

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

2

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; Ignavibacteriae; Ignavibacteria	85.9 (YP_006526890) Fe-only hydrogenase, catalytic subunit alpha [ <i>Meliobacter 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	Dictyoglomi; 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_001113004) 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 (YP_003640841) hydrogenase, Fe-only [ <i>Thermincola potens</i> JR]
P28_hydA272	D4ZHLFP1:60:D2HDNACXX:2:2314:4574:35683: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 (YP_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 (YP_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 (YP_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 (YP_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 (YP_004969732) hydrogenase, Fe-only [ <i>Desulfosporosinus orientis</i> DSM 765]
P28_hydA287	D4ZHLFP1:60:D2HDNACXX:2:1302:16282:18416:GGATGT	Firmicutes; Clostridia; Clostridiales	57.0 (YP_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 (YP_003640841) hydrogenase, Fe-only [ <i>Thermincola potens</i> JR]
P28_hydA298	D4ZHLFP1:60:D2HDNACXX:2:2310:11693:54229:GGATGT	Firmicutes; Clostridia; Clostridiales	82.0 (YP_0077035) 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_hydA300	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 (YP_001113007) hydrogenase [ <i>Desulfotomaculum reducens</i> MI-1]
P28_hydA303	D4ZHLFP1:60:D2HDNACXX:2:2106:7935:41866:GGATGT	Firmicutes; Clostridia; Clostridiales	87.0 (YP_001212560) hydrogenase subunit [ <i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA304	D4ZHLFP1:60:D2HDNACXX:2:2315:4334:79513:GGATGT	Firmicutes; Clostridia; Clostridiales	84.7 (YP_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 (YP_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 (YP_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:2:1105:7395:56887:GGATGT	Firmicutes; Clostridia; Clostridiales	72.4 (GAE88236) hydrogenase [ <i>Clostridium straminisolvans</i> JCM 21531]
P28_hydA310	D4ZHLFP1:60:D2HDNACXX:2:2306:18542:41819:GGATGT	Firmicutes; Clostridia; Clostridiales	51.2 (YP_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 (YP_001212560) hydrogenase subunit [ <i>Pelotomaculum thermopropionicum</i> SI]
P28_hydA321	D4ZHLFP1:60:D2HDNACXX:2:1314:6888:24210:GGATGT	Firmicutes; Clostridia; Clostridiales	69.3 (YP_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 (YP_004496996) hydrogenase, Fe-only [ <i>Desulfotomaculum carboxydivorans</i> CO-1-SRB]
P28_hydA324	D4ZHLFP1:60:D2HDNACXX:2:1108:14667:21673:GGATGT	Firmicutes; Clostridia; Clostridiales	84.7 (YP_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 (YP_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 (YP_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>Lachno Clostridium</i> ]
P28_hydA338	D4ZHLFP1:60:D2HDNACXX:2:1111:1445:80970: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 (YP_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 (YP_001717478) hydrogenase, Fe-only [ <i>Candidatus Desulfuridis audauxiator</i> MP104C]
P28_hydA355	D4ZHLFP1:60:D2HDNACXX:2:1108:1063:76207:GGATGT	Firmicutes; Clostridia; Clostridiales	92.0 (YP_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 (YP_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 (YP_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 (YP_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 (YP_001113007) hydrogenase [ <i>Desulfotomaculum reducens</i> MI-1]
P28_hydA366	D4ZHLFP1:60:D2HDNACXX:2:2311:7920:97575:GGATGT	Firmicutes; Clostridia; Clostridiales	69.3 (YP_004517644) hydrogenase, Fe-only [ <i>Desulfotomaculum kuznetsovii</i> DSM 6115]









P28_hydA22	D4ZHLFP1:60:D2HDNACXX:2:2313:16296:62472:GGATGT	<i>Thermotogae; Thermotogales</i>	56.2	(YP_001409760)	hydrogenase, Fe-only [ <i>Ferriobacterium nodosum</i> Rt17-B1]
P28_hydA438	D4ZHLFP1:60:D2HDNACXX:2:1108:421:176573:GGATGT	<i>Verrucomicrobia; Opitutales</i>	61.6	(YP_001818428)	hydrogenase, Fe-only [ <i>Opitutus terrae</i> PB90-1]
P28_hydA245	D4ZHLFP1:60:D2HDNACXX:2:2311:1:16033:61947: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:2:2311:1:17889:19912:GGATGT	Paddy field soil, Japan	68.2	(BAM65975)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA37	D4ZHLFP1:60:D2HDNACXX:2:1301:1:1581:79121: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:2:2109:20719:77364: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	80.7	(BAM65973)	[FeFe]-hydrogenase, partial [uncultured bacterium]
P28_hydA49	D4ZHLFP1:60:D2HDNACXX:2:2306:14493:52422:GGATGT	Paddy field soil, Japan	86.1	(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:2:1311:19109:53485: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 subDjected to CO <sub>2</sub> and water-flooding	91.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA275	D4ZHLFP1:60:D2HDNACXX:2:1311:18238:99456:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	67.4	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA347	D4ZHLFP1:60:D2HDNACXX:2:2115:11101:29212:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	98.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA397	D4ZHLFP1:60:D2HDNACXX:2:1305:14634:49470:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	92.8	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA417	D4ZHLFP1:60:D2HDNACXX:2:1112:12296:56649:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	62.0	(AGU38565)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA181	D4ZHLFP1:60:D2HDNACXX:2:2315:7477:90219:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	99.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA133	D4ZHLFP1:60:D2HDNACXX:2:1315:18802:34017:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	92.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA319	D4ZHLFP1:60:D2HDNACXX:2:2305:7572:15250:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	92.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA350	D4ZHLFP1:60:D2HDNACXX:2:2314:8112:100475:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	72.4	(AGU38572)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA356	D4ZHLFP1:60:D2HDNACXX:2:2309:11330:76283:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	78.2	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA59	D4ZHLFP1:60:D2HDNACXX:2:2104:21112:2451:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	75.9	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA318	D4ZHLFP1:60:D2HDNACXX:2:1303:1708:62889:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	96.7	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA409	D4ZHLFP1:60:D2HDNACXX:2:2305:14962:93264:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	93.6	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA61	D4ZHLFP1:60:D2HDNACXX:2:2312:9596:27580:GGATGT	Oil fields subDjected to CO <sub>2</sub> and water-flooding	92.0	(AGU38562)	FeFe-hydrogenase, partial [uncultured prokaryote]
P28_hydA111	D4ZHLFP1:60:D2HDNACXX:2:2315:8361:45741:GGATGT	Oil fields subDjected to CO <sub>2</sub> 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:2:2306:6557:88665: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]

3

4