

Table 1. *B. thetaiotaomicron* genes that are regulated by the presence of *M. smithii* in vivo

COG Category	COG totals (Bt/Ms vs. Bt)	Gene ID	Annotation	GeneChip		
				Fold difference	P value	
Translation [J]	48 up-regulated (170)*	BT3430	Ribosomal protein S20	6.5	5.2E-03	
		BT2161	50S ribosomal protein L9	5.7	6.3E-03	
		BT3995	Alanyl-tRNA synthetase	3.7	1.9E-03	
		BT2162	30S ribosomal protein S18	3.2	2.3E-03	
		BT1669	Phenylalanyl-tRNA synthetase alpha chain	3.1	7.2E-03	
		BT0810	Hypothetical protein	3.1	2.2E-03	
		BT3877	30S ribosomal protein S2 (BS1)	2.9	2.5E-03	
		BT3876	30S ribosomal protein S9	2.6	3.2E-03	
		BT2163	30S ribosomal protein S6	2.6	1.9E-03	
		BT3878	Elongation factor Ts (EF-Ts)	2.6	6.4E-03	
		BT3709	Elongation factor P	2.5	6.1E-03	
		BT3875	50S ribosomal protein L13	2.5	4.9E-03	
		BT2729	Elongation factor G	2.5	5.5E-03	
		BT2705	Translation initiation factor IF-1	2.4	8.8E-03	
		BT0425	50S ribosomal protein L20	2.4	5.7E-03	
		BT2004	RimM protein, required for 16S rRNA processing	2.3	9.5E-03	
		BT2718	30S ribosomal protein S17	2.3	1.3E-03	
		BT2736	Ribosomal protein L10	2.3	6.3E-03	
		BT0916	50S ribosomal protein L28	2.3	5.9E-03	
		BT3611	Glycyl-tRNA synthetase	2.2	8.4E-03	
		BT4313	50S ribosomal protein L27	2.2	5.5E-03	
		BT2727	50S ribosomal protein L3	2.2	5.1E-03	
		BT2726	50S ribosomal protein L4	2.2	6.5E-03	
		BT3710	50S ribosomal protein L34	2.1	2.5E-03	
		BT2720	50S ribosomal protein L16	2.1	5.8E-03	
		BT2737	50S ribosomal protein L1	2.1	6.4E-03	
		BT2717	50S ribosomal protein L14	2.0	3.8E-03	
		BT2738	50S ribosomal protein L11	2.0	6.6E-03	
		BT2730	30S ribosomal protein S7	2.0	4.8E-03	
		BT2731	30S ribosomal protein S12	2.0	1.3E-03	
		BT4562	Hypothetical protein	2.0	3.7E-03	
		BT2735	50S ribosomal protein L7/L12	2.0	3.8E-03	
		BT2728	30S ribosomal protein S10	2.0	6.8E-03	
		BT0872	Aspartyl-tRNA synthetase	2.0	6.4E-03	
		BT0915	50S ribosomal protein L33	2.0	5.9E-03	
		BT4312	Seryl-tRNA synthetase	1.9	6.6E-03	
		BT0423	Translation initiation factor IF-3	1.9	5.2E-03	
		BT3833	50S ribosomal protein L32 (Ribosomal protein I)	1.9	7.0E-03	
		BT1360	tRNA/rRNA methyltransferase	1.9	6.2E-05	
		BT0424	50S ribosomal protein L35	1.8	3.0E-03	
		BT2725	50S ribosomal protein L23	1.8	5.8E-03	
		BT2719	50S ribosomal protein L29	1.8	6.2E-03	
		BT3772	Ribosomal large subunit pseudouridine synthase D	1.7	8.1E-03	
		BT2716	50S ribosomal protein L24	1.7	8.6E-03	
		BT2723	30S ribosomal protein S19	1.7	9.0E-03	
		BT2933	Methionyl-tRNA synthetase	1.5	6.9E-03	
		BT3945	Methionyl-tRNA formyltransferase	1.5	3.8E-03	
		BT4323	tRNA delta(2)-isopentenylpyrophosphate transferase	1.4	2.4E-03	
