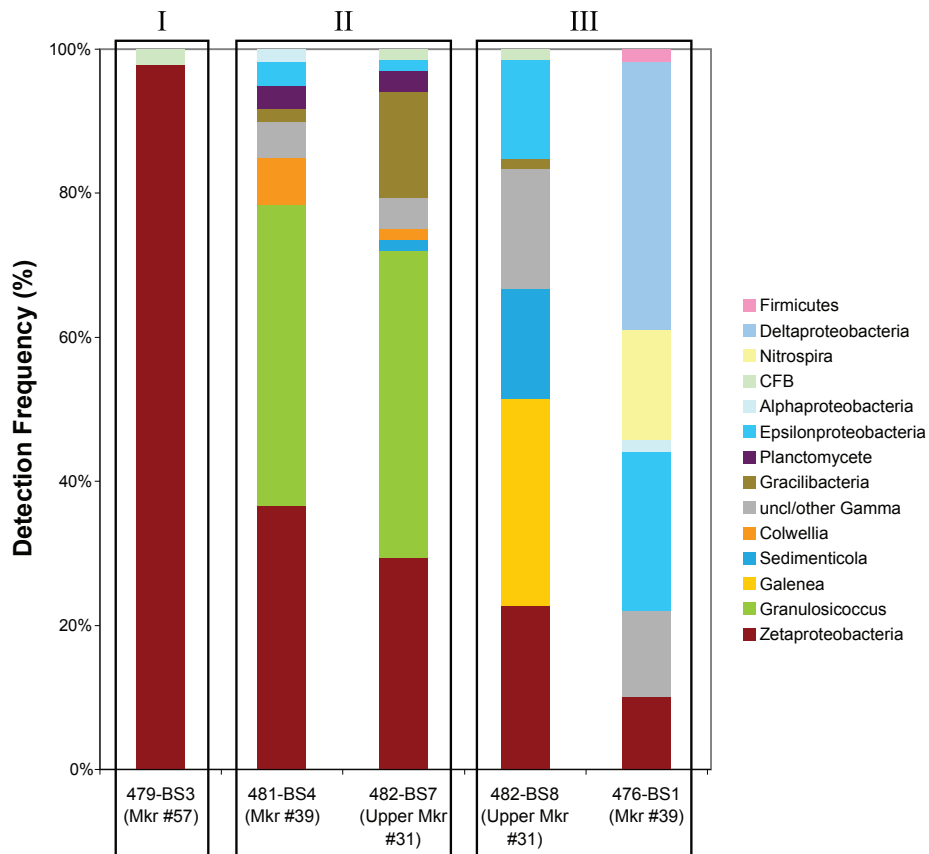
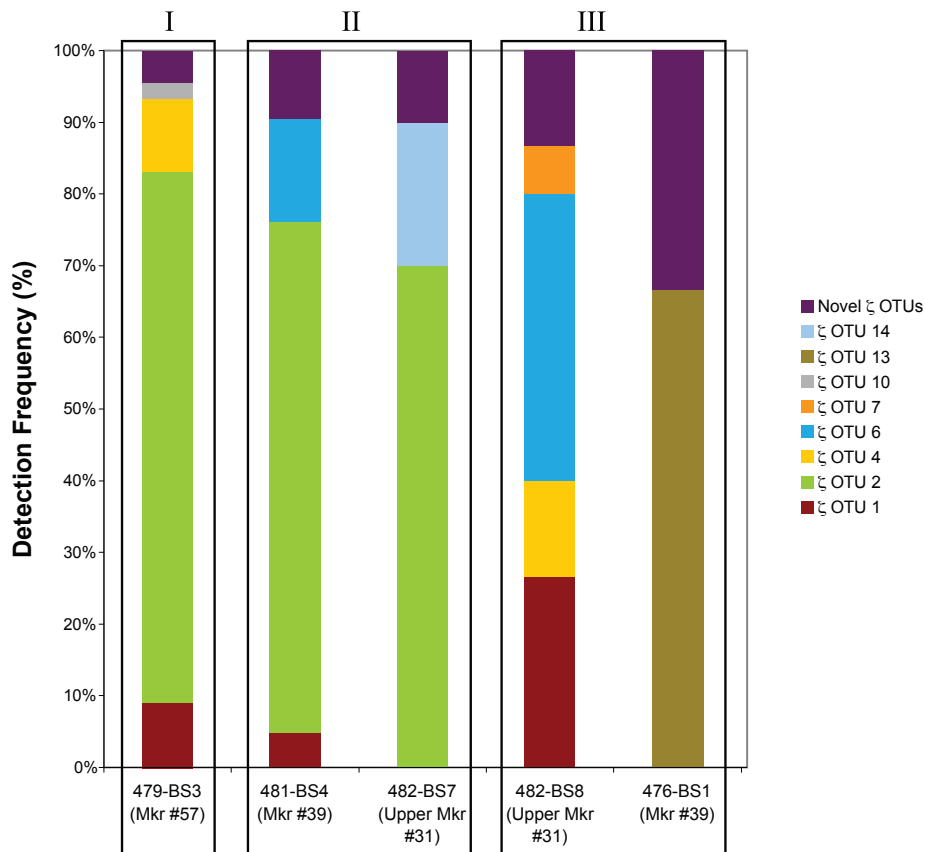


