	98.2	(YP_001212560)	hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA471	D4ZHLFP1:60:D2HDNACXX:2:1308:8193:42336:GGATGT	Firmicutes; Clostridia; Clostridiales	99.0	(YP_001716352)	hydrogenase, Fe-only [<i>Candidatus Desulfurodus audaxviator</i> MP104C]
P28_hydA475	D4ZHLFP1:60:D2HDNACXX:2:2313:8363:60911:GGATGT	Firmicutes; Clostridia; Clostridiales	83.2	(YP_004518239)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA50	D4ZHLFP1:60:D2HDNACXX:2:1113:11592:79933:GGATGT	Firmicutes; Clostridia; Clostridiales	82.0	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA51	D4ZHLFP1:60:D2HDNACXX:2:2316:12094:16372:GGATGT	Firmicutes; Clostridia; Clostridiales	74.7	(YP_004518238)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA56	D4ZHLFP1:60:D2HDNACXX:2:1116:9777:2233:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5	(WP_022071136)	hydrogenase Fe-only [<i>Clostridium bartlettii</i> CAG:1329]
P28_hydA66	D4ZHLFP1:60:D2HDNACXX:2:2106:4911:95193:GGATGT	Firmicutes; Clostridia; Clostridiales	81.3	(WP_008410059)	Iron hydrogenase 1 [<i>Desulfotomaculum hydrothermale</i>]
P28_hydA69	D4ZHLFP1:60:D2HDNACXX:2:2304:12327:89856:GGATGT	Firmicutes; Clostridia; Clostridiales	82.8	(YP_001113004)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA73	D4ZHLFP1:60:D2HDNACXX:2:2303:6298:51820:GGATGT	Firmicutes; Clostridia; Clostridiales	61.2	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA75	D4ZHLFP1:60:D2HDNACXX:2:1102:16085:50822:GGATGT	Firmicutes; Clostridia; Clostridiales	70.5	(YP_003640841)	hydrogenase, Fe-only [<i>Thermincula potens</i> JR]
P28_hydA76	D4ZHLFP1:60:D2HDNACXX:2:1113:5070:77194:GGATGT	Firmicutes; Clostridia; Clostridiales	80.9	(YP_004498193)	hydrogenase, Fe-only [<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA79	D4ZHLFP1:60:D2HDNACXX:2:2110:14682:4653:GGATGT	Firmicutes; Clostridia; Clostridiales	82.4	(YP_004517644)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA8	D4ZHLFP1:60:D2HDNACXX:2:2105:19592:29920:GGATGT	Firmicutes; Clostridia; Clostridiales	80.5	(YP_001113004)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA84	D4ZHLFP1:60:D2HDNACXX:2:2114:2666:53657:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5	(YP_008699055)	hydrogenase, Fe-only [<i>Clostridium autoethanogenum</i> DSM 10061]
P28_hydA85	D4ZHLFP1:60:D2HDNACXX:2:2109:19628:92874:GGATGT	Firmicutes; Clostridia; Clostridiales	77.0	(YP_001212560)	hydrogenase subunit [<i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA86	D4ZHLFP1:60:D2HDNACXX:2:1308:8109:90227:GGATGT	Firmicutes; Clostridia; Clostridiales	83.2	(YP_004518239)	hydrogenase, Fe-only [<i>Desulfotomaculum kuznetsovii</i> DSM 6115]
P28_hydA88	D4ZHLFP1:60:D2HDNACXX:2:1303:11762:71086:GGATGT	Firmicutes; Clostridia; Clostridiales	50.8	(YP_003640841)	hydrogenase, Fe-only [<i>Thermincula potens</i> JR]
P28_hydA9	D4ZHLFP1:60:D2HDNACXX:2:1116:4572:23493:GGATGT	Firmicutes; Clostridia; Clostridiales	63.5	(YP_004496996)	hydrogenase, Fe-only [<i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA91	D4ZHLFP1:60:D2HDNACXX:2:1306:14960:38560:GGATGT	Firmicutes; Clostridia; Clostridiales	54.7	(YP_001113004)	hydrogenase [<i>Desulfotomaculum reducens</i> MI-1]
P28_hydA95	D4ZHLFP1:60:D2HDNACXX:2:1301:13034:98797:GGATGT	Firmicutes; Clostridia; Clostridiales	97.0	(YP_001717478)	hydrogenase, Fe-only [<i>Candidatus Desulfurodus audaxviator</i> MP104C]
P28_hydA11	D4ZHLFP1:60:D2HDNACXX:2:1311:11947:31607:GGATGT	Firmicutes; Clostridia; Clostridiales	70.5	(YP_003640841)	hydrogenase, Fe-only [<i>Thermincula potens</i> JR]

P28_hydA113	D4ZHLFP1:60:D2HDNACXX:2:1315:19200:83174:GGATGT	Firmicutes; Clostridia; Clostridiales	97.1	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 771]
P28_hydA116	D4ZHLFP1:60:D2HDNACXX:2:2306:11088:25324:GGATGT	Firmicutes; Clostridia; Clostridiales	93.6	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P28_hydA117	D4ZHLFP1:60:D2HDNACXX:2:2116:3269:29850:GGATGT	Firmicutes; Clostridia; Clostridiales	89.7	(YP_004545921)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P28_hydA121	D4ZHLFP1:60:D2HDNACXX:2:2313:10137:45526:GGATGT	Firmicutes; Clostridia; Clostridiales	90.8	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA123	D4ZHLFP1:60:D2HDNACXX:2:2107:16945:52378:GGATGT	Firmicutes; Clostridia; Clostridiales	91.3	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA124	D4ZHLFP1:60:D2HDNACXX:2:1112:15984:85021:GGATGT	Firmicutes; Clostridia; Clostridiales	89.4	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 771]
P28_hydA126	D4ZHLFP1:60:D2HDNACXX:2:1101:12401:26344:GGATGT	Firmicutes; Clostridia; Clostridiales	93.6	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA127	D4ZHLFP1:60:D2HDNACXX:2:2114:18376:91305:GGATGT	Firmicutes; Clostridia; Clostridiales	85.1	(YP_004497002)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P28_hydA130	D4ZHLFP1:60:D2HDNACXX:2:2111:20908:32283:GGATGT	Firmicutes; Clostridia; Clostridiales	89.0	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P28_hydA134	D4ZHLFP1:60:D2HDNACXX:2:1114:16202:5057:GGATGT	Firmicutes; Clostridia; Clostridiales	69.7	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA137	D4ZHLFP1:60:D2HDNACXX:2:2102:3729:17264:GGATGT	Firmicutes; Clostridia; Clostridiales	79.3	(YP_001212560)	hydrogenase subunit [Pelotomaculum thermopropionicum SI]
P28_hydA139	D4ZHLFP1:60:D2HDNACXX:2:1108:11575:34060:GGATGT	Firmicutes; Clostridia; Clostridiales	66.2	(WP_023062885)	hydrogenase, Fe-only [Clostridium thermocellum]
P28_hydA14	D4ZHLFP1:60:D2HDNACXX:2:1304:3003:11855:GGATGT	Firmicutes; Clostridia; Clostridiales	77.0	(YP_004969732)	hydrogenase, Fe-only [Desulfovorusinus orientis DSM 765]
P28_hydA144	D4ZHLFP1:60:D2HDNACXX:2:2316:10303:37616:GGATGT	Firmicutes; Clostridia; Clostridiales	90.1	(YP_001113007)	hydrogenase [Desulfotomaculum reducens MI-1]
P28_hydA145	D4ZHLFP1:60:D2HDNACXX:2:2310:1848:85387:GGATGT	Firmicutes; Clostridia; Clostridiales	78.6	(YP_001212560)	hydrogenase subunit [Pelotomaculum thermopropionicum SI]
P28_hydA146	D4ZHLFP1:60:D2HDNACXX:2:2304:4583:85850:GGATGT	Firmicutes; Clostridia; Clostridiales	87.4	(YP_004545921)	hydrogenase, Fe-only [Desulfotomaculum ruminis DSM 2154]