		3 down-regulated (170)	BT3592	Alpha-galactosidase precursor	-1.6	4.8E-03
			BT3024	Putative outer membrane protein, probably involved in nutrient binding	-1.9	1.2E-03
BT4295	Putative chitinase		-2.4	4.3E-03		
Coenzyme transport and metabolism [H]	16 up-regulated (108)	BT1763	Putative outer membrane protein, probably involved in nutrient binding	11.8	3.0E-03	
		BT3226	Hypothetical protein	3.6	6.9E-03	
		BT0575	Hypothetical protein	2.6	7.1E-03	
		BT4560	Thiamine biosynthesis lipoprotein apbE precursor	2.6	6.0E-04	
		BT4594	Putative dephospho-CoA kinase	2.5	2.7E-03	
		BT2168	Coproporphyrinogen III oxidase	2.1	7.0E-03	
		BT3117	Putative oxidoreductase	2.1	2.2E-03	
		BT1836	Thiamine biosynthesis protein ThiH	2.0	6.3E-04	
		BT4253	6,7-dimethyl-8-ribityllumazine synthase	1.9	5.7E-03	
		BT4216	Ubiquinone/menaquinone biosynthesis	1.8	1.2E-04	
		BT4563	Hypothetical protein	1.8	3.6E-03	

		BT2011	Putative nicotinate-nucleotide adenyltransferase	1.8	7.7E-03
		BT4258	Putative 5-formyltetrahydrofolate cyclo-ligase	1.7	8.4E-03
		BT0891	Dihydroorotate dehydrogenase electron transfer	1.6	2.5E-03
		BT3918	Pyridoxal phosphate biosynthetic protein pdxJ	1.5	8.2E-03
		BT2396	Putative membrane transporter involved in nicotinamide mononucleotide transport	1.5	5.3E-03
	4 down-regulated (108)	BT2238	Putative biotin--(acetyl-CoA carboxylase) synthetase	-1.3	5.7E-03
		BT1403	1-deoxy-D-xylulose 5-phosphate synthase	-1.4	7.5E-03
		BT0343	Methylcobamide:CoM methyltransferase mtbA	-1.5	9.6E-03
		BT4298	Putative outer membrane protein, probably involved in nutrient binding	-2.5	1.6E-03
<b>Cell motility [N]</b>	1 up-regulated (21)	BT4219	Hypothetical protein	1.9	8.1E-05
	1 down-regulated (21)	BT0345	Hypothetical protein	-1.6	2.0E-03
<b>Defense mechanisms [V]</b>	4 up-regulated (105)	BT1600	BexA, membrane proein	1.8	5.6E-03
		BT3119	Chloramphenicol acetyltransferase	1.8	1.5E-03
		BT4318	ATP-binding protein	1.7	9.2E-03
		BT4507	Beta-lactamase precursor	1.4	2.1E-03
	5 down-regulated (105)	BT0300	Cation efflux system (AcrB/AcrD/AcrF family)	-1.4	7.8E-03
		BT2377	Cation efflux pump	-1.4	6.3E-03
		BT2118	Transporter, AcrB/D/F family	-1.6	3.7E-03
		BT4408	Hypothetical protein	-1.7	9.3E-04
		BT4627	DNA modification methylase	-1.7	6.3E-03
<b>Cell wall/membrane bioogenesis [M]</b>	15 up-regulated (357)	BT1370	NAD dependent nucleotide-diphosphate-sugar epimerase	2.6	1.2E-04
		BT0829	UDP-glucose 6-dehydrogenase	2.5	6.0E-03
		BT1730	Putative dTDP-4-dehydrorhamnose reductase	2.5	7.1E-03
		BT2937	Putative glycosyltransferase	2.4	1.3E-03
		BT3814	Rod shape-determining protein	2.4	1.6E-03
		BT2798	Carboxy-terminal processing protease precursor	2.4	2.9E-03