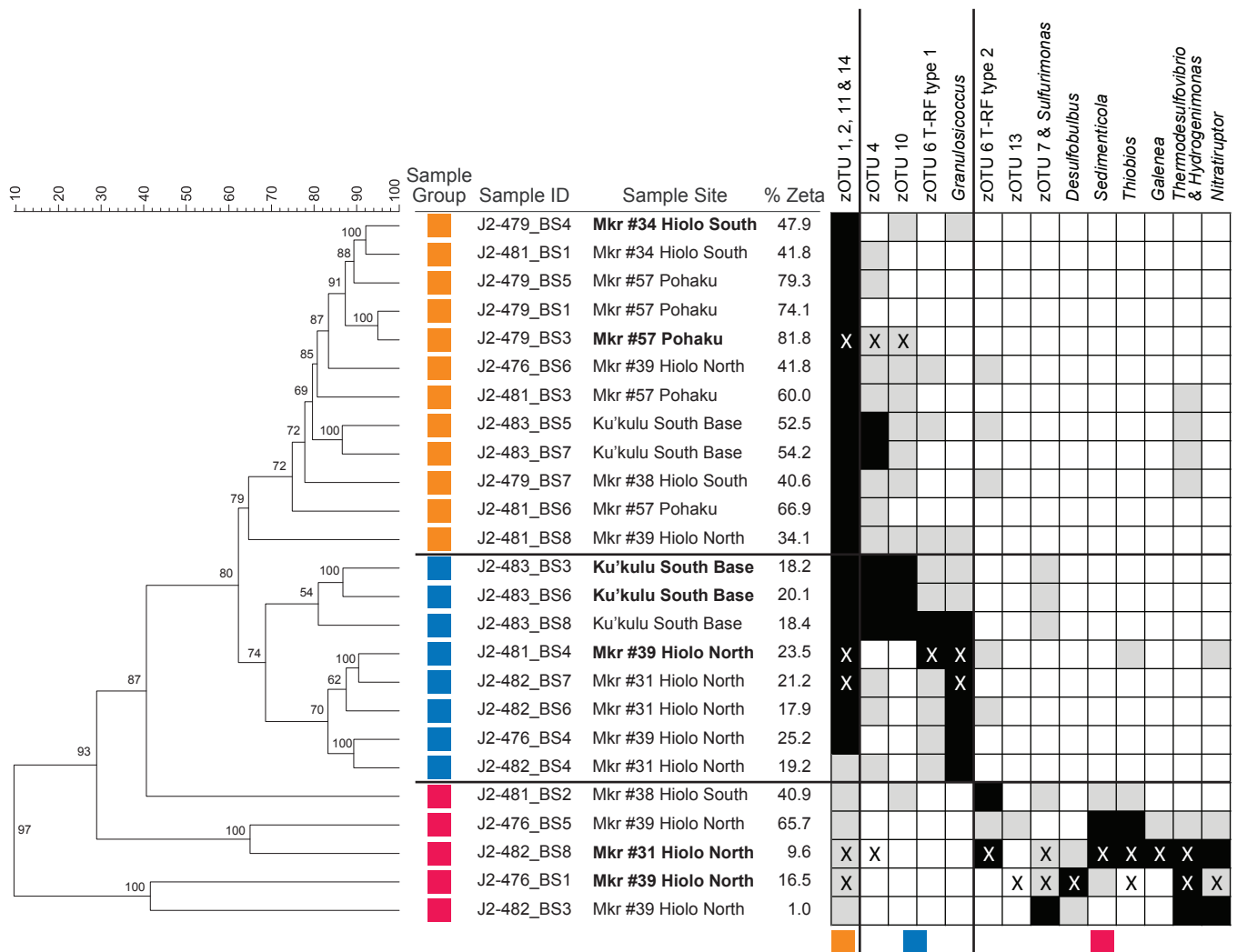
# Bacterial Community



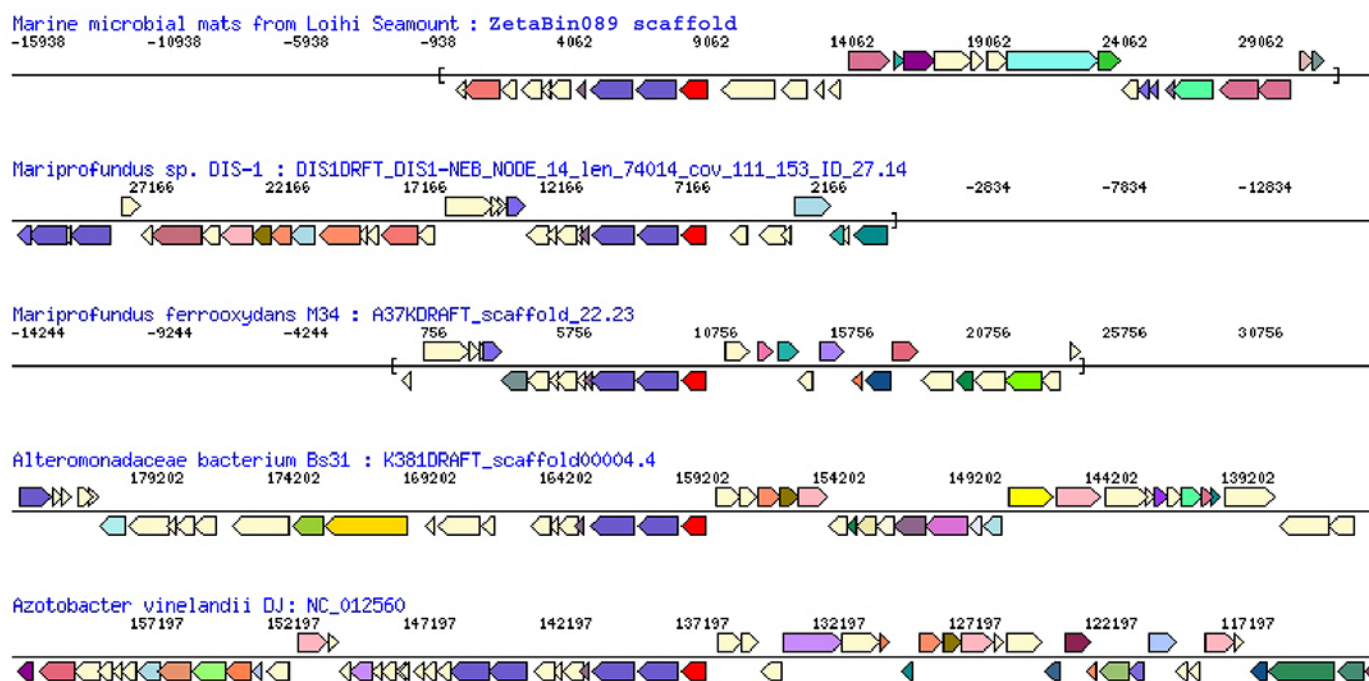
# Zetaproteobacteria Only



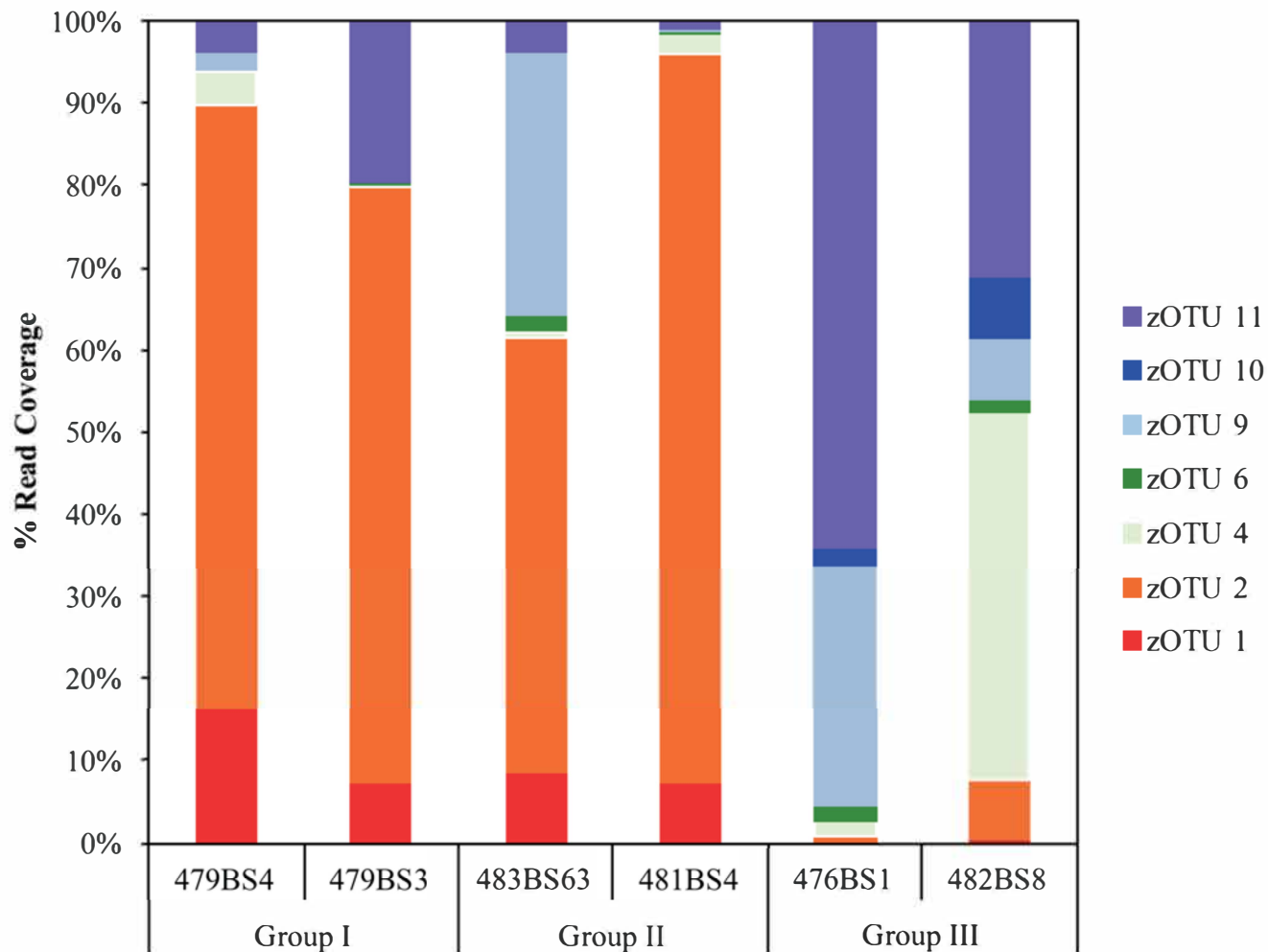
**Supplemental Figure 1.** Detection frequency for all Bacteria (top) and Zetaproteobacteria OTUs (bottom) as determined by SSU rRNA gene clone libraries constructed for T-RFLP assessment.



**Supplemental Figure 2.** Addendum to Figure 3, including identification of specific terminal-restriction fragments used to identify putative phylotypes showing a distinct pattern among each group, driven by changes in abundance of Zetaproteobacteria, Granulosicoccus (Gammaproteobacteria), and sulfur- and hydrogen-metabolizing organisms, including Epsilonproteobacteria. Black boxes represent strong peaks; grey boxes represent low abundance peaks; white boxes represent no peak. X's mark those peaks that were detected in the SSU rDNA gene clone libraries.



**Supplemental Figure 3.** Synteny plot of the *nifH* region. The red is the *nifH* gene and the purple are the *nifD*, *nifK* and *nifT* genes. The top genome fragment is a scaffold from ZetaBin089.



**Supplemental Figure 4.** Distribution of Zetaproteobacteria genome bins and their read coverage by taxonomic placement. Genome bins were assessed for taxonomic classification using CheckM. Zetaproteobacteria genome bins were sorted by their closest zOTU as determined by ANI.