P28_hydA147	D4ZHLFP1:60:D2HDNACXX:2:2108:19118:60589:GGATGT	Firmicutes; Clostridia; Clostridiales	84.3	(WP_022038410)	hydrogenase Fe-only [Ruminococcus gnavus CAG:126]
P28_hydA150	D4ZHLFP1:60:D2HDNACXX:2:2303:14872:83867:GGATGT	Firmicutes; Clostridia; Clostridiales	82.4	(YP_001716352)	hydrogenase, Fe-only [Candidatus Desulfoturillus audaxviator MP104C]
P28_hydA152	D4ZHLFP1:60:D2HDNACXX:2:1316:19452:70846:GGATGT	Firmicutes; Clostridia; Clostridiales	74.7	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA160	D4ZHLFP1:60:D2HDNACXX:2:2111:19543:12745:GGATGT	Firmicutes; Clostridia; Clostridiales	75.9	(WP_023055471)	[FeFe] hydrogenase, group A [Peptoniphilus sp. BV3C26]
P28_hydA162	D4ZHLFP1:60:D2HDNACXX:2:1313:8325:90007:GGATGT	Firmicutes; Clostridia; Clostridiales	85.9	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P28_hydA165	D4ZHLFP1:60:D2HDNACXX:2:1315:17668:96907:GGATGT	Firmicutes; Clostridia; Clostridiales	88.6	(YP_003828850)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabicum DSM 5501]
P28_hydA166	D4ZHLFP1:60:D2HDNACXX:2:1304:14131:84579:GGATGT	Firmicutes; Clostridia; Clostridiales	76.6	(YP_007946226)	hydrogenase, Fe-only [Desulfotomaculum gibsoniae DSM 7213]
P28_hydA167	D4ZHLFP1:60:D2HDNACXX:2:1312:17917:68044:GGATGT	Firmicutes; Clostridia; Clostridiales	57.4	(WP_023062885)	hydrogenase, Fe-only [Clostridium thermocellum]
P28_hydA168	D4ZHLFP1:60:D2HDNACXX:2:1312:6724:38486:GGATGT	Firmicutes; Clostridia; Clostridiales	92.0	(YP_004518293)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA17	D4ZHLFP1:60:D2HDNACXX:2:2114:16346:87258:GGATGT	Firmicutes; Clostridia; Clostridiales	77.4	(YP_004545921)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P28_hydA172	D4ZHLFP1:60:D2HDNACXX:2:21104:17994:78933:GGATGT	Firmicutes; Clostridia; Clostridiales	82.8	(WP_022288920)	putative uptake hydrogenase subunit HupA [Oscillibacter sp. CAG:155]
P28_hydA173	D4ZHLFP1:60:D2HDNACXX:2:2316:17949:94326:GGATGT	Firmicutes; Clostridia; Clostridiales	81.6	(YP_007715799)	hydrogenase [Clostridium asparagiforme]
P28_hydA175	D4ZHLFP1:60:D2HDNACXX:2:2318:18562:77270:GGATGT	Firmicutes; Clostridia; Clostridiales	88.2	(YP_004092838)	hydrogenase, Fe-only [Ethanologenins harbinense YUAN-3]
P28_hydA178	D4ZHLFP1:60:D2HDNACXX:2:1108:17079:23070:GGATGT	Firmicutes; Clostridia; Clostridiales	94.7	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 771]
P28_hydA18	D4ZHLFP1:60:D2HDNACXX:2:1116:9957:88271:GGATGT	Firmicutes; Clostridia; Clostridiales	68.6	(YP_001318525)	hydrogenase, Fe-only [Alkaliphilus metallireducens QYMF]
P28_hydA188	D4ZHLFP1:60:D2HDNACXX:2:1110:10828:80546:GGATGT	Firmicutes; Clostridia; Clostridiales	74.7	(WP_016146995)	hypothetical protein [Butyrivibrio pullicaeorum]
P28_hydA191	D4ZHLFP1:60:D2HDNACXX:2:1315:12108:32506:GGATGT	Firmicutes; Clostridia; Clostridiales	69.3	(WP_02194567)	Fe-only hydrogenase catalytic subunit alpha [Clostridium sp. CAG:967]
P28_hydA193	D4ZHLFP1:60:D2HDNACXX:2:1316:2809:12394:GGATGT	Firmicutes; Clostridia; Clostridiales	74.7	(YP_004545925)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P28_hydA194	D4ZHLFP1:60:D2HDNACXX:2:1115:12420:59393:GGATGT	Firmicutes; Clostridia; Clostridiales	90.1	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P28_hydA196	D4ZHLFP1:60:D2HDNACXX:2:2308:4906:84336:GGATGT	Firmicutes; Clostridia; Clostridiales	86.3	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA2	D4ZHLFP1:60:D2HDNACXX:2:2115:20070:69253:GGATGT	Firmicutes; Clostridia; Clostridiales	82.4	(WP_001212560)	hydrogenase subunit [Pelotomaculum thermopropionicum SI]
P28_hydA200	D4ZHLFP1:60:D2HDNACXX:2:2109:13328:77971:GGATGT	Firmicutes; Clostridia; Clostridiales	50.1	(WP_0212560)	hydrogenase subunit [Pelotomaculum thermopropionicum SI]
P28_hydA202	D4ZHLFP1:60:D2HDNACXX:2:1108:7452:41914:GGATGT	Firmicutes; Clostridia; Clostridiales	69.7	(WP_023062885)	hydrogenase, Fe-only [Clostridium thermocellum]
P28_hydA203	D4ZHLFP1:60:D2HDNACXX:2:2314:8087:63697:GGATGT	Firmicutes; Clostridia; Clostridiales	86.7	(YP_007946226)	hydrogenase, Fe-only [Desulfotomaculum gibsoniae DSM 7213]
P28_hydA205	D4ZHLFP1:60:D2HDNACXX:2:1112:11042:33174:GGATGT	Firmicutes; Clostridia; Clostridiales	79.3	(YP_004545921)	hydrogenase Fe-only [Desulfotomaculum ruminis DSM 2154]
P28_hydA209	D4ZHLFP1:60:D2HDNACXX:2:1107:15147:89949:GGATGT	Firmicutes; Clostridia; Clostridiales	62.8	(YP_754500)	NADH dehydrogenase I subunit G [Syntrophomonas wolfei subsp. wolfei str. Goettingen G311]
P28_hydA211	D4ZHLFP1:60:D2HDNACXX:2:2115:15:4317:46474:GGATGT	Firmicutes; Clostridia; Clostridiales	98.6	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA214	D4ZHLFP1:60:D2HDNACXX:2:1112:2518:55363:GGATGT	Firmicutes; Clostridia; Clostridiales	91.7	(GAE88236)	hydrogenase [Clostridium straminisolvens JCM 21531]
P28_hydA221	D4ZHLFP1:60:D2HDNACXX:2:2115:6996:51259:GGATGT	Firmicutes; Clostridia; Clostridiales	82.8	(YP_004496996)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P28_hydA223	D4ZHLFP1:60:D2HDNACXX:2:1311:20330:21663:GGATGT	Firmicutes; Clostridia; Clostridiales	77.8	(YP_004497002)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P28_hydA224	D4ZHLFP1:60:D2HDNACXX:2:2111:19537:17191:GGATGT	Firmicutes; Clostridia; Clostridiales	73.9	(WP_004630049)	hydrogenase, Fe-only [Clostridium termitidis]
P28_hydA225	D4ZHLFP1:60:D2HDNACXX:2:1308:15996:39808:GGATGT	Firmicutes; Clostridia; Clostridiales	79.7	(YP_003189750)	hydrogenase, Fe-only [Desulfotomaculum acetoxidans DSM 771]
P28_hydA226	D4ZHLFP1:60:D2HDNACXX:2:1113:12356:62433:GGATGT	Firmicutes; Clostridia; Clostridiales	95.5	(WP_0064440667)	ferredoxin [Clostridium hylomenae]
P28_hydA230	D4ZHLFP1:60:D2HDNACXX:2:2310:11723:51125:GGATGT	Firmicutes; Clostridia; Clostridiales	68.6	(WP_003779039)	oxidoreductase [Clostridium ljungdahlii DSM 13528]