		BT1613	Hypothetical protein	2.0	4.8E-03
		BT3118	Prolipoprotein diacylglycerol transferase	1.9	6.8E-03
		BT2944	Putative UDP-N-acetylglucosamine 2-epimerase	1.9	1.6E-03
		BT4283	Hypothetical protein	1.7	1.9E-03
		BT3372	Glycosyltransferase	1.6	8.0E-03
		BT3376	Nucleotide sugar transaminase	1.5	4.4E-03
		BT4703	Chloromuconate cycloisomerase	1.4	5.7E-03
		BT1608	Capsule biosynthesis protein capA	1.4	8.7E-03
		BT3996	Putative peptidase	1.4	6.3E-03
	18 down-regulated (357)	BT1194	Outer membrane protein, OmpA family	-1.3	6.5E-03
		BT4129	Outer membrane assembly protein	-1.3	4.9E-03
		BT3905	Putative alkaline protease aprF	-1.4	7.2E-03
		BT4410	Hypothetical protein	-1.4	9.1E-03
		BT2665	TonB	-1.5	3.4E-03
		BT2927	Conserved hypothetical protein, putative cell wall-associated protein precursor	-1.5	8.8E-04
		BT1313	Muconate cycloisomerase	-1.5	2.7E-03
		BT1550	Hypothetical protein	-1.5	8.2E-03
		BT1213	Periplasmic component of efflux system	-1.5	7.9E-03
		BT3026	Glycosylhydrolase, putative xylanase	-1.5	2.3E-03
		BT4153	Exopolygalacturonase precursor	-1.5	2.9E-03
		BT4304	Putative glycosyltransferase	-1.6	7.1E-03
		BT2117	Outer membrane protein, putative	-1.6	1.9E-03
		BT0610	Lipopolysaccharide biosynthesis protein, putative glycosyltransferase	-1.7	1.6E-03
		BT0813	TonB	-1.7	8.7E-04
		BT0669	Putative cation efflux system protein	-1.8	2.9E-03
		BT2086	Choloylglycine hydrolase	-1.8	6.0E-03
		BT2762	TonB	-1.9	4.6E-03
<b>Replication, recombination and repair [L]</b>	12 up-regulated (278)	BT1499	DNA-binding protein HU	2.6	1.7E-03
		BT2143	Chromosomal replication initiator protein dnaA	2.5	2.8E-03
		BT3979	Putative methyltransferase	2.4	7.3E-04
		BT2236	Hypothetical protein	1.9	7.3E-03
		BT3255	Putative N6-adenine-specific DNA methylase	1.9	5.6E-03
		BT3938	ATP-dependent DNA helicase recQ	1.8	4.5E-03
		BT3478	Integrase	1.8	2.3E-03
		BT1671	Endonuclease III	1.6	4.5E-03
		BT0570	Excinuclease ABC subunit B	1.5	3.3E-03
		BT0419	Putative endonuclease	1.5	6.2E-04
		BT0578	Excinuclease ABC subunit A	1.4	4.5E-03
		BT2056	Hypothetical protein	1.2	7.2E-03

	17 down-regulated (278)	BT2272	Hypothetical protein	-1.3	4.4E-03
		BT4343	Hypothetical protein	-1.4	4.6E-03
		BT1509	Integrase	-1.5	6.1E-03
		BT1411	Methylated-DNA--protein-cysteine methyltransferase	-1.5	4.0E-03
		BT2294	Conserved protein found in conjugate transposon	-1.5	6.4E-03
		BT0615	Hypothetical protein	-1.6	4.8E-03
		BT3860	Hypothetical protein	-1.6	3.9E-03
		BT2830	DNA-binding protein HU-beta	-1.6	5.2E-04
		BT2488	Integrase	-1.6	2.8E-03
		BT0291	Integrase	-1.7	3.4E-04
		BT2349	Transposase	-1.7	6.8E-04
		BT4469	Hypothetical protein	-1.7	1.7E-03
		BT3020	Hypothetical protein	-1.8	4.7E-03