**Supplemental Table 1.** Read Statistics.

| Sample Name | Cycles  | Sequencer | Before Normalization | After Normalization |
|-------------|---------|-----------|----------------------|---------------------|
| 476-BS1     | 2 x 308 | MiSeq     | 62,704,746           | 28,197,716          |
| 479-BS4     | 2 x 308 | MiSeq     | 40,807,268           | 12,391,396          |
| 479-BS3     | 2 x 101 | HiSeq     | 293,219,592          | 36,324,362          |
| 481-BS4     | 2 x 308 | MiSeq     | 49,135,240           | 11,227,026          |
| 482-BS8     | 2 x 308 | MiSeq     | 41,426,814           | 15,618,046          |
| 483-BS63    | 2 x 84  | MiSeq     | 41,991,914           | 6,906,718           |

**Supplemental Table 2.** Genes identified as similar to *M. ferrooxydans* PV-1 *cyc1* (DAA64808.1).

| Scaffold          | Class              | Genome Bin      | Locus Tag           | Gene Product Name   |
|-------------------|--------------------|-----------------|---------------------|---|
| Ga0117756_1001273 | Zetaproteobacteria | LoihiMaxBin_011 | Ga0117756_100127326 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1000092 | Zetaproteobacteria | LoihiMaxBin_040 | Ga0117756_100009214 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1001286 | Zetaproteobacteria | LoihiMaxBin_041 | Ga0117756_100128619 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1002578 | Zetaproteobacteria | LoihiMaxBin_042 | Ga0117756_100257812 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1001746 | Zetaproteobacteria | LoihiMaxBin_043 | Ga0117756_100174666 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1028789 | Zetaproteobacteria | LoihiMaxBin_047 | Ga0117756_10287891  | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1001836 | Zetaproteobacteria | LoihiMaxBin_050 | Ga0117756_100183621 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1051079 | Zetaproteobacteria | LoihiMaxBin_055 | Ga0117756_10510791  | Cytochrome c553   |
| Ga0117756_1038594 | Zetaproteobacteria | LoihiMaxBin_056 | Ga0117756_10385943  | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1030170 | Zetaproteobacteria | LoihiMaxBin_059 | Ga0117756_10301701  | Cytochrome c553   |
| Ga0117756_1003929 | Zetaproteobacteria | LoihiMaxBin_065 | Ga0117756_100392910 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1058088 | Zetaproteobacteria | LoihiMaxBin_065 | Ga0117756_10580881  | Cytochrome c553   |
| Ga0117756_1000364 | Zetaproteobacteria | LoihiMaxBin_066 | Ga0117756_100036422 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1003301 | Zetaproteobacteria | LoihiMaxBin_066 | Ga0117756_10033016  | thiosulfate dehydrogenase   |
| Ga0117756_1006226 | Zetaproteobacteria | LoihiMaxBin_077 | Ga0117756_10062266  | Cytochrome c553/Tetraheme cytochrome c subunit of nitrate or TMAO reductase |
| Ga0117756_1008594 | Zetaproteobacteria | LoihiMaxBin_077 | Ga0117756_10085946  | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1001414 | Zetaproteobacteria | LoihiMaxBin_079 | Ga0117756_100141411 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1000939 | Zetaproteobacteria | LoihiMaxBin_080 | Ga0117756_100093923 | thiosulfate dehydrogenase   |
| Ga0117756_1040683 | Zetaproteobacteria | LoihiMaxBin_084 | Ga0117756_10406832  | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1049104 | Zetaproteobacteria | LoihiMaxBin_084 | Ga0117756_10491041  | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1000815 | Zetaproteobacteria | LoihiMaxBin_088 | Ga0117756_100081524 | Cytochrome c553   |
| Ga0117756_1003270 | Zetaproteobacteria | LoihiMaxBin_088 | Ga0117756_10032707  | Cytochrome c553/Tetraheme cytochrome c subunit of nitrate or TMAO reductase |
| Ga0117756_1000031 | Zetaproteobacteria | LoihiMaxBin_089 | Ga0117756_100003124 | Cytochrome c553/Cytochrome c553   |
| Ga0117756_1017374 | Zetaproteobacteria | LoihiMaxBin_091 | Ga0117756_10173745  | Cytochrome c553/Cytochrome c553   |