P28_hydA231	D4ZHLFP1:60:D2HDNACXX:2:2311:17268:51711:GGATGT	Firmicutes; Clostridia; Clostridiales	58.9	(YP_004496996)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P28_hydA238	D4ZHLFP1:60:D2HDNACXX:2:1112:6714:70609:GGATGT	Firmicutes; Clostridia; Clostridiales	97.0	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA242	D4ZHLFP1:60:D2HDNACXX:2:1304:6732:92947:GGATGT	Firmicutes; Clostridia; Clostridiales	84.0	(YP_004497002)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P28_hydA241	D4ZHLFP1:60:D2HDNACXX:2:2101:6362:31381:GGATGT	Firmicutes; Clostridia; Clostridiales	80.1	(YP_004517644)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA242	D4ZHLFP1:60:D2HDNACXX:2:2113:6122:96554:GGATGT	Firmicutes; Clostridia; Clostridiales	75.5	(YP_004518295)	hydrogenase, Fe-only [Desulfotomaculum kuznetsovii DSM 6115]
P28_hydA246	D4ZHLFP1:60:D2HDNACXX:2:1315:18621:94191:GGATGT	Firmicutes; Clostridia; Clostridiales	84.3	(YP_007946226)	hydrogenase, Fe-only [Desulfotomaculum gibsoniae DSM 7213]
P28_hydA247	D4ZHLFP1:60:D2HDNACXX:2:1108:2356:26602:GGATGT	Firmicutes; Clostridia; Clostridiales	82.4	(WP_021908252)	hydrogenase, Fe-only [Eubacterium sp. CAG:146]
P28_hydA248	D4ZHLFP1:60:D2HDNACXX:2:1105:4287:47028:GGATGT	Firmicutes; Clostridia; Clostridiales	72.4	(YP_001212560)	hydrogenase subunit [Pelotomaculum thermopropionicum SI]
P28_hydA249	D4ZHLFP1:60:D2HDNACXX:2:2109:14906:83643:GGATGT	Firmicutes; Clostridia; Clostridiales	59.7	(WP_021675481)	putative ferredoxin hydrogenase [Peptostreptococcaceae bacterium oral taxon 113]
P28_hydA250	D4ZHLFP1:60:D2HDNACXX:2:1302:11377:92286:GGATGT	Firmicutes; Clostridia; Clostridiales	93.0	(YP_004545921)	hydrogenase, Fe-only [Desulfotomaculum ruminis DSM 2154]
P28_hydA253	D4ZHLFP1:60:D2HDNACXX:2:1102:2651:71684:GGATGT	Firmicutes; Clostridia; Clostridiales	81.6	(YP_007947570)	hydrogenase, Fe-only [Desulfotomaculum gibsoniae DSM 7213]
P28_hydA289	D4ZHLFP1:60:D2HDNACXX:2:1116:10190:42803:GGATGT	Firmicutes; Clostridia; Clostridiales	47.0	(YP_001113004)	hydrogenase [Desulfotomaculum reducens MI-1]
P28_hydA102	D4ZHLFP1:60:D2HDNACXX:2:2115:5878:10051:GGATGT	Firmicutes; Clostridia; Clostridiales	83.2	(YP_004498193)	hydrogenase, Fe-only [Desulfotomaculum carboxydivorans CO-1-SRB]
P28_hydA110	D4ZHLFP1:60:D2HDNACXX:2:2109:4033:21864:GGATGT	Firmicutes; Clostridia; Clostridiales	72.8	(WP_008410059)	Iron hydrogenase 1 [Desulfotomaculum hydrothermale]
P28_hydA13	D4ZHLFP1:60:D2HDNACXX:2:1301:7743:36721:GGATGT	Firmicutes; Clostridia; Clostridiales	67.0	(GAE88236)	hydrogenase [Clostridium straminisolvens JCM 21531]

P28_hydA240	D4ZHLFP1:60:D2HDNACXX:2:1102:10549:18234:GGATGT	Firmicutes; Clostridia; Halanaerobiales	84.7	(YP_003828850)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA262	D4ZHLFP1:60:D2HDNACXX:2:1311:7479:6204:GGATGT	Firmicutes; Clostridia; Halanaerobiales	56.6	(YP_003826883)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA280	D4ZHLFP1:60:D2HDNACXX:2:2315:18278:80300:GGATGT	Firmicutes; Clostridia; Halanaerobiales	91.7	(YP_003828451)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Acetohalobium arabaticum DSM 5501]
P28_hydA31	D4ZHLFP1:60:D2HDNACXX:2:2305:8863:73684:GGATGT	Firmicutes; Clostridia; Halanaerobiales	75.1	(YP_007316252)	hydrogenase, Fe-only [Halobacteroides halobius DSM 5150]
P28_hydA313	D4ZHLFP1:60:D2HDNACXX:2:1107:5724:58972:GGATGT	Firmicutes; Clostridia; Halanaerobiales	87.8	(YP_005836915)	NAD(P)-dependent iron-only hydrogenase iron-sulfur protein [Halanaerobium praevalens DSM 2228]
P28_hydA328	D4ZHLFP1:60:D2HDNACXX:2:1103:3193:8355:GGATGT	Firmicutes; Clostridia; Halanaerobiales	86.3	(YP_003828850)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA336	D4ZHLFP1:60:D2HDNACXX:2:1106:16335:17264:GGATGT	Firmicutes; Clostridia; Halanaerobiales	54.7	(YP_005836913)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Halanaerobium praevalens DSM 2228]
P28_hydA353	D4ZHLFP1:60:D2HDNACXX:2:1112:11959:67712:GGATGT	Firmicutes; Clostridia; Halanaerobiales	53.5	(YP_007316252)	hydrogenase, Fe-only [Halobacteroides halobius DSM 5150]
P28_hydA372	D4ZHLFP1:60:D2HDNACXX:2:2107:9997:60658:GGATGT	Firmicutes; Clostridia; Halanaerobiales	77.4	(YP_003828850)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA419	D4ZHLFP1:60:D2HDNACXX:2:1313:15899:71497:GGATGT	Firmicutes; Clostridia; Halanaerobiales	68.9	(YP_005836915)	NAD(P)-dependent iron-sulfur protein [Halanaerobium praevalens DSM 2228]
P28_hydA425	D4ZHLFP1:60:D2HDNACXX:2:2103:7854:41623:GGATGT	Firmicutes; Clostridia; Halanaerobiales	61.2	(YP_005836915)	NAD(P)-dependent iron-only hydrogenase iron-sulfur protein [Halanaerobium praevalens DSM 2228]
P28_hydA55	D4ZHLFP1:60:D2HDNACXX:2:2307:15234:42821:GGATGT	Firmicutes; Clostridia; Halanaerobiales	69.7	(YP_003826885)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA80	D4ZHLFP1:60:D2HDNACXX:2:2305:7709:26197:GGATGT	Firmicutes; Clostridia; Halanaerobiales	78.6	(YP_003828850)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Acetohalobium arabaticum DSM 5501]
P28_hydA143	D4ZHLFP1:60:D2HDNACXX:2:1312:17755:31435:GGATGT	Firmicutes; Clostridia; Halanaerobiales	73.9	(YP_003826883)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA151	D4ZHLFP1:60:D2HDNACXX:2:1306:8606:79764:GGATGT	Firmicutes; Clostridia; Halanaerobiales	65.5	(YP_005836913)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Halanaerobium praevalens DSM 2228]
P28_hydA15	D4ZHLFP1:60:D2HDNACXX:2:2306:2069:49841:GGATGT	Firmicutes; Clostridia; Halanaerobiales	63.5	(WP_018249208)	NADH dehydrogenase [Orenia marismortui]
P28_hydA120	D4ZHLFP1:60:D2HDNACXX:2:2111:6873:11974:GGATGT	Firmicutes; Clostridia; Halanaerobiales	57.0	(YP_003826883)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA158	D4ZHLFP1:60:D2HDNACXX:2:1107:14111:95140:GGATGT	Firmicutes; Clostridia; Halanaerobiales	53.9	(YP_003826885)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Acetohalobium arabaticum DSM 5501]
P28_hydA177	D4ZHLFP1:60:D2HDNACXX:2:1114:17220:95674:GGATGT	Firmicutes; Clostridia; Halanaerobiales	80.1	(YP_003828850)	NAD(P)-dependent iron-only hydrogenase [Acetohalobium arabaticum DSM 5501]
P28_hydA218	D4ZHLFP1:60:D2HDNACXX:2:2116:15353:54799:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	81.6	(YP_430562)	Iron hydrogenase, small subunit [Moorella thermoacetica ATCC 39073]