		BT0795	Hypothetical protein	-1.8	1.7E-03
		BT1424	Hypothetical protein	-1.9	4.3E-03
		BT4021	Integrase	-2.0	5.5E-04
		BT1980	Transposase	-2.4	1.7E-04
<b>Nucleotide transport and metabolism [F]</b>	13 up-regulated (80)	BT4582	Amidophosphoribosyltransferase precursor	4.8	6.9E-03
		BT4387	Adenylate kinase (ATP-AMP transphosphatase)	3.1	2.3E-03
		BT0748	Ribose-phosphate pyrophosphokinase	3.1	4.6E-03
		BT2791	Uracil phosphoribosyltransferase	3.0	4.7E-03
		BT3989	Hypothetical protein	2.6	1.0E-04
		BT3267	Adenine phosphoribosyltransferase	2.4	1.5E-03
		BT2145	Ribonucleoside-diphosphate reductase alpha chain	2.1	7.8E-03
		BT0651	Thiamine biosynthesis protein ThiG	2.1	6.0E-03
		BT1733	Putative phosphoribosylformylglycinamide synthase	2.1	4.1E-03
		BT0590	CTP synthase (UTP-ammonia ligase)	2.0	4.8E-03
		BT4217	Phosphoribosylamidoimidazole-succinocarboxamide synthase	1.9	3.2E-04
		BT0686	Putative uracil permease (uracil transporter)	1.7	2.2E-03
		BT2060	Cytidylate kinase	1.5	6.2E-03
		BT2527	Uridine kinase (uridine monophosphokinase)	-1.4	4.1E-03
		BT2566	HIT family protein	-1.4	8.7E-03
		BT0888	AMP nucleosidase	-1.5	1.1E-03
		BT1588	Hypothetical protein	-1.5	3.4E-03
<b>Secondary metabolites biosynthesis, transport and catabolism [Q]</b>	1 up-regulated (31)	BT3771	3-oxoacyl-[acyl-carrier protein] reductase	1.5	6.6E-04
	2 down-regulated (31)	BT0199	Hypothetical protein	-1.7	3.7E-03
		BT2692	Imidazolonepropionase	-2.0	6.0E-03
<b>Intracellular trafficking and secretion [U]</b>	3 up-regulated (54)	BT1601	Putative signal recognition protein	2.6	7.9E-03
		BT2835	Protein-export membrane protein SecD/SecE	2.3	1.9E-03
		BT4103	Putative Sec-independent protein translocase	1.5	3.3E-03
	4 down-regulated (54)	BT2668	MotA/TolQ/ExbB proton channel	-1.7	9.8E-05
		BT1108	Conserved hypothetical protein, putative integral membrane protein	-1.9	6.0E-03
		BT1072	Hypothetical protein	-2.0	1.8E-03
		BT3347	Hypothetical protein	-2.2	6.2E-03
<b>Lipid transport and metabolism [I]</b>	8 up-regulated (70)	BT3358	3-oxoacyl-[acyl-carrier-protein] synthase II	2.6	2.9E-03
		BT1526	Myo-inositol-1-phosphate synthase	2.2	1.2E-03
		BT1523	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	2.1	9.4E-03
		BT3834	3-oxoacyl-[acyl-carrier-protein] synthase III	1.9	4.3E-03
		BT3884	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.7	1.3E-03
		BT4322	Conserved hypothetical protein, with a diacylglycerol kinase catalytic domain	1.6	5.6E-04
		BT0122	3-oxoacyl-[acyl-carrier-protein] synthase III	1.6	9.8E-03
		BT1806	Acyl-CoA dehydrogenase	1.6	8.1E-05
	6 down-regulated (70)	BT3978	Putative cardiolipin synthetase	-1.3	2.4E-03
