

Supplemental Table S1 - Putative 3-OH Propionate Genes and their corresponding hidden Markov model hits

Enzyme ¹	Step in pathway
Acetyl/propionyl-CoA carboxylase, carboxyltransferase alpha subunit	1/4
Acetyl/propionyl-CoA carboxylase, carboxyltransferase beta subunit	1/4
Acetyl/propionyl-CoA carboxylase, biotin carboxyl carrier protein subunit	1/4
Acetyl/propionyl-CoA carboxylase, carboxyltransferase subunit (CT1)	1/4
Acetyl/propionyl-CoA carboxylase, carboxyltransferase subunit (CT2)	1/4
Acetyl/propionyl-CoA carboxylase, carboxyltransferase subunit (CT3)	1/4
Acetyl/propionyl-CoA carboxylase, carboxyltransferase subunit (CT4)	1/4
Acetyl/propionyl-CoA carboxylase, biotin carboxylase subunit	1/4
Acetyl/propionyl-CoA carboxylase, biotin carboxylase subunit	1/4
Acetyl/propionyl-CoA carboxylase, biotin carboxylase subunit	1/4
Malonyl-CoA reductase	2
Propionyl-CoA synthase	3
Methylmalonyl-CoA epimerase	5
Methylmalonyl-CoA mutase, C-terminus	6
Methylmalonyl-CoA mutase, N-terminus	6
Methylmalonyl-CoA mutase, N-terminus	6
Methylmalonyl-CoA mutase, N-terminus	6
Succinate dehydrogenase/fumarate reductase, b-cytochrome subunit	7
Succinate dehydrogenase/fumarate reductase, FeS subunit	7
Succinate dehydrogenase/fumarate reductase FeS subunit	7
Fumarate hydratase	7
Succinyl-CoA:L-malyl-CoA transferase, alpha subunit	8
Succinyl-CoA:L-malyl-CoA transferase, beta subunit	8
L-malyl-CoA lyase	9
succinyl-CoA:D-citramalate CoA transferase	12
D-citramalyl-CoA lyase	13

¹ Initial identification of 3-hydroxypropionate genes in *C. aurantiacus* J-10-fl genome used combination of profile HMMs, automatic genome annotations, and blastp analysis of 3-OHP gene sequences in OK-70-fl. Homologs in other genomes were determined by blastp analyses as described in Table 1 footnotes.

² Red text indicates HMM hit is above Noise Cutoff (NC) but not above the Trusted Cutoff (TC) in TIGRFAM database (see <http://www.tigr.org/TIGRFAMs/Explanations.shtml>).