**Supplemental Table 3.** Genes identified as similar to *M. ferrooxydans* PV-1 *cyc2* (AKN35166.1).

| Scaffold          | Class              | Genome Bin | Locus Tag           | Gene Product Name    |
|-------------------|--------------------|------------|---------------------|----------------------|
| Ga0117756_1000082 | Zetaproteobacteria | ZetaBin080 | Ga0117756_100008262 | hypothetical protein |
| Ga0117756_1000169 | Zetaproteobacteria | ZetaBin035 | Ga0117756_10001694  | hypothetical protein |
| Ga0117756_1000281 | Zetaproteobacteria | ZetaBin040 | Ga0117756_100028141 | hypothetical protein |
| Ga0117756_1000517 | Zetaproteobacteria | ZetaBin042 | Ga0117756_100051734 | hypothetical protein |
| Ga0117756_1001027 | Zetaproteobacteria | ZetaBin041 | Ga0117756_10010279  | hypothetical protein |
| Ga0117756_1001197 | Zetaproteobacteria | ZetaBin066 | Ga0117756_10011974  | hypothetical protein |
| Ga0117756_1001197 | Zetaproteobacteria | ZetaBin066 | Ga0117756_10011973  | hypothetical protein |
| Ga0117756_1001926 | Zetaproteobacteria | ZetaBin035 | Ga0117756_100192620 | hypothetical protein |
| Ga0117756_1001926 | Zetaproteobacteria | ZetaBin035 | Ga0117756_100192618 | hypothetical protein |
| Ga0117756_1002147 | Zetaproteobacteria | ZetaBin043 | Ga0117756_100214710 | hypothetical protein |
| Ga0117756_1002914 | Zetaproteobacteria | ZetaBin088 | Ga0117756_10029141  | hypothetical protein |
| Ga0117756_1003808 | Zetaproteobacteria | ZetaBin089 | Ga0117756_10038085  | hypothetical protein |
| Ga0117756_1004200 | Zetaproteobacteria | ZetaBin050 | Ga0117756_10042008  | hypothetical protein |
| Ga0117756_1005281 | Zetaproteobacteria | ZetaBin050 | Ga0117756_10052816  | hypothetical protein |
| Ga0117756_1007026 | Zetaproteobacteria | ZetaBin090 | Ga0117756_10070261  | hypothetical protein |
| Ga0117756_1007675 | Zetaproteobacteria | ZetaBin011 | Ga0117756_10076751  | hypothetical protein |
| Ga0117756_1011041 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10110416  | hypothetical protein |
| Ga0117756_1012992 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10129924  | hypothetical protein |
| Ga0117756_1013610 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10136104  | hypothetical protein |
| Ga0117756_1013891 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10138912  | hypothetical protein |
| Ga0117756_1014268 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10142681  | hypothetical protein |
| Ga0117756_1016945 | Zetaproteobacteria | ZetaBin065 | Ga0117756_10169454  | hypothetical protein |
| Ga0117756_1025359 | Zetaproteobacteria | ZetaBin091 | Ga0117756_10253592  | hypothetical protein |
| Ga0117756_1028748 | Zetaproteobacteria | ZetaBin088 | Ga0117756_10287482  | hypothetical protein |
| Ga0117756_1029363 | Zetaproteobacteria | ZetaBin084 | Ga0117756_10293631  | hypothetical protein |
| Ga0117756_1029874 | Zetaproteobacteria | ZetaBin035 | Ga0117756_10298741  | hypothetical protein |
| Ga0117756_1030386 | Zetaproteobacteria | ZetaBin084 | Ga0117756_10303861  | hypothetical protein |
| Ga0117756_1031186 | Zetaproteobacteria | ZetaBin084 | Ga0117756_10311861  | hypothetical protein |
| Ga0117756_1033024 | Zetaproteobacteria | ZetaBin064 | Ga0117756_10330242  | hypothetical protein |
| Ga0117756_1034066 | Zetaproteobacteria | ZetaBin062 | Ga0117756_10340661  | hypothetical protein |
| Ga0117756_1036278 | Zetaproteobacteria | ZetaBin084 | Ga0117756_10362781  | hypothetical protein |
| Ga0117756_1038273 | Zetaproteobacteria | ZetaBin059 | Ga0117756_10382731  | hypothetical protein |
| Ga0117756_1038911 | Zetaproteobacteria | ZetaBin065 | Ga0117756_10389111  | hypothetical protein |
| Ga0117756_1041107 | Zetaproteobacteria | ZetaBin069 | Ga0117756_10411071  | hypothetical protein |
| Ga0117756_1045285 | Zetaproteobacteria | ZetaBin090 | Ga0117756_10452851  | hypothetical protein |
| Ga0117756_1047975 | Zetaproteobacteria | ZetaBin011 | Ga0117756_10479752  | hypothetical protein |
| Ga0117756_1048244 | Zetaproteobacteria | ZetaBin090 | Ga0117756_10482441  | hypothetical protein |
| Ga0117756_1051193 | Zetaproteobacteria | ZetaBin089 | Ga0117756_10511931  | hypothetical protein |
| Ga0117756_1052798 | Zetaproteobacteria | ZetaBin060 | Ga0117756_10527981  | hypothetical protein |
| Ga0117756_1053486 | Zetaproteobacteria | ZetaBin084 | Ga0117756_10534862  | hypothetical protein |
| Ga0117756_1079919 | Zetaproteobacteria | ZetaBin037 | Ga0117756_10799191  | hypothetical protein |

**Supplemental Table 4.** Genes identified as similar to *M.ferrooxydans* PV-1 Mob (SPV1\_03948).

| Scaffold          | Class              | GenomeBin  | Locus Tag           | Gene Product Name   |
|-------------------|--------------------|------------|---------------------|---|
| Ga0117756_1001425 | Zetaproteobacteria | ZetaBin011 | Ga0117756_100142513 | NADH-quinone oxidoreductase subunit G   |
| Ga0117756_1002014 | Zetaproteobacteria | ZetaBin011 | Ga0117756_100201417 | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1003853 | Zetaproteobacteria | ZetaBin011 | Ga0117756_10038531  | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1038481 | Zetaproteobacteria | ZetaBin011 | Ga0117756_10384811  | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1018933 | Zetaproteobacteria | ZetaBin037 | Ga0117756_10189332  | formate dehydrogenase major subunit   |
| Ga0117756_1001039 | Zetaproteobacteria | ZetaBin040 | Ga0117756_100103913 | assimilatory nitrate reductase catalytic subunit  |
| Ga0117756_1003809 | Zetaproteobacteria | ZetaBin040 | Ga0117756_10038098  | nitrate reductase NapA  |
| Ga0117756_1001693 | Zetaproteobacteria | ZetaBin043 | Ga0117756_10016938  | nitrate reductase NapA  |
| Ga0117756_1003962 | Zetaproteobacteria | ZetaBin047 | Ga0117756_10039626  | NADH-quinone oxidoreductase subunit G   |
| Ga0117756_1021850 | Zetaproteobacteria | ZetaBin047 | Ga0117756_10218501  | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1038467 | Zetaproteobacteria | ZetaBin047 | Ga0117756_10384673  | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1052450 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10524501  | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1055985 | Zetaproteobacteria | ZetaBin049 | Ga0117756_10559851  | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1001959 | Zetaproteobacteria | ZetaBin050 | Ga0117756_100195912 | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1002724 | Zetaproteobacteria | ZetaBin050 | Ga0117756_10027244  | NADH-quinone oxidoreductase subunit G   |
| Ga0117756_1001247 | Zetaproteobacteria | ZetaBin066 | Ga0117756_100124739 | prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit |
| Ga0117756_1006226 | Zetaproteobacteria | ZetaBin077 | Ga0117756_10062265  | Anaerobic selenocysteine-containing dehydrogenase                                       |
| Ga0117756_1000082 | Zetaproteobacteria | ZetaBin080 | Ga0117756_10000828  | NADH-quinone oxidoreductase subunit G   |
| Ga0117756_1038571 | Zetaproteobacteria | ZetaBin084 | Ga0117756_10385712  | formate dehydrogenase major subunit   |
| Ga0117756_1003270 | Zetaproteobacteria | ZetaBin088 | Ga0117756_10032708  | Anaerobic selenocysteine-containing dehydrogenase                                       |
| Ga0117756_1007462 | Zetaproteobacteria | ZetaBin089 | Ga0117756_10074623  | nitrate reductase NapA  |
| Ga0117756_1038643 | Zetaproteobacteria | ZetaBin089 | Ga0117756_10386431  | assimilatory nitrate reductase catalytic subunit  |
| Ga0117756_1004180 | Zetaproteobacteria | ZetaBin090 | Ga0117756_10041807  | nitrate reductase NapA  |
| Ga0117756_1016962 | Zetaproteobacteria | ZetaBin091 | Ga0117756_10169623  | assimilatory nitrate reductase catalytic subunit  |
| Ga0117756_1004665 | Zetaproteobacteria | ZetaBin092 | Ga0117756_10046658  | nitrate reductase NapA  |
| Ga0117756_1021839 | Zetaproteobacteria | ZetaBin092 | Ga0117756_10218391  | NADH-quinone oxidoreductase subunit G   |
| Ga0117756_1023392 | Zetaproteobacteria | ZetaBin092 | Ga0117756_10233921  | NADH-quinone oxidoreductase subunit G   |
| Ga0117756_1051284 | Zetaproteobacteria | ZetaBin092 | Ga0117756_10512841  | nitrate reductase NapA  |