		BT0260	Acyltransferase family protein	-1.3	6.5E-03
		BT0135	Hypothetical protein	-1.4	6.1E-03
		BT1449	Biotin carboxylase	-2.3	5.1E-03
		BT0316	Putative hemin receptor	-2.3	2.4E-03
		BT1450	Propionyl-CoA carboxylase beta chain	-2.5	4.1E-03
<b>Amino acid transport and metabolism [E]</b>	12 up-regulated (209)	BT3866	Glutamine-dependent carbamyl phosphate synthetase	3.7	2.0E-03
		BT1288	Spermidine/putrescine ABC transporter	3.3	7.4E-03
		BT3760	Argininosuccinate synthase	2.8	5.0E-03
		BT3759	N-acetyl-gamma-glutamyl-phosphate reductase	2.7	4.9E-03

		BT2834	Peptidyl-dipeptidase	2.2	4.1E-03	
		BT4215	Shikimate 5-dehydrogenase	2.2	6.8E-05	
		BT0569	Hypothetical protein	2.0	5.1E-04	
		BT4257	Putative histidinol-phosphatase	2.0	2.4E-03	
		BT3395	Putative acetylglutamate kinase	1.9	9.8E-04	
		BT0457	Sialic acid-specific 9-O-acetyltransferase	1.7	3.5E-03	
		BT0674	Carboxynorspermidine decarboxylase	1.6	3.0E-03	
		BT1789	Aminopeptidase C (bleomycin hydrolase)	1.3	8.6E-03	
	18 down-regulated (209)	BT4584	Putative aminomethyltransferase	-1.4	9.3E-03	
		BT2522	Xaa-Pro aminopeptidase	-1.5	2.8E-03	
		BT4424	Sorbitol dehydrogenase	-1.5	7.1E-03	
		BT4150	Putative rhamnogalacturonan acetyltransferase	-1.5	8.7E-03	
		BT4412	Hypothetical protein	-1.5	3.9E-03	
		BT4502	Hypothetical protein	-1.5	4.5E-04	
		BT2621	Hypothetical protein	-1.7	1.3E-03	
		BT4078	Hypothetical protein	-1.8	2.3E-03	
		BT2691	Methenyltetrahydrofolate cyclohydrolase	-1.9	2.1E-03	
		BT1743	Hypothetical protein	-1.9	3.5E-04	
		BT2404	L-asparaginase I	-2.0	6.4E-03	
		BT1064	Hypothetical protein	-2.0	8.0E-04	
		BT1492	Tyrosine phenol-lyase	-2.0	3.1E-03	
		BT3734	Oxidoreductase	-2.1	3.4E-03	
		BT2690	Histidine ammonia-lyase	-2.3	9.9E-03	
		BT2693	Formiminotransferase-cyclodeaminase	-2.6	1.7E-03	
		BT2694	Putative urocanate hydratase	-3.0	1.5E-04	
		BT1554	Alanine dehydrogenase	-3.5	5.0E-05	
General function prediction only [R]	32 up-regulated (394)	BT3220	TPR-repeat-containing protein	5.6	6.2E-04	
		BT2160	Putative regulatory protein	3.0	8.8E-03	
		BT4388	GTP-binding protein	3.0	8.4E-03	
		BT4595	Hypothetical protein	2.9	6.6E-04	
		BT3373	Spermidine n1-acetyltransferase	2.8	2.4E-04	
		BT2035	Putative ABC transporter ATP-binding protein	2.6	2.2E-03	
		BT2542	Putative haloacid dehalogenase-like hydrolase	2.6	1.3E-03	
		BT0883	Hypothetical protein	2.5	3.7E-03	
		BT4339	Glutamine synthetase	2.4	5.9E-03	
		BT0822	Putative metallo-beta-lactamase superfamily hydrolase	2.4	4.7E-03	
		BT3730	Putative regulatory protein	2.3	6.5E-04	
		BT4320	Putative zinc protease	2.0	1.3E-03	
		BT4254	Hypothetical protein	2.0	5.6E-03	
		BT0334	Hypothetical protein	1.8	3.2E-03	