<i>C. aurantiacus</i> J-10-fl				
Accession #	TIGRFAM ²	E-value	PFAM	E-value
ZP_00765934	TIGR00513 (accA)	4.10E-123	PF03255.4 (ACCA)	3.20E-051
ZP_00765933	TIGR00515 (accD)	2.20E-119	None	None
ZP_00765701	TIGR00531 (BCCP, accB)	5.00E-048		
ZP_00766450	None	None	PF01039.11 (carboxyltransferase domain)	5.00E-213
ZP_00766333	None	None	PF01039.11 (carboxyltransferase domain)	1.50E-256
ZP_00768256	None	None	PF01039.11 (carboxyltransferase domain)	8.40E-300
ZP_00767776	None	None	PF01039.11 (carboxyltransferase domain)	4.10E-256
ZP_00767008	TIGR00514 (accC)	6.90E-217	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	2.30E-103 5.30E-049 1.00E-045 3.10E-023
ZP_00768624	TIGR00514 (accC)	5.00E-265	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	5.20E-099 2.20E-047 1.20E-059 1.00E-024
ZP_00766319	TIGR00514 (accC)	1.80E-290	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C)	7.20E-111 1.20E-047 1.60E-061
ZP_00767341	None	None	PF00106.15 (adh_short, short chain dehydrogenase) PF01370.11 (Epimerase, NAD dep.)	6.30E-029 5.10E-004
ZP_00767417	None	None	PF00501.17 (AMP-binding) PF00378.9 (ECH: Enoyl-CoA hydratase family, GroES-like dom) PF08240.2 (ADH_N: alcohol dehydrnase, GroES domain)	3.30E-056 3.80E-049 2.40E-005
ZP_00767758	None	None	PF00903.15 (Glyoxalase)	2.90E-011
ZP_00768755	TIGR00640 (methylmalonyl-CoA mutase Cterm)	2.50E-048	PF02310.8 (B-12 binding)	6.40E-039
ZP_00768570	TIGR00641 (methylmalonyl-CoA mutase Nterm)	3.10E-285	PF01642.11 (MM_CoA_mutase)	0
	TIGR00640 (methylmalonyl-CoA mutase Cterm)	8.70E-065	PF02310.8 (B-12 binding)	7.10E-031
ZP_00768571	TIGR00641 (methylmalonyl-CoA mutase Nterm)	1.70E-107	PF01642.11 (MM_CoA_mutase)	1.50E-121
	TIGR00642 (methylmalonyl-CoA mutase small sub)	8.20E-109		
	TIGR00640 (methylmalonyl-CoA mutase Cterm)	2.90E-003		
ZP_00766014	TIGR00641 (methylmalonyl-CoA mutase Nterm)	4.20E-235	PF01642.11 (MM_CoA_mutase)	3.00E-255
ZP_00769191	TIGR02046 (sdhC b558 sub.)	2.10E-060	None	None
ZP_00769189	TIGR00384 (dhsB)	4.20E-015	PF00037.16 (Fer4, 4Fe-4S) PF00111.17 (Fer2, 2Fe-2S)	4.40E-005 7.60E-002
ZP_00769190	TIGR01811 (sdhA flavoprot. Sub)	0	PF00890.13 (FAD_binding_2) PF02910.10 (Succ_DH_flav_C) PF01266.13 (DAO)	6.70E-059 8.20E-010 1.40E-004
ZP_00766645	TIGR00839 (aspA)	1.10E-193	PF00206.10 (Lyase_1)	6.80E-135
ZP_00767840	None	None	PF02515.6 (CoA_transf_3)	9.90E-061
ZP_00767841	None	None	PF02515.6 (CoA_transf_3)	7.80E-065
ZP_00767843	None	None	PF03328.4 (HpcH_Hpal)	1.10E-012
ZP_00768727	None	None	PF02515.6 (CoA_transf_3)	6.10E-067
ZP_00768726	None	None	PF00682.8 (HMGL-like)	9.60E-032