**Supplemental Table 5.** The taxonomic placement and genome bins of the RubisCO Large Chain protein along with the closest BlastP database hit.

| Scaffold          | Locus Tag           | Closest Blast hit               | Type        | pid   | length | eval   | bitscore | Gene Name                                     | Class                   | GenomeBin       |
|-------------------|---------------------|---------------------------------|-------------|-------|--------|--------|----------|---|-------------------------|-----------------|
| Ga0117756_1036952 | Ga0117756_10369521  | gi 517099781 ref WP_018288599.1 | II          | 89.7  | 468    | 0      | 884      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin091      |
| Ga0117756_1006443 | Ga0117756_10064431  | gi 517092680 ref WP_018281498.1 | II          | 97.9  | 388    | 0      | 793      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin089      |
| Ga0117756_1009661 | Ga0117756_10096614  | gi 517092680 ref WP_018281498.1 | II          | 96.1  | 76     | 2E-44  | 159      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin089      |
| Ga0117756_1016164 | Ga0117756_10161643  | gi 517097112 ref WP_018285930.1 | II          | 93.0  | 445    | 0      | 876      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin084      |
| Ga0117756_1000143 | Ga0117756_100014332 | gi 517097112 ref WP_018285930.1 | II          | 96.4  | 472    | 0      | 950      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin080      |
| Ga0117756_1008592 | Ga0117756_10085926  | gi 517097112 ref WP_018285930.1 | II          | 95.7  | 187    | 8E-129 | 382      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin079      |
| Ga0117756_1017913 | Ga0117756_10179133  | gi 517097112 ref WP_018285930.1 | II          | 95.9  | 170    | 2E-113 | 342      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin079      |
| Ga0117756_1010223 | Ga0117756_10102234  | gi 517097112 ref WP_018285930.1 | II          | 92.8  | 472    | 0      | 916      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin077      |
| Ga0117756_1001224 | Ga0117756_100122415 | gi 497537089 ref WP_009851287.1 | II          | 76.6  | 469    | 0      | 758      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin066      |
| Ga0117756_1009325 | Ga0117756_10093251  | gi 517097112 ref WP_018285930.1 | II          | 100.0 | 58     | 1E-29  | 117      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin065      |
| Ga0117756_1025537 | Ga0117756_10255372  | gi 517099781 ref WP_018288599.1 | II          | 91.5  | 472    | 0      | 902      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin065      |
| Ga0117756_1045447 | Ga0117756_10454471  | gi 517097112 ref WP_018285930.1 | II          | 95.5  | 201    | 7E-137 | 404      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin059      |
| Ga0117756_1036909 | Ga0117756_10369091  | gi 517097112 ref WP_018285930.1 | II          | 96.7  | 366    | 0      | 744      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin058      |
| Ga0117756_1040564 | Ga0117756_10405641  | gi 517097112 ref WP_018285930.1 | II          | 95.5  | 424    | 0      | 863      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin057      |
| Ga0117756_1011633 | Ga0117756_10116331  | gi 517099781 ref WP_018288599.1 | II          | 89.8  | 472    | 0      | 890      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin055      |
| Ga0117756_1008234 | Ga0117756_10082342  | gi 659893037 ref WP_029939712.1 | II          | 77.2  | 465    | 0      | 761      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin050      |
| Ga0117756_1010010 | Ga0117756_10100105  | gi 657350008 ref WP_029406688.1 | II          | 79.1  | 177    | 1E-93  | 291      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin050      |
| Ga0117756_1010712 | Ga0117756_10107121  | gi 497537089 ref WP_009851287.1 | II          | 83.4  | 151    | 2E-86  | 272      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin049      |
| Ga0117756_1030307 | Ga0117756_10303073  | gi 659893037 ref WP_029939712.1 | II          | 76.7  | 223    | 9E-121 | 363      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin047      |
| Ga0117756_1039135 | Ga0117756_10391352  | gi 659893037 ref WP_029939712.1 | II          | 77.9  | 199    | 2E-106 | 326      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin047      |
| Ga0117756_1050695 | Ga0117756_10506951  | gi 659893037 ref WP_029939712.1 | II          | 76.2  | 390    | 0      | 630      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin047      |
| Ga0117756_1002262 | Ga0117756_100226216 | gi 517099781 ref WP_018288599.1 | II          | 100.0 | 471    | 0      | 979      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin043      |
| Ga0117756_1000102 | Ga0117756_10001023  | gi 517097112 ref WP_018285930.1 | II          | 92.4  | 472    | 0      | 912      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin042      |
| Ga0117756_1002917 | Ga0117756_100291713 | gi 517097112 ref WP_018285930.1 | II          | 95.8  | 472    | 0      | 956      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin041      |
| Ga0117756_1000051 | Ga0117756_100005126 | gi 517092680 ref WP_018281498.1 | II          | 100.0 | 468    | 0      | 973      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin040      |
| Ga0117756_1019077 | Ga0117756_10190771  | gi 517092680 ref WP_018281498.1 | II          | 74.9  | 179    | 3E-89  | 280      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin037      |
| Ga0117756_1003323 | Ga0117756_10033234  | gi 737402008 ref WP_035383183.1 | II          | 92.3  | 470    | 0      | 905      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin035      |
| Ga0117756_1022954 | Ga0117756_10229541  | gi 517099781 ref WP_018288599.1 | II          | 92.7  | 385    | 0      | 757      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin022      |
| Ga0117756_1050794 | Ga0117756_10507941  | gi 490178889 ref WP_004077508.1 | I           | 65.9  | 82     | 2E-29  | 118      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin022      |
| Ga0117756_1002975 | Ga0117756_10029751  | gi 659893037 ref WP_029939712.1 | II          | 78.1  | 465    | 0      | 759      | ribulose-bisphosphate carboxylase large chain | Zetaproteobacteria      | ZetaBin011      |
| Ga0117756_1137224 | Ga0117756_11372241  | gi 496642367 ref WP_011323101.1 | III         | 57.1  | 133    | 4E-42  | 155      | ribulose-bisphosphate carboxylase large chain | IMG=Alphaproteobacteria | unbinned        |
| Ga0117756_1056354 | Ga0117756_10563541  | gi 517097112 ref WP_018285930.1 | II          | 95.0  | 160    | 1E-107 | 327      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1067788 | Ga0117756_10677881  | gi 740417597 ref WP_038250565.1 | II          | 87.8  | 302    | 0      | 563      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1070361 | Ga0117756_10703611  | gi 759380765 ref WP_043107373.1 | II          | 98.6  | 293    | 0      | 603      | ribulose-bisphosphate carboxylase large chain | IMG=Gammaproteobacteria | unbinned        |