		BT1229	Conserved hypothetical protein, putative membrane protein	1.7	8.6E-03	
		BT4369	Hypothetical protein	1.7	9.0E-03	
		BT2417	Hypothetical protein	1.7	3.5E-03	
		BT1186	ABC transporter ATP-binding protein	1.6	3.2E-03	
		BT2832	Rhomboid family protein	1.6	8.1E-03	
		BT3837	ABC transporter ATP-binding protein	1.6	3.4E-04	
		BT4315	HPr(Ser) phosphatase	1.6	6.2E-03	
		BT2134	Putative HD superfamily hydrolase	1.6	4.1E-03	
		BT3405	Hypothetical protein	1.6	7.0E-03	
		BT4214	Hypothetical protein	1.6	7.4E-03	
		BT0766	Hypothetical protein	1.5	5.5E-04	
		BT2207	Putative ATPase/GTPase	1.5	1.6E-03	
		BT3459	Hemolysin A	1.5	9.6E-04	
		BT1666	Hydrolase, haloacid dehalogenase-like hydrolase	1.5	2.4E-03	
		BT4346	Conserved hypothetical protein, with a Metallo-beta-lactamase superfamily domain	1.4	1.5E-03	
		BT2018	Hypothetical protein	1.4	5.9E-03	
		BT0774	Conserved protein with a conserved patatin-like phospholipase domain	1.4	7.4E-03	
		BT1851	TPR-repeat-containing protein	1.3	1.4E-03	
		36 down-regulated (394)	BT2371	Putative protease/amidase	-1.2	6.0E-03
			BT3432	Hypothetical protein	-1.3	7.6E-03
			BT4509	Hypothetical protein	-1.4	3.8E-03
			BT0278	Hypothetical protein	-1.4	9.2E-03
			BT0168	Hypothetical protein	-1.4	3.9E-03
			BT2384	Acetyltransferase	-1.4	9.5E-03
			BT2209	Putative nucleotidyltransferase	-1.5	9.5E-03
			BT2385	Hypothetical protein	-1.5	8.1E-03

		BT3023	Hypothetical protein	-1.5	1.4E-03		
		BT3401	Hypothetical protein	-1.5	6.2E-03		
		BT0585	Hypothetical protein	-1.5	8.1E-04		
		BT4556	Hypothetical protein	-1.5	2.7E-03		
		BT4140	Hypothetical protein	-1.5	2.9E-03		
		BT1707	Hypothetical protein	-1.6	1.5E-03		
		BT1894	TPR-repeat-containing proteins	-1.6	2.8E-03		
		BT0057	Hypothetical protein	-1.6	4.8E-03		
		BT1263	Putative protease I	-1.6	1.5E-03		
		BT0164	Hypothetical protein	-1.6	5.7E-03		
		BT1839	Hypothetical protein	-1.6	5.5E-03		
		BT0479	Putative glycosyltransferase	-1.6	2.1E-03		
		BT2756	Anaerobic C4-dicarboxylate transporter dcuB	-1.7	7.3E-03		
		BT3467	Putative glycosylhydrolase	-1.7	8.3E-04		
		BT0448	Hypothetical protein	-1.7	3.1E-03		
		BT4108	Hypothetical protein	-1.7	7.0E-03		
		BT1016	Conserved protein with a conserved patatin-like phospholipase domain	-1.7	8.7E-03		
		BT1924	Putative metal-dependent hydrolase	-1.7	4.0E-04		
		BT2174	ABC transporter ATP-binding protein	-1.7	2.7E-03		
		BT2769	Putative serine/threonine-protein kinase pknB	-1.7	4.6E-03		
		BT0163	Hypothetical protein	-1.7	1.7E-04		
		BT2771	Putative serine/threonine-protein kinase pknB	-1.8	8.5E-03		
		BT3947	Competence protein	-1.8	3.6E-03		
		BT1383	Oxidoreductase, aldo/keto reductase	-1.9	1.8E-04		
		BT0673	NADP(H) oxidoreductase	-1.9	5.0E-03		