<i>C. aggregans</i>				
Accession #	TIGRFAM	E-value	PFAM	E-value
ZP_01517425	TIGR00513 (accA)	2.60E-130	PF03255.4 (ACCA)	2.90E-050
ZP_01517424	TIGR00515 (accD)	1.00E-123	None	None
ZP_01516850	TIGR00531 (BCCP, accB)	6.60E-046		
ZP_01514351	None	None	PF01039.11 (carboxyltransferase domain)	4.70E-214
ZP_01515866	None	None	PF01039.11 (carboxyltransferase domain)	7.80E-262
ZP_01515721	None	None	PF01039.11 (carboxyltransferase domain)	2.80E-081
ZP_01514651	None	None	PF01039.11 (carboxyltransferase domain)	8.60E-261
ZP_01516463	TIGR00514 (accC)	2.90E-216	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	9.60E-102 2.20E-048 2.60E-047 2.60E-021
ZP_01515126	TIGR00514 (accC)	6.40E-259	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	1.10E-096 4.30E-046 1.60E-059 6.00E-024
ZP_01516152	TIGR00514 (accC)	2.70E-292	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C)	8.90E-110 1.70E-047 1.50E-061
ZP_01514509	None	None	PF00106.15 (adh_short, short chain dehydrogenase) PF01370.11 (NAD dep. epimerase/dehydratase)	1.70E-036 8.50E-004
ZP_01517350	None	None	PF00378.9 (ECH: Enoyl-CoA hydratase family, GroES-like dom) PF08240.2 (ADH_N: alcohol dehydrnase, GroES domain)	8.50E-008 3.40E-005
ZP_01514668	None	None	PF00903.15 (Glyoxalase)	1.00E-013
ZP_01515264	TIGR00640 (methylmalonyl-CoA mutase Cterm)	1.20E-048	PF02310.8 (B-12 binding)	1.00E-038
ZP_01517339	TIGR00641 (methylmalonyl-CoA mutase Nterm) TIGR00640 (methylmalonyl-CoA mutase Cterm)	5.00E-283 1.80E-064	PF01642.11 (MM_CoA_mutase) PF02310.8 (B-12 binding)	0 2.50E-032
ZP_01517338	TIGR00641 (methylmalonyl-CoA mutase Nterm) TIGR00642 (methylmalonyl-CoA mutase small sub) TIGR00640 (methylmalonyl-CoA mutase Cterm)	1.80E-104 2.50E-128 3.30E-003	PF01642.11 (MM_CoA_mutase)	1.60E-127
ZP_01515118	TIGR00641 (methylmalonyl-CoA mutase Nterm)	5.30E-237	PF01642.11 (MM_CoA_mutase)	1.30E-254
ZP_01514963	TIGR02046 (sdhC b558 sub.)	1.70E-061	None	None
ZP_01514965	TIGR00384 (dhsB)	6.40E-016	PF00037.16 (Fer4, 4Fe-4S) PF00111.17 (Fer2, 2Fe-2S)	4.40E-005 1.00E-001
ZP_01514964	TIGR01811 (sdhA flavoprot. Sub)	0	PF00890.13 (FAD_binding_2) PF02910.10 (Succ_DH_flav_C) PF01266.13 (DAO)	9.20E-059 4.60E-010 1.50E-004
ZP_01516094	TIGR00839 (aspA)	3.60E-191	PF00206.10 (Lyase_1)	6.30E-137
ZP_01516527	None	None	PF02515.6 (CoA_transf_3)	8.10E-066
ZP_01516526	None	None	PF02515.6 (CoA_transf_3)	1.00E-063
ZP_01516524	None	None	PF03328.4 (HpcH_Hpal)	1.10E-010
ZP_01514248	None	None	PF02515.6 (CoA_transf_3)	3.40E-064
ZP_01514247	None	None	PF00682.8 (HMGL-like)	5.10E-033