P28_hydA259	D4ZHLFP1:60:D2HDNACXX:2:1304:15254:15255:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	81.3	(WP_004401666)	hydrogenase, Fe-only [Thermoanaerobacter thermohydroxyluricus]
P28_hydA284	D4ZHLFP1:60:D2HDNACXX:2:1302:4272:3726:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	84.0	(YP_004461911)	hydrogenase, Fe-only [Tepidanaerobacter acetatoxydans Re1]
P28_hydA285	D4ZHLFP1:60:D2HDNACXX:2:1116:10437:74421:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	73.6	(GAF24846)	Fe-only hydrogenase large subunit, C-terminal domain [Moorella thermoacetica Y72]
P28_hydA286	D4ZHLFP1:60:D2HDNACXX:2:2301:14265:87761:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	67.4	(YP_004461324)	hydrogenase, Fe-only [Tepidanaerobacter acetatoxydans Re1]
P28_hydA288	D4ZHLFP1:60:D2HDNACXX:2:1108:9442:99025:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	59.3	(YP_003239720)	hydrogenase, Fe-only [Ammonifex degensii KC4]
P28_hydA300	D4ZHLFP1:60:D2HDNACXX:2:2307:5041:20659:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	68.9	(GAF24846)	Fe-only hydrogenase large subunit, C-terminal domain [Moorella thermoacetica Y72]
P28_hydA308	D4ZHLFP1:60:D2HDNACXX:2:2304:10101:67081:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	79.0	(YP_002246551)	hydrogenase [Coprothermobacter proteolyticus DSM 5265]
P28_hydA32	D4ZHLFP1:60:D2HDNACXX:2:1316:17659:45702:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	82.0	(GAF24846)	Fe-only hydrogenase large subunit, C-terminal domain [Moorella thermoacetica Y72]
P28_hydA327	D4ZHLFP1:60:D2HDNACXX:2:1308:16700:99537:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	73.2	(YP_003825085)	NAD(P)-dependent iron-only hydrogenase [Thermoselminibacter oceanii DSM 16646]
P28_hydA383	D4ZHLFP1:60:D2HDNACXX:2:2315:12231:55852:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	73.9	(YP_001180640)	hydrogenase, Fe-only [Caldicellulosiruptor saccharolyticus DSM 8903]
P28_hydA39	D4ZHLFP1:60:D2HDNACXX:2:2103:7070:24853:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	69.3	(YP_001180640)	hydrogenase, Fe-only [Caldicellulosiruptor saccharolyticus DSM 8903]
P28_hydA393	D4ZHLFP1:60:D2HDNACXX:2:1305:9485:70857:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	70.1	(YP_004461326)	NAD(P)-dependent iron-only hydrogenase iron-sulfur protein [Tepidanaerobacter acetatoxydans Re1]
P28_hydA411	D4ZHLFP1:60:D2HDNACXX:2:2111:8329:58755:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	72.4	(YP_002246551)	hydrogenase [Coprothermobacter proteolyticus DSM 5265]
P28_hydA434	D4ZHLFP1:60:D2HDNACXX:2:2303:15736:81598:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	72.4	(YP_002246551)	hydrogenase [Coprothermobacter proteolyticus DSM 5265]
P28_hydA451	D4ZHLFP1:60:D2HDNACXX:2:2314:3668:64579:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	88.2	(YP_007298421)	hydrogenase, Fe-only [Thermoanaerobacterium thermosaccharolyticum M0795]
P28_hydA466	D4ZHLFP1:60:D2HDNACXX:2:1308:11913:50654:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	85.5	(YP_004463270)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Mahella australiensis 50-1 BON]
P28_hydA469	D4ZHLFP1:60:D2HDNACXX:2:1303:16259:55923:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	69.7	(GAF24846)	Fe-only hydrogenase large subunit [Moorella thermoacetica Y72]
P28_hydA470	D4ZHLFP1:60:D2HDNACXX:2:2106:4343:70694:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	75.9	(GAF24846)	Fe-only hydrogenase large subunit [Moorella thermoacetica Y72]
P28_hydA60	D4ZHLFP1:60:D2HDNACXX:2:2115:7729:59693:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	94.0	(YP_004438253)	hydrogenase, Fe-only [Thermodesulfobium narugense DSM 14796]
P28_hydA98	D4ZHLFP1:60:D2HDNACXX:2:2305:19517:28054:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	59.3	(YP_001180640)	hydrogenase, Fe-only [Caldicellulosiruptor saccharolyticus DSM 8903]
P28_hydA184	D4ZHLFP1:60:D2HDNACXX:2:1306:7062:27269:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	77.8	(YP_003239720)	hydrogenase, Fe-only [Ammonifex degensii KC4]
P28_hydA164	D4ZHLFP1:60:D2HDNACXX:2:2301:9841:57513:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	79.3	(YP_002246551)	hydrogenase [Coprothermobacter proteolyticus DSM 5265]
P28_hydA21	D4ZHLFP1:60:D2HDNACXX:2:2108:11337:43438:GGATGT	Firmicutes; Clostridia; Thermoanaerobacterales	95.5	(YP_007298421)	hydrogenase, Fe-only [Thermoanaerobacterium thermosaccharolyticum M0795]
P28_hydA212	D4ZHLFP1:60:D2HDNACXX:2:2109:7268:98405:GGATGT	Firmicutes; Negativicutes; Selenomonadales	81.3	(WP_021167212)	NADP-reducing hydrogenase subunit Hndc [Sporomusa ovata]
P28_hydA291	D4ZHLFP1:60:D2HDNACXX:2:1314:7803:60983:GGATGT	Firmicutes; Negativicutes; Selenomonadales	50.1	(WP_021167102)	NADP-reducing hydrogenase subunit Hndc [Sporomusa ovata]
P28_hydA0	D4ZHLFP1:60:D2HDNACXX:2:1107:8897:81612:GGATGT	Firmicutes; Negativicutes; Selenomonadales	40.0	(ET592418)	[FeFe] hydrogenase, group A [Veillonella sp. AS16]
P28_hydA103	D4ZHLFP1:60:D2HDNACXX:2:1108:18262:37422:GGATGT	Firmicutes; Negativicutes; Selenomonadales	56.6	(WP_021167212)	NADP-reducing hydrogenase subunit Hndc [Sporomusa ovata]
P28_hydA106	D4ZHLFP1:60:D2HDNACXX:2:2111:6537:97386:GGATGT	Firmicutes; Negativicutes; Selenomonadales	42.0	(ET592418)	[FeFe] hydrogenase, group A [Veillonella sp. AS16]
P28_hydA109	D4ZHLFP1:60:D2HDNACXX:2:1101:12380:24778:GGATGT	Firmicutes; Negativicutes; Selenomonadales	70.5	(WP_021167102)	NADP-reducing hydrogenase subunit Hndc [Sporomusa ovata]
P28_hydA403	D4ZHLFP1:60:D2HDNACXX:2:2313:4078:52817:GGATGT	Fusobacteria; Fusobacteriales	84.0	(YP_003966824)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Ilyobacter polytopus DSM 2926]
P28_hydA180	D4ZHLFP1:60:D2HDNACXX:2:2309:6802:75822:GGATGT	Ignavibacteriia; Ignavibacteriales	87.4	(YP_005845237)	Iron-only hydrogenase large subunit [Ignavibacterium album JCM 16511]
P28_hydA243	D4ZHLFP1:60:D2HDNACXX:2:2314:9574:61300:GGATGT	Ignavibacteriia; Ignavibacteriales	87.0	(YP_006526890)	Fe-only hydrogenase, catalytic subunit alpha [Meliobacter roseus P3M-2]