| Ga0117756_1070520 | Ga0117756_10705201  | gi 517097112 ref WP_018285930.1 | II          | 98.6  | 73     | 2E-40  | 148      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1077249 | Ga0117756_10772491  | gi 503057046 ref WP_013292022.1 | II          | 74.9  | 227    | 2E-121 | 365      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1079512 | Ga0117756_10795121  | gi 740417597 ref WP_038250565.1 | II          | 88.6  | 262    | 1E-173 | 499      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1083217 | Ga0117756_10832171  | gi 517097112 ref WP_018285930.1 | II          | 100.0 | 249    | 0      | 522      | ribulose-bisphosphate carboxylase large chain | IMG=Betaproteobacteria  | unbinned        |
| Ga0117756_1084274 | Ga0117756_10842742  | gi 517097112 ref WP_018285930.1 | II          | 90.3  | 31     | 8E-10  | 61.6     | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1084399 | Ga0117756_10843991  | gi 517099781 ref WP_018288599.1 | II          | 92.8  | 249    | 2E-170 | 491      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1095397 | Ga0117756_10953971  | gi 759380765 ref WP_043107373.1 | II          | 91.0  | 145    | 4E-90  | 281      | ribulose-bisphosphate carboxylase large chain | IMG=Gammaproteobacteria | unbinned        |
| Ga0117756_1106676 | Ga0117756_11066761  | gi 517092680 ref WP_018281498.1 | II          | 90.1  | 201    | 2E-131 | 389      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1110271 | Ga0117756_11102711  | gi 506245542 ref WP_015765417.1 | II          | 91.8  | 195    | 9E-128 | 379      | ribulose-bisphosphate carboxylase large chain | IMG=Gammaproteobacteria | unbinned        |
| Ga0117756_1111400 | Ga0117756_11114001  | gi 517092680 ref WP_018281498.1 | II          | 74.7  | 142    | 5E-66  | 219      | ribulose-bisphosphate carboxylase large chain | IMG=Gammaproteobacteria | unbinned        |
| Ga0117756_1114043 | Ga0117756_11140431  | gi 517097112 ref WP_018285930.1 | II          | 91.1  | 190    | 5E-124 | 370      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1128243 | Ga0117756_11282431  | gi 517097112 ref WP_018285930.1 | II          | 93.6  | 172    | 3E-114 | 345      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1144663 | Ga0117756_11446631  | gi 764556396 ref WP_044418808.1 | II          | 89.6  | 154    | 2E-95  | 295      | ribulose-bisphosphate carboxylase large chain | IMG=Alphaproteobacteria | unbinned        |
| Ga0117756_1151383 | Ga0117756_11513832  | gi 502888301 ref WP_013123277.1 | II          | 90.5  | 63     | 3E-32  | 125      | ribulose-bisphosphate carboxylase large chain | IMG=Zetaproteobacteria  | unbinned        |
| Ga0117756_1085828 | Ga0117756_10858281  | gi 737267451 ref WP_035251360.1 | I           | 87.9  | 58     | 2E-26  | 108      | ribulose-bisphosphate carboxylase large chain | IMG=Alphaproteobacteria | unbinned        |
| Ga0117756_1061759 | Ga0117756_10617591  | gi 518005896 ref WP_019176104.1 | I           | 53.4  | 262    | 2E-82  | 265      | ribulose-bisphosphate carboxylase large chain | IMG=Methanomicrobium    | unbinned        |
| Ga0117756_1076488 | Ga0117756_10764882  | gi 759380759 ref WP_043107369.1 | I           | 100.0 | 37     | 4E-17  | 82.4     | ribulose-bisphosphate carboxylase large chain | IMG=Gammaproteobacteria | unbinned        |
| Ga0117756_1083288 | Ga0117756_10832881  | gi 759380759 ref WP_043107369.1 | I           | 99.5  | 198    | 4E-138 | 406      | ribulose-bisphosphate carboxylase large chain | IMG=Gammaproteobacteria | unbinned        |
| Ga0117756_1152120 | Ga0117756_11521201  | gi 504020534 ref WP_014254528.1 | -           | 66.9  | 151    | 2E-63  | 210      | ribulose-bisphosphate carboxylase large chain | IMG=Methanomicrobium    | unbinned        |
| Ga0117756_1000071 | Ga0117756_100007122 | gi 924870411 ref WP_053549117.1 | not rubisco | 56.6  | 129    | 2E-46  | 160      | ribulose-bisphosphate carboxylase large chain | Nitrospirae             | NitroBin001     |
| Ga0117756_1000235 | Ga0117756_10002351  | gi 504865161 ref WP_015052263.1 | -           | 74.7  | 474    | 0      | 775      | ribulose-bisphosphate carboxylase large chain | Unclassified Archaea    | LoihiMaxBin001  |
| Ga0117756_1000202 | Ga0117756_100020230 | gi 518331021 ref WP_019501228.1 | I           | 67.7  | 464    | 0      | 656      | ribulose-bisphosphate carboxylase large chain | Caldilineae             | CaldiBin024     |
| Ga0117756_1022958 | Ga0117756_10229581  | gi 506220048 ref WP_015739823.1 | III         | 52.0  | 177    | 6E-51  | 180      | ribulose-bisphosphate carboxylase large chain | Anaerolineae            | AaeroBin020     |
| Ga0117756_1015772 | Ga0117756_10157722  | gi 503448813 ref WP_013683474.1 | III         | 55.3  | 423    | 1E-162 | 477      | ribulose-bisphosphate carboxylase large chain | Unclassified Archaea    | LoihiMaxBin012  |
| Ga0117756_1020642 | Ga0117756_10206421  | gi 495361790 ref WP_008086508.1 | III         | 57.3  | 419    | 4E-170 | 496      | ribulose-bisphosphate carboxylase large chain | IgnaviBacteria          | IgnaviMaxBin015 |
| Ga0117756_1000079 | Ga0117756_10000797  | gi 918697881 ref WP_052567263.1 | not rubisco | 40.6  | 527    | 2E-132 | 407      | ribulose-bisphosphate carboxylase large chain | gemmatimonadetes        | GemmaBin005     |
| Ga0117756_1003443 | Ga0117756_10034437  | gi 500421767 ref WP_011930036.1 | II          | 91.3  | 460    | 0      | 884      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin093     |
| Ga0117756_1000371 | Ga0117756_100037123 | gi 656108512 ref WP_029132057.1 | II          | 83.7  | 459    | 0      | 824      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin082     |
| Ga0117756_1000877 | Ga0117756_10008773  | gi 500421767 ref WP_011930036.1 | II          | 91.7  | 460    | 0      | 889      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin076     |
| Ga0117756_1032300 | Ga0117756_10323002  | gi 928926965 ref WP_053951892.1 | II          | 95.0  | 460    | 0      | 909      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin063     |
| Ga0117756_1021618 | Ga0117756_10216181  | gi 640165948 ref WP_024807638.1 | II          | 71.6  | 461    | 0      | 707      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin045     |
| Ga0117756_1046377 | Ga0117756_10463771  | gi 497537089 ref WP_009851287.1 | II          | 94.6  | 388    | 0      | 770      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin045     |
| Ga0117756_1057876 | Ga0117756_10578761  | gi 751599392 ref WP_041067559.1 | II          | 94.5  | 274    | 0      | 546      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin045     |
| Ga0117756_1025798 | Ga0117756_10257982  | gi 759392796 ref WP_043117722.1 | I           | 96.9  | 413    | 0      | 842      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin045     |
| Ga0117756_1002875 | Ga0117756_10028757  | gi 521063127 ref WP_020395078.1 | II          | 90.7  | 461    | 0      | 886      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin038     |
| Ga0117756_1006138 | Ga0117756_10061384  | gi 983348972 ref WP_060528669.1 | II          | 94.4  | 461    | 0      | 919      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin038     |
| Ga0117756_1043410 | Ga0117756_10434101  | gi 983348972 ref WP_060528669.1 | II          | 92.0  | 162    | 8E-105 | 318      | ribulose-bisphosphate carboxylase large chain | Gammaproteobacteria     | GammaBin038     |