Roseiflexus sp.RS-1				
Accession #	TIGRFAM	E-value	PFAM	E-value
ZP_01355546	TIGR00513 (accA)	8.10E-134	PF03255.4 (ACCA)	5.40E-046
ZP_01357316	TIGR00513 (accA)	1.10E-121	PF03255.4 (ACCA)	2.40E-048
ZP_01355547	TIGR00515 (accD)	1.20E-123	None	None
ZP_01357318	TIGR00515 (accD)	2.30E-104	None	None
ZP_01355575	TIGR00531 (BCCP, accB)	5.30E-042	None	None
ZP_01356591	None	None	PF01039.11 (carboxyltransferase domain)	7.90E-218
ZP_01356719	None	None	PF01039.11 (carboxyltransferase domain)	8.60E-269
ZP_01356342	None	None	PF01039.11 (carboxyltransferase domain)	1.80E-301
ZP_01359695	None	None	PF01039.11 (carboxyltransferase domain)	8.00E-264
ZP_01357276	TIGR00514 (accC)	3.40E-207	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	6.10E-106 8.10E-048 1.10E-045 4.70E-017
ZP_01356809	TIGR00514 (accC)	7.40E-254	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	5.80E-103 5.80E-049 2.20E-062 4.20E-019
ZP_01355543	TIGR00514 (accC)	6.40E-284	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C)	7.30E-113 5.30E-045 2.00E-063
ZP_01355545	None	None	PF00106.15 (adh_short, short chain dehydrogenase) PF03807.6 (NADP oxidoreduc, F420 dep.)	4.90E-031 4.50E-003
ZP_01355544	None	None	PF00501.17 (AMP-binding) PF00378.9 (ECH: Enoyl-CoA hydratase family, GroES-like dom) PF08240.2 (ADH_N: alcohol dehydrnase, GroES domain)	4.50E-062 1.00E-045 3.80E-005
ZP_01357008	None	None	PF00903.15 (Glyoxalase)	6.60E-020
ZP_01356241	TIGR00640 (methylmalonyl-CoA mutase Cterm)	3.60E-043	PF02310.8 (B-12 binding)	1.30E-036
ZP_01356321	TIGR00641 (methylmalonyl-CoA mutase Nterm) TIGR00640 (methylmalonyl-CoA mutase Cterm)	1.40E-282 2.60E-064	PF01642.11 (MM_CoA_mutase) PF02310.8 (B-12 binding)	0 4.40E-028
ZP_01356322	TIGR00641 (methylmalonyl-CoA mutase Nterm) TIGR00642 (methylmalonyl-CoA mutase small sub) TIGR00640 (methylmalonyl-CoA mutase Cterm)	3.50E-115 6.50E-116 6.60E-005	PF01642.11 (MM_CoA_mutase)	6.40E-130
ZP_01359158	TIGR00641 (methylmalonyl-CoA mutase Nterm)	6.90E-240	PF01642.11 (MM_CoA_mutase)	1.60E-254
ZP_01357781	TIGR02046 (sdhC b558 sub.)	1.90E-066	None	None
ZP_01357783	TIGR00384 (dhsB)	2.40E-017	PF00037.16 (Fer4, 4Fe-4S) PF00111.17 (Fer2, 2Fe-2S)	6.70E-005 2.00E-002
ZP_01357782	TIGR01811 (sdhA flavoprot. Sub)	0	PF00890.13 (FAD_binding_2) PF02910.10 (Succ_DH_flav_C) PF01266.13 (DAO)	4.30E-057 5.00E-012 3.20E-005
ZP_01359213	TIGR00839 (aspA)	6.40E-185	PF00206.10 (Lyase_1)	1.80E-130
ZP_01357610	None	None	PF02515.6 (CoA_transf_3)	1.50E-065
ZP_01357611	None	None	PF02515.6 (CoA_transf_3)	1.60E-066
ZP_01357613	None	None	PF03328.4 (HpcH_Hpal)	1.90E-010
ZP_01356548	None	None	PF02515.6 (CoA_transf_3)	8.90E-071
ZP_01356547	None	None	PF00682.8 (HMGL-like)	1.90E-034