P28_hydA33	D4ZHLFP1:60:D2HDNACXX:2:1310:8731:83856:GGATGT	Ignavibacteriia; Ignavibacteriales	75.9	(YP_005845237)	Fe-only hydrogenase large subunit [Ignavibacterium album JCM 16511]
P28_hydA118	D4ZHLFP1:60:D2HDNACXX:2:2111:2061:77159:GGATGT	Deltaproteobacteria; Desulfobacterales	88.6	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA138	D4ZHLFP1:60:D2HDNACXX:2:1311:13431:91130:GGATGT	Deltaproteobacteria; Desulfobacterales	82.8	(YP_002952160)	Fe hydrogenase [Desulfovibrio magnetricus RS-1]
P28_hydA142	D4ZHLFP1:60:D2HDNACXX:2:2107:9900:26341:GGATGT	Deltaproteobacteria; Desulfobacterales	77.8	(WP_023407578)	hypothetical protein [uncultured Desulfotilus sp. PB-SRB1]
P28_hydA206	D4ZHLFP1:60:D2HDNACXX:2:1310:16127:97033:GGATGT	Deltaproteobacteria; Desulfobacterales	63.9	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA223	D4ZHLFP1:60:D2HDNACXX:2:2311:4184:36432:GGATGT	Deltaproteobacteria; Desulfobacterales	86.3	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA25	D4ZHLFP1:60:D2HDNACXX:2:2102:9683:12556:GGATGT	Deltaproteobacteria; Desulfobacterales	79.7	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA258	D4ZHLFP1:60:D2HDNACXX:2:2108:11702:74298:GGATGT	Deltaproteobacteria; Desulfobacterales	63.9	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA421	D4ZHLFP1:60:D2HDNACXX:2:2316:12545:22203:GGATGT	Deltaproteobacteria; Desulfobacterales	69.7	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA436	D4ZHLFP1:60:D2HDNACXX:2:1105:10075:54351:GGATGT	Deltaproteobacteria; Desulfobacterales	61.6	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA440	D4ZHLFP1:60:D2HDNACXX:2:1308:9791:16364:GGATGT	Deltaproteobacteria; Desulfobacterales	87.4	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA448	D4ZHLFP1:60:D2HDNACXX:2:2308:11112:4719:GGATGT	Deltaproteobacteria; Desulfobacterales	52.0	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]
P28_hydA58	D4ZHLFP1:60:D2HDNACXX:2:2308:11112:4719:GGATGT	Deltaproteobacteria; Desulfobacterales	66.2	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [Desulfobulbus propionicus DSM 2032]

P28_hydA354	D4ZHLFP1:60:D2HDNACXX:2:1308:15477:10829:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	90.1	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfovibrio magneticus</i>]
P28_hydA389	D4ZHLFP1:60:D2HDNACXX:2:2315:17485:12079:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	85.9	(YP_002952160)	Fe hydrogenase [<i>Desulfovibrio magneticus RS-1</i>]
P28_hydA391	D4ZHLFP1:60:D2HDNACXX:2:2115:13942:46150:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	83.6	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus DSM 2032</i>]
P28_hydA44	D4ZHLFP1:60:D2HDNACXX:2:1105:16776:32194:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	77.4	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfovibrio magneticus</i>]
P28_hydA446	D4ZHLFP1:60:D2HDNACXX:2:1316:8749:40017:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	88.2	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfovibrio magneticus</i>]
P28_hydA64	D4ZHLFP1:60:D2HDNACXX:2:2302:1649:3807:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	95.5	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfovibrio magneticus</i>]
P28_hydA83	D4ZHLFP1:60:D2HDNACXX:2:1312:9567:93217:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	55.1	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfovibrio magneticus</i>]
P28_hydA295	D4ZHLFP1:60:D2HDNACXX:2:1312:7905:70603:GGATGT	<i>Deltaproteobacteria; Desulfuromonadales</i>	62.0	(YP_901164)	hydrogenase, Fe-only [<i>Pelobacter propionicus DSM 2379</i>]
P28_hydA256	D4ZHLFP1:60:D2HDNACXX:2:1101:7156:4545:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	93.2	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans MPOB</i>]
P28_hydA401	D4ZHLFP1:60:D2HDNACXX:2:1111:5768:93829:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	95.0	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans MPOB</i>]
P28_hydA441	D4ZHLFP1:60:D2HDNACXX:2:1102:8008:40859:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	84.3	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans MPOB</i>]
P28_hydA416	D4ZHLFP1:60:D2HDNACXX:2:2111:21254:19461:GGATGT	<i>Deltaproteobacteria; Desulfovibionales</i>	50.1	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus DSM 2032</i>]
P28_hydA455	D4ZHLFP1:60:D2HDNACXX:2:2310:9367:11409:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	62.4	(YP_462897)	2Fe-2S and 4Fe-4S iron-sulfur protein [<i>Syntrophus aciditrophicus SB</i>]
P28_hydA458	D4ZHLFP1:60:D2HDNACXX:2:1107:6062:45666:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	71.6	(YP_462897)	2Fe-2S and 4Fe-4S iron-sulfur protein [<i>Syntrophus aciditrophicus SB</i>]
P28_hydA57	D4ZHLFP1:60:D2HDNACXX:2:1307:18676:50166:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	78.6	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans MPOB</i>]
P28_hydA67	D4ZHLFP1:60:D2HDNACXX:2:1108:2150:17747:GGATGT	<i>Deltaproteobacteria; Syntrophobacterales</i>	87.8	(YP_844976)	hydrogenase, Fe-only [<i>Syntrophobacter fumaroxidans MPOB</i>]
P28_hydA101	D4ZHLFP1:60:D2HDNACXX:2:1108:15132:54838:GGATGT	<i>Deltaproteobacteria; Desulfovibrionales</i>	86.3	(WP_006921111)	hydrogenase, Fe-only, partial [<i>Desulfovibrio magneticus</i>]
P28_hydA140	D4ZHLFP1:60:D2HDNACXX:2:2311:12290:15501:GGATGT	<i>Deltaproteobacteria; Desulfovibionales</i>	50.1	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus DSM 2032</i>]
P28_hydA149	D4ZHLFP1:60:D2HDNACXX:2:2109:3943:11784:GGATGT	<i>Deltaproteobacteria; Desulfovibionales</i>	88.6	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus DSM 2032</i>]
P28_hydA15	D4ZHLFP1:60:D2HDNACXX:2:2114:13414:98639:GGATGT	<i>Deltaproteobacteria; Desulfuromonadales</i>	83.6	(YP_901164)	hydrogenase, Fe-only [<i>Pelobacter propionicus DSM 2379</i>]
P28_hydA16	D4ZHLFP1:60:D2HDNACXX:2:2116:6328:14789:GGATGT	<i>Deltaproteobacteria; Desulfovibionales</i>	63.9	(YP_004195044)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Desulfobulbus propionicus DSM 2032</i>]