**Supplemental Table 6.** Genes identified as ATP-citrate lyase Beta-subunits.

| Scaffold          | Class                 | Genome Bin    | Locus Tag           | Gene Name                      | Closes species as identified by IMG       |
|-------------------|-----------------------|---------------|---------------------|--------------------------------|---|
| Ga0117756_1000566 | Epsilonproteobacteria | EpsilonBin032 | Ga0117756_100056631 | ATP-citrate lyase beta-subunit | Sulfurovum sp. AR                         |
| Ga0117756_1004299 | Epsilonproteobacteria | EpsilonBin027 | Ga0117756_10042996  | ATP-citrate lyase beta-subunit | Nitratiruptor sp. SB155-2                 |
| Ga0117756_1006995 | Epsilonproteobacteria | EpsilonBin053 | Ga0117756_10069953  | ATP-citrate lyase beta-subunit | Sulfurovum sp. AR                         |
| Ga0117756_1047188 | Epsilonproteobacteria | EpsilonBin071 | Ga0117756_10471882  | ATP-citrate lyase beta-subunit | Sulfurovum sp. AR                         |
| Ga0117756_1059723 | Epsilonproteobacteria | EpsilonBin033 | Ga0117756_10597232  | ATP-citrate lyase beta-subunit | Sulfurimonas autotrophica OK10, DSM 16294 |
| Ga0117756_1137333 | NA                    | NA            | Ga0117756_11373331  | ATP-citrate lyase beta-subunit | Sulfurimonas autotrophica OK10, DSM 16294 |
| Ga0117756_1139997 | NA                    | NA            | Ga0117756_11399971  | ATP-citrate lyase beta-subunit | Sulfurimonas autotrophica OK10, DSM 16294 |