<i>R. castenholzii</i>				
Accession #	TIGRFAM	E-value	PFAM	E-value
ZP_01531379	TIGR00513 (accA)	2.20E-130	PF03255.4 (ACCA)	1.50E-048
ZP_01530807	TIGR00513 (accA)	2.60E-127	PF03255.4 (ACCA)	7.40E-048
ZP_01531380	TIGR00515 (accD)	1.80E-120	None	None
ZP_01530809	TIGR00515 (accD)	7.50E-109	None	None
ZP_01531408	TIGR00531 (BCCP, accB)	1.50E-042	None	None
ZP_01530384	None	None	PF01039.11 (carboxyltransferase domain)	2.10E-214
ZP_01530368	None	None	PF01039.11 (carboxyltransferase domain)	2.40E-270
ZP_01531322	None	None	PF01039.11 (carboxyltransferase domain)	2.30E-300
ZP_01531424	None	None	PF01039.11 (carboxyltransferase domain)	2.30E-300
ZP_01530388	TIGR00514 (accC)	5.00E-213	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	1.60E-105 1.10E-047 3.30E-047 2.80E-014
ZP_01533205	TIGR00514 (accC)	8.40E-259	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	8.80E-104 5.80E-049 3.50E-060 3.50E-020
ZP_01531376	TIGR00514 (accC)	3.20E-279	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C)	1.50E-110 7.30E-045 1.60E-063
ZP_01531378	None	None	PF00106.15 (adh_short, short chain dehydrogenase)	1.10E-029
ZP_01531377	None	None	PF00501.17 (AMP-binding) PF00378.9 (ECH: Enoyl-CoA hydratase family, GroES-like dom) PF08240.2 (ADH_N: alcohol dehydrnase, GroES domain)	1.10E-059 1.00E-045 2.00E-005
ZP_01531892	None	None	PF00903.15 (Glyoxalase)	1.10E-019
ZP_01532326	TIGR00640 (methylmalonyl-CoA mutase Cterm)	2.10E-046	PF02310.8 (B-12 binding)	2.10E-037
ZP_01533144	TIGR00641 (methylmalonyl-CoA mutase Nterm) TIGR00640 (methylmalonyl-CoA mutase Cterm)	1.70E-283 8.00E-063	PF01642.11 (MM_CoA_mutase) PF02310.8 (B-12 binding)	0 1.30E-030
ZP_01533145	TIGR00641 (methylmalonyl-CoA mutase Nterm) TIGR00642 (methylmalonyl-CoA mutase small sub) TIGR00640 (methylmalonyl-CoA mutase Cterm)	1.90E-116 1.70E-120 9.20E-004	PF01642.11 (MM_CoA_mutase)	3.00E-140
ZP_01533682	TIGR00641 (methylmalonyl-CoA mutase Nterm)	5.70E-240	PF01642.11 (MM_CoA_mutase)	2.70E-256
ZP_01531119	TIGR02046 (sdhC b558 sub.)	1.20E-066	None	None
ZP_01531117	TIGR00384 (dhsB)	2.80E-017	PF00037.16 (Fer4, 4Fe-4S) PF00111.17 (Fer2, 2Fe-2S)	1.40E-004 3.70E-002
ZP_01531118	TIGR01811 (sdhA flavoprot. Sub)	0	PF00890.13 (FAD_binding_2) PF02910.10 (Succ_DH_flav_C) PF01266.13 (DAO)	1.60E-054 5.90E-012 5.20E-005
ZP_01531632	TIGR00839 (aspA)	5.20E-182	PF00206.10 (Lyase_1)	3.70E-129
ZP_01531617	None	None	PF02515.6 (CoA_transf_3)	1.30E-064
ZP_01531618	None	None	PF02515.6 (CoA_transf_3)	1.50E-067
ZP_01531620	None	None	PF03328.4 (HpcH_Hpal)	
ZP_01532409	None	None	PF02515.6 (CoA_transf_3)	2.50E-65
ZP_01532408	None	None	PF00682.8 (HMGL-like)	3.10E-31