P28_hydA197	D4ZHLFP1:60:D2HDNACXX:2:2101:14114:73636:GGATGT	<i>Spirochaetes; Spirochaetales</i>	93.6	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA210	D4ZHLFP1:60:D2HDNACXX:2:2302:1998:88206:GGATGT	<i>Spirochaetes; Spirochaetales</i>	79.7	(YP_003802215)	hydrogenase, Fe-only [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA217	D4ZHLFP1:60:D2HDNACXX:2:2303:12031:86571:GGATGT	<i>Spirochaetes; Spirochaetales</i>	88.2	(YP_003802215)	hydrogenase, Fe-only [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA227	D4ZHLFP1:60:D2HDNACXX:2:1311:8720:79761:GGATGT	<i>Spirochaetes; Spirochaetales</i>	72.0	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA229	D4ZHLFP1:60:D2HDNACXX:2:1110:6655:64887:GGATGT	<i>Spirochaetes; Spirochaetales</i>	80.9	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA237	D4ZHLFP1:60:D2HDNACXX:2:2107:8025:67535:GGATGT	<i>Spirochaetes; Spirochaetales</i>	97.4	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA251	D4ZHLFP1:60:D2HDNACXX:2:2115:16128:90091:GGATGT	<i>Spirochaetes; Spirochaetales</i>	83.2	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA252	D4ZHLFP1:60:D2HDNACXX:2:2309:8988:94473:GGATGT	<i>Spirochaetes; Spirochaetales</i>	76.3	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA254	D4ZHLFP1:60:D2HDNACXX:2:1115:16928:10462:GGATGT	<i>Spirochaetes; Spirochaetales</i>	70.5	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA279	D4ZHLFP1:60:D2HDNACXX:2:2109:15795:73802:GGATGT	<i>Spirochaetes; Spirochaetales</i>	79.3	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA290	D4ZHLFP1:60:D2HDNACXX:2:2307:14352:43488:GGATGT	<i>Spirochaetes; Spirochaetales</i>	75.9	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA317	D4ZHLFP1:60:D2HDNACXX:2:2101:9681:95732:GGATGT	<i>Spirochaetes; Spirochaetales</i>	86.7	(YP_003802215)	hydrogenase, Fe-only [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA351	D4ZHLFP1:60:D2HDNACXX:2:1310:12256:38899:GGATGT	<i>Spirochaetes; Spirochaetales</i>	80.1	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA386	D4ZHLFP1:60:D2HDNACXX:2:1108:9206:11716:GGATGT	<i>Spirochaetes; Spirochaetales</i>	64.7	(YP_005061073)	hydrogenase, Fe-only [<i>Sphaerochaeta pleomorpha str. Grapes</i>]
P28_hydA387	D4ZHLFP1:60:D2HDNACXX:2:2103:8711:61592:GGATGT	<i>Spirochaetes; Spirochaetales</i>	77.8	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA398	D4ZHLFP1:60:D2HDNACXX:2:1105:3172:49214:GGATGT	<i>Spirochaetes; Spirochaetales</i>	87.8	(YP_003802215)	hydrogenase, Fe-only [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA418	D4ZHLFP1:60:D2HDNACXX:2:1109:3864:42746:GGATGT	<i>Spirochaetes; Spirochaetales</i>	85.1	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA422	D4ZHLFP1:60:D2HDNACXX:2:2114:20411:45230:GGATGT	<i>Spirochaetes; Spirochaetales</i>	90.1	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA444	D4ZHLFP1:60:D2HDNACXX:2:1108:15662:57230:GGATGT	<i>Spirochaetes; Spirochaetales</i>	71.2	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA447	D4ZHLFP1:60:D2HDNACXX:2:1314:12915:31002:GGATGT	<i>Spirochaetes; Spirochaetales</i>	91.0	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA456	D4ZHLFP1:60:D2HDNACXX:2:1107:9964:40383:GGATGT	<i>Spirochaetes; Spirochaetales</i>	60.8	(YP_006044637)	hydrogenase, Fe-only [<i>Spirochaeta thermophiles DSM 6578</i>]
P28_hydA460	D4ZHLFP1:60:D2HDNACXX:2:1302:5716:41810:GGATGT	<i>Spirochaetes; Spirochaetales</i>	81.3	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA62	D4ZHLFP1:60:D2HDNACXX:2:2310:16315:59036:GGATGT	<i>Spirochaetes; Spirochaetales</i>	82.8	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA266	D4ZHLFP1:60:D2HDNACXX:2:1108:15952:64033:GGATGT	<i>Spirochaetes; Spirochaetales</i>	95.1	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA10	D4ZHLFP1:60:D2HDNACXX:2:1308:5318:45616:GGATGT	<i>Spirochaetes; Spirochaetales</i>	71.2	(YP_003802215)	hydrogenase, Fe-only [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA108	D4ZHLFP1:60:D2HDNACXX:2:1303:8337:4917:GGATGT	<i>Spirochaetes; Spirochaetales</i>	66.2	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA125	D4ZHLFP1:60:D2HDNACXX:2:1302:18912:63674:GGATGT	<i>Spirochaetes; Spirochaetales</i>	73.2	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA136	D4ZHLFP1:60:D2HDNACXX:2:1316:16229:71422:GGATGT	<i>Spirochaetes; Spirochaetales</i>	62.4	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA148	D4ZHLFP1:60:D2HDNACXX:2:2313:15953:28598:GGATGT	<i>Spirochaetes; Spirochaetales</i>	73.9	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA161	D4ZHLFP1:60:D2HDNACXX:2:1102:12280:94355:GGATGT	<i>Spirochaetes; Spirochaetales</i>	66.6	(YP_006044637)	hydrogenase, Fe-only [<i>Spirochaeta thermophiles DSM 6578</i>]
P28_hydA185	D4ZHLFP1:60:D2HDNACXX:2:2311:19480:99240:GGATGT	<i>Spirochaetes; Spirochaetales</i>	92.8	(YP_003802215)	NAD(P)-dependent iron-only hydrogenase catalytic subunit [<i>Spirochaeta smaragdinae DSM 11293</i>]
P28_hydA189	D4ZHLFP1:60:D2HDNACXX:2:1309:11913:24310:GGATGT	<i>Spirochaetes; Spirochaetales</i>	60.8	(YP_006044637)	hydrogenase, Fe-only [<i>Spirochaeta thermophiles DSM 6578</i>]
P28_hydA19	D4ZHLFP1:60:D2HDNACXX:2:1309:2702:32676:GGATGT	<i>Spirochaetes; Spirochaetales</i>	73.2	(YP_005475514)	hydrogenase, Fe-only [<i>Spirochaeta africana DSM 8902</i>]
P28_hydA163	D4ZHLFP1:60:D2HDNACXX:2:1114:3565:23768:GGATGT	<i>Thermotogae; Thermotogales</i>	88.6	(YP_002939902)	hydrogenase, Fe-only [<i>Kosmotoga olearia TBF 19.5.1</i>]
P28_hydA255	D4ZHLFP1:60:D2HDNACXX:2:2311:13944:72440:GGATGT	<i>Thermotogae; Thermotogales</i>	70.9	(YP_002939902)	hydrogenase, Fe-only [<i>Kosmotoga olearia TBF 19.5.1</i>]
P28_hydA257	D4ZHLFP1:60:D2HDNACXX:2:1309:3954:78696:GGATGT	<i>Thermotogae; Thermotogales</i>	79.7	(YP_002939902)	hydrogenase, Fe-only [<i>Kosmotoga olearia TBF 19.5.1</i>]
P28_hydA265	D4ZHLFP1:60:D2HDNACXX:2:2110:8245:52454:GGATGT	<i>Thermotogae; Thermotogales</i>	82.4	(YP_005470551)	hydrogenase, Fe-only [<i>Fervidobacterium pennivorans DSM 9078</i>]
P28_hydA343	D4ZHLFP1:60:D2HDNACXX:2:1316:10526:19921:GGATGT	<i>Thermotogae; Thermotogales</i>	73.6	(YP_005096723)	hydrogenase, Fe-only [<i>Marinotoga piezophila KA3</i>]
P28_hydA373	D4ZHLFP1:60:D2HDNACXX:2:2315:7515:50488:GGATGT	<i>Thermotogae; Thermotogales</i>	82.4	(YP_002939902)	hydrogenase, Fe-only [<i>Kosmotoga olearia TBF 19.5.1</i>]
P28_hydA385	D4ZHLFP1:60:D2HDNACXX:2:1309:15282:15883:GGATGT	<i>Thermotogae; Thermotogales</i>	79.7	(YP_005096723)	hydrogenase, Fe-only [<i>Marinotoga piezophila KA3</i>]
P28_hydA424	D4ZHLFP1:60:D2HDNACXX:2:2312:16959:78448:GGATGT	<i>Thermotogae; Thermotogales</i>	72.8	(YP_002939902)	hydrogenase, Fe-only [<i>Kosmotoga olearia TBF 19.5.1</i>]
P28_hydA70	D4ZHLFP1:60:D2HDNACXX:2:2106:4783:93650:GGATGT	<i>Thermotogae; Thermotogales</i>	64.3	(YP_005470551)	hydrogenase, Fe-only [<i>Fervidobacterium pennivorans DSM 9078</i>]
P28_hydA72	D4ZHLFP1:60:D2HDNACXX:2:2303:6153:42186:GGATGT	<i>Thermotogae; Thermotogales</i>	87.4	(YP_002939902)	hydrogenase, Fe-only [<i>Kosmotoga olearia TBF 19.5.1</i>]

P28_hydA22	D4ZHLFP1:60:D2HDNACXX:2:2313:16296:62472:GGATGT	<i>Thermotogae; Thermotogales</i>	56.2	(YP_001409760)	hydrogenase, Fe-only [<i>Fervidobacterium nodosum</i> Rt17-B1]
P28_hydA438	D4ZHLFP1:60:D2HDNACXX:2:1108:4211:76573:GGATGT	<i>Verrucomicrobia; Opitutales</i>	61.6	(YP_001818428)	hydrogenase, Fe-only [<i>Opitutus terreus</i> PB90-1]
P28_hydA245	D4ZHLFP1:60:D2HDNACXX:2:2311:16033:61947:GGATGT	Paddy field soil, Japan	72.8	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA263	D4ZHLFP1:60:D2HDNACXX:2:1316:4581:3244:GGATGT	Paddy field soil, Japan	83.6	(BAM65873)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA264	D4ZHLFP1:60:D2HDNACXX:2:2316:10927:9465:GGATGT	Paddy field soil, Japan	82.4	(BAM66122)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA270	D4ZHLFP1:60:D2HDNACXX:2:1113:12148:29276:GGATGT	Paddy field soil, Japan	82.8	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA219	D4ZHLFP1:60:D2HDNACXX:2:1108:5767:25663:GGATGT	Paddy field soil, Japan	61.2	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA220	D4ZHLFP1:60:D2HDNACXX:2:1105:12304:22767:GGATGT	Paddy field soil, Japan	74.7	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA235	D4ZHLFP1:60:D2HDNACXX:2:2306:12066:75508:GGATGT	Paddy field soil, Japan	75.1	(BAM65873)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA169	D4ZHLFP1:60:D2HDNACXX:2:2305:3576:73977:GGATGT	Paddy field soil, Japan	77.8	(BAM66149)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA131	D4ZHLFP1:60:D2HDNACXX:2:1303:20757:91605:GGATGT	Paddy field soil, Japan	85.5	(BAM66039)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA452	D4ZHLFP1:60:D2HDNACXX:2:2302:6322:95743:GGATGT	Paddy field soil, Japan	75.9	(BAM66084)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA128	D4ZHLFP1:60:D2HDNACXX:2:1106:16034:41315:GGATGT	Paddy field soil, Japan	68.6	(BAM66175)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA174	D4ZHLFP1:60:D2HDNACXX:2:1112:5107:21749:GGATGT	Paddy field soil, Japan	77.4	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA201	D4ZHLFP1:60:D2HDNACXX:2:2301:20855:80465:GGATGT	Paddy field soil, Japan	85.9	(BAM65965)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA104	D4ZHLFP1:60:D2HDNACXX:2:1109:9142:36449:GGATGT	Paddy field soil, Japan	91.3	(BAM66117)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA107	D4ZHLFP1:60:D2HDNACXX:2:2304:3378:12314:GGATGT	Paddy field soil, Japan	79.7	(BAM66175)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA3	D4ZHLFP1:60:D2HDNACXX:2:1104:13776:58918:GGATGT	Paddy field soil, Japan	80.1	(BAM66149)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA34	D4ZHLFP1:60:D2HDNACXX:2:1113:8868:88278:GGATGT	Paddy field soil, Japan	84.0	(BAM66175)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA346	D4ZHLFP1:60:D2HDNACXX:2:2311:17889:19912:GGATGT	Paddy field soil, Japan	68.2	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA37	D4ZHLFP1:60:D2HDNACXX:2:1301:11581:79121:GGATGT	Paddy field soil, Japan	66.2	(BAM65845)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA377	D4ZHLFP1:60:D2HDNACXX:2:1313:9467:66814:GGATGT	Paddy field soil, Japan	78.2	(BAM66088)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA380	D4ZHLFP1:60:D2HDNACXX:2:2103:7160:7503:GGATGT	Paddy field soil, Japan	72.4	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA384	D4ZHLFP1:60:D2HDNACXX:2:2111:5306:87159:GGATGT	Paddy field soil, Japan	81.3	(BAM65965)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA52	D4ZHLFP1:60:D2HDNACXX:2:1310:6679:37596:GGATGT	Paddy field soil, Japan	94.7	(BAM66117)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA53	D4ZHLFP1:60:D2HDNACXX:2:1105:12680:81935:GGATGT	Paddy field soil, Japan	93.2	(BAM66088)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA54	D4ZHLFP1:60:D2HDNACXX:2:1315:12857:40287:GGATGT	Paddy field soil, Japan	86.7	(BAM66117)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA78	D4ZHLFP1:60:D2HDNACXX:2:2309:1879:88698:GGATGT	Paddy field soil, Japan	85.1	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA82	D4ZHLFP1:60:D2HDNACXX:2:1111:13288:34560:GGATGT	Paddy field soil, Japan	79.3	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA89	D4ZHLFP1:60:D2HDNACXX:2:1306:8669:10318:GGATGT	Paddy field soil, Japan	49.7	(BAM66154)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA112	D4ZHLFP1:60:D2HDNACXX:2:1104:16777:32264:GGATGT	Paddy field soil, Japan	86.3	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA155	D4ZHLFP1:60:D2HDNACXX:2:1101:19725:90289:GGATGT	Paddy field soil, Japan	79.3	(BAM65896)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA244	D4ZHLFP1:60:D2HDNACXX:2:2109:2079:77364:GGATGT	Paddy field soil, Japan	94.7	(BAM66232)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA28	D4ZHLFP1:60:D2HDNACXX:2:1107:21082:64239:GGATGT	Paddy field soil, Japan	79.0	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA99	D4ZHLFP1:60:D2HDNACXX:2:1110:1283:40053:GGATGT	Paddy field soil, Japan	90.5	(BAM66117)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA337	D4ZHLFP1:60:D2HDNACXX:2:1313:15865:35313:GGATGT	Paddy field soil, Japan	81.6	(BAM66175)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA439	D4ZHLFP1:60:D2HDNACXX:2:2315:5629:86143:GGATGT	Paddy field soil, Japan	80.1	(BAM65973)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA49	