<i>H. aurantiacus</i>				
Accession #	TIGRFAM	E-value	PFAM	E-value
ZP_01427913	TIGR00513 (accA)	1.70E-139	PF03255.4 (ACCA)	1.30E-045
ZP_01427914	TIGR00515 (accD)	9.90E-126	None	None
ZP_01423245	TIGR00531 (BCCP, accB)	5.40E-040		
ZP_01426128	None	None	PF01039.11 (carboxyltransferase domain)	1.70E-209
ZP_01423344	None	None	PF01039.11 (carboxyltransferase domain)	2.90E-301
ZP_01426793	TIGR00514 (accC)	5.20E-227	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	5.70E-097 9.20E-050 1.20E-048 6.90E-024
ZP_01425029	TIGR00514 (accC)	6.90E-255	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C) PF00364.12 (Biotin_lipoyl)	2.90E-101 3.70E-046 5.60E-058 2.40E-018
ZP_01424256	TIGR00514 (accC)	1.80E-294	PF02786.7 (CPSase_L_D2) PF00289.12 (CPSase_L_chain) PF02785.8 (Biotin_carb_C)	2.40E-108 1.10E-046 2.70E-058
ZP_01423212	TIGR00839 (aspA)	4.30E-194	PF00206.10 (lyase)	2.50E-128
ZP_01425095	TIGR02188 (AcsA)	0	PF00501.17 (AMP-binding)	2.20E-134
ZP_01423940	None	None	PF00903.15 (Glyoxalase)	1.30E-013
ZP_01424623	TIGR00640 (methylmalonyl-CoA mutase Cterm)	2.40E-043	PF02310.8 (B-12 binding)	1.40E-035
ZP_01425886	TIGR00641 (methylmalonyl-CoA mutase Nterm)	3.40E-223	PF01642.11 (MM_CoA_mutase)	1.60E-234
ZP_01427428	TIGR00641 (methylmalonyl-CoA mutase Nterm)	2.60E-233	PF01642.11 (MM_CoA_mutase)	9.10E-248
ZP_01427428	TIGR00641 (methylmalonyl-CoA mutase Nterm)	2.60E-233	PF01642.11 (MM_CoA_mutase)	9.10E-248
ZP_01424827	TIGR02046 (sdhC b558 sub.)	1.80E-084	None	None
ZP_01424829	TIGR00384 (chsB)	1.10E-013	PF00037.16 (Fer4, 4Fe-4S) PF00111.17 (Fer2, 2Fe-2S)	4.50E-005 8.00E-002
ZP_01424828	TIGR01811 (sdhA flavoprot. Sub)	0	PF00890.13 (FAD_binding_2) PF02910.10 (Succ_DH_flav_C) PF01266.13 (DAO)	3.60E-044 2.20E-009 5.20E-004
ZP_01423212	TIGR00839 (aspA)	4.30E-194	PF00206.10 (Lyase_1)	2.50E-128
ZP_01424508	None	None	PF02515.6 (CoA_transf_3)	4.50E-062
ZP_01424508	None	None	PF02515.6 (CoA_transf_3)	4.50E-062
ZP_01426861	None	None	PF03328.4 (HpcH_Hpal)	4.90E-046
ZP_01424508	None	None	PF02515.6 (CoA_transf_3)	4.50E-062
ZP_01424269	None	None	PF00682.8 (HMGL-like)	5.80E-046

Supplemental Table S2 – Metagenome libraries

Sample	Temperature	Layer	Lysis Procedure	Clone Insert Size	# of Reads
Octopus Spring High Temperature	58-67°C	0-1 mm	Enzymatic	2-3 kb	4216
		0-1 mm	Enzymatic	10-12 kb	3838
Octopus Spring Low Temperature	53.5-63.4°C	0-1 mm	Enzymatic	2-3 kb	19142
		0-1 mm	Enzymatic	10-12 kb	79674
Octopus Spring Total (collected November 5th 2004)					106870
Sample	Temperature	Layer	Lysis Procedure	Clone Insert Size	# of Reads
Mushroom Spring High Temperature	65°C	0-1 mm	Enzymatic	2-3 kb	8001
		0-1 mm	Enzymatic	10-12 kb	7280
		0-1 mm	Mechanical	2-3 kb	689
		0-1 mm	Mechanical	10-12 kb	722
		1-2 mm	Mechanical	3-4 kb	5759
		1-2 mm	Mechanical	5-6 kb	5427
		7-8 mm	Mechanical	4-5 kb	5772
Mushroom Spring Low Temperature	60°C	0-1 mm	Enzymatic	3-4 kb	15837
		0-1 mm	Enzymatic	8-9 kb	23341
		0-1 mm	Mechanical	3-4 kb	5650
		0-1 mm	Mechanical	5-6 kb	5661
		1-2 mm	Mechanical	5-6 kb	5679
		4-5 mm	Mechanical	5-6 kb	5643
Mushroom Spring Total (collected October 2nd 2003)					95461
Metagenome Total					202331