D4ZHLFP1:60:D2HDNACXX:2:2306:14493:52422:GGATGT	Paddy field soil, Japan	86.7	(BAM66042)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA94	D4ZHLFP1:60:D2HDNACXX:2:1316:14939:47564:GGATGT	Paddy field soil, Japan	78.6	(BAM66088)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA216	D4ZHLFP1:60:D2HDNACXX:2:2310:20634:25267:GGATGT	Paddy field soil, Japan	99.4	(BAM66088)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA415	D4ZHLFP1:60:D2HDNACXX:2:2110:9798:11682:GGATGT	Paddy field soil, Japan	90.1	(BAM66173)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA360	D4ZHLFP1:60:D2HDNACXX:2:2311:19109:53485:GGATGT	Paddy field soil, Japan	77.0	(BAM65965)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA77	D4ZHLFP1:60:D2HDNACXX:2:2310:3887:27231:GGATGT	Paddy field soil, Japan	83.2	(BAM66084)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA207	D4ZHLFP1:60:D2HDNACXX:2:2111:5017:69311:GGATGT	Paddy field soil, Japan	68.9	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA430	D4ZHLFP1:60:D2HDNACXX:2:2312:11983:94515:GGATGT	Paddy field soil, Japan	98.6	(BAM66117)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA239	D4ZHLFP1:60:D2HDNACXX:2:2114:3737:84393:GGATGT	Oil fields subducted to CO ₂ and water-flooding	91.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA275	D4ZHLFP1:60:D2HDNACXX:2:1311:18238:99456:GGATGT	Oil fields subducted to CO ₂ and water-flooding	67.4	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA347	D4ZHLFP1:60:D2HDNACXX:2:2115:11101:29212:GGATGT	Oil fields subducted to CO ₂ and water-flooding	98.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA397	D4ZHLFP1:60:D2HDNACXX:2:1305:14634:49470:GGATGT	Oil fields subducted to CO ₂ and water-flooding	92.8	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA417	D4ZHLFP1:60:D2HDNACXX:2:1112:12296:56649:GGATGT	Oil fields subducted to CO ₂ and water-flooding	62.0	(AGU38565)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA181	D4ZHLFP1:60:D2HDNACXX:2:2315:7477:90219:GGATGT	Oil fields subducted to CO ₂ and water-flooding	99.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA133	D4ZHLFP1:60:D2HDNACXX:2:1315:18802:34017:GGATGT	Oil fields subducted to CO ₂ and water-flooding	92.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA319	D4ZHLFP1:60:D2HDNACXX:2:2305:7572:15250:GGATGT	Oil fields subducted to CO ₂ and water-flooding	92.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA350	D4ZHLFP1:60:D2HDNACXX:2:2314:8112:100475:GGATGT	Oil fields subducted to CO ₂ and water-flooding	72.4	(AGU38572)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA356	D4ZHLFP1:60:D2HDNACXX:2:2309:11330:76283:GGATGT	Oil fields subducted to CO ₂ and water-flooding	78.2	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA59	D4ZHLFP1:60:D2HDNACXX:2:2104:21112:2451:GGATGT	Oil fields subducted to CO ₂ and water-flooding	75.9	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA318	D4ZHLFP1:60:D2HDNACXX:2:1303:1708:62889:GGATGT	Oil fields subducted to CO ₂ and water-flooding	96.7	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA409	D4ZHLFP1:60:D2HDNACXX:2:2305:14962:93264:GGATGT	Oil fields subducted to CO ₂ and water-flooding	93.6	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA61	D4ZHLFP1:60:D2HDNACXX:2:2312:9596:27580:GGATGT	Oil fields subducted to CO ₂ and water-flooding	92.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA111	D4ZHLFP1:60:D2HDNACXX:2:2315:8361:45741:GGATGT	Oil fields subducted to CO ₂ and water-flooding	96.7	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA170	D4ZHLFP1:60:D2HDNACXX:2:2113:3747:95005:GGATGT	Saline microbial mat community, Mexico	95.9	(ACM67558)	iron-dependent hydrogenase [uncultured organism]
P28_hydA122	D4ZHLFP1:60:D2HDNACXX:2:2114:4910:91263:GGATGT	Saline microbial mat community, Mexico	97.4	(ACM67558)	iron-dependent hydrogenase [uncultured organism]
P28_hydA426	D4ZHLFP1:60:D2HDNACXX:2:2315:9602:86691:GGATGT	Saline microbial mat community, Mexico	93.2	(ACM67558)	iron-dependent hydrogenase [uncultured organism]
P28_hydA204	D4ZHLFP1:60:D2HDNACXX:2:2316:11718:88709:GGATGT	Saline microbial mat community, Mexico	91.3	(ACM67558)	iron-dependent hydrogenase [uncultured organism]
P28_hydA443	D4ZHLFP1:60:D2HDNACXX:2:2306:6557:86865:GGATGT	Acidic fen	86.7	(CAY56136)	[Fe-Fe] hydrogenase large subunit [uncultured bacterium]

P28_hydA213	D4ZHLFP1:60:D2HDNACXX:2:1311:19242:44860:GGATGT	Acidic fen	90.1	(CAY56138)	[Fe-Fe] hydrogenase large subunit [uncultured bacterium]
P28_hydA457	D4ZHLFP1:60:D2HDNACXX:2:1310:6776:26173:GGATGT	Water column of the Great Salt Lake, USA	95.5	(ADC53611)	[Fe-Fe] hydrogenase [uncultured bacterium]
P28_hydA90	D4ZHLFP1:60:D2HDNACXX:2:1314:14350:90820:GGATGT	Water column of the Great Salt Lake, USA	92.4	(ADC53611)	[Fe-Fe] hydrogenase [uncultured bacterium]
P28_hydA114	D4ZHLFP1:60:D2HDNACXX:2:2305:14681:91239:GGATGT	Earthworm gut contents	67.0	(CBX44190)	[FeFe]-hydrogenase large subunit, partial [uncultured bacterium]
P28_hydA182	D4ZHLFP1:60:D2HDNACXX:2:2302:19922:61154:GGATGT	Phreatic limestone sinkholes in Mexico	57.4	(ACQ94905)	[Fe-Fe] hydrogenase [uncultured bacterium]
P28_hydA359	D4ZHLFP1:60:D2HDNACXX:2:2107:7975:61393:GGATGT	Biogas digester system	62.4	(AEK22103)	FeFe-hydrogenase [uncultured organism]
P28_hydA410	D4ZHLFP1:60:D2HDNACXX:2:2308:6226:88233:GGATGT	Anaerobic domestic sewage sludge	82.8	(AGF90866)	FeFe-hydrogenase large subunit, partial [uncultured bacterium]
P28_hydA7	D4ZHLFP1:60:D2HDNACXX:2:2108:1486:27443:GGATGT	Biogas digester system	85.9	(AET11788)	Fe-hydrogenase [uncultured organism]
P28_hydA179	D4ZHLFP1:60:D2HDNACXX:2:1306:2483:74069:GGATGT	Biogas digester system	70.1	(AET11789)	hydrogenase [uncultured organism]
P28_hydA431	D4ZHLFP1:60:D2HDNACXX:2:2307:14244:49092:GGATGT	Water column of the Great Salt Lake, USA	88.2	(ADQ86057)	[FeFe]-hydrogenase subunit A large subunit [uncultured bacterium]
P28_hydA335	D4ZHLFP1:60:D2HDNACXX:2:1303:8667:76848:GGATGT	Termite gut microbiota	65.5	(AFH54065)	[Fe-Fe] hydrogenase large subunit, partial [uncultured bacterium]

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