		BT0187	Hypothetical protein	-1.9	2.6E-03		
		BT2434	Pyridine nucleotide-disulphide oxidoreductase	-2.0	1.3E-03		
		BT0755	Hypothetical protein	-2.2	1.9E-04		
<b>Posttranslational modification, protein turnover, chaperones [O]</b>	14 up-regulated (107)	BT3841	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	3.9	6.2E-03		
		BT0897	Chaperone protein htpG (heat shock protein htpG)	2.4	5.1E-03		
		BT2977	Peptidylprolyl isomerase	2.3	1.5E-03		
		BT4371	Peptidyl-prolyl cis-trans isomerase	2.2	4.5E-03		
		BT3612	Putative FKBP-type peptidyl-prolyl cis-trans isomerase fkpA	2.2	6.0E-03		
		BT1829	60 kDa chaperonin (groEL)	2.1	2.3E-03		
		BT2976	FKBP-type peptidyl-prolyl cis-trans isomerase, outer membrane protein precursor	2.0	7.2E-03		
		BT0920	Putative O-sialoglycoprotein endopeptidase	1.8	5.0E-03		
		BT1830	10 kDa chaperonin (groES)	1.8	7.3E-03		
		BT0149	Peptidase	1.7	8.4E-03		
		BT1055	Pyruvate formate-lyase activating enzyme	1.6	2.5E-03		
		BT4615	Chaperone protein dnaK	1.6	9.5E-03		
		BT2564	Hypothetical protein	1.6	2.1E-03		
		BT3810	Putative endothelin-converting enzyme	1.5	2.3E-04		
	10 down-regulated (107)	BT3322	Putative thioredoxin family protein	-1.3	7.2E-03		
		BT0781	Hypothetical protein	-1.5	3.2E-03		
		BT3897	Putative thiol:disulfide interchange protein DsbE	-1.6	4.5E-03		
		BT2499	Peptide methionine sulfoxide reductase msrA/msrB	-1.7	7.9E-03		
		BT0987	Putative cytochrome C-type biogenesis protein	-1.7	5.8E-03		
		BT2811	Alkyl hydroperoxide reductase subunit F	-1.7	4.5E-03		
		BT4194	Putative integral membrane protein	-1.7	6.5E-03		
		BT0565	Putative heat shock protein	-1.9	9.4E-03		
		BT1329	Putative thiol peroxidase	-2.0	3.8E-03		
		BT3971	Glutathione peroxidase	-2.1	4.0E-03		
		<b>Energy production and conversion [C]</b>	19 up-regulated (162)	BT4064	NADH dehydrogenase I, chain H	3.7	2.2E-03
				BT1159	Na <sup>+</sup> -translocating NADH-quinone reductase subunit	3.4	7.0E-03
				BT4066	NADH dehydrogenase I, chain B	3.0	5.7E-03
				BT1157	Na <sup>+</sup> -translocating NADH-quinone reductase subunit	2.9	7.3E-03
BT1160	Na <sup>+</sup> -translocating NADH-quinone reductase subunit			2.6	7.9E-04		
BT1207	Glycerate dehydrogenase (NADH-dependent)			2.3	4.3E-03		
BT1158	Na <sup>+</sup> -translocating NADH-quinone reductase subunit			2.1	9.7E-03		
		BT0617	Na <sup>+</sup> -transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfB	2.0	2.5E-04		

		BT0618	Na <sup>+</sup> -transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein mfc	2.0	1.2E-03
		BT1155	Na <sup>+</sup> -translocating NADH-quinone reductase subunit	1.9	5.8E-03
		BT4065	NADH dehydrogenase I, chain D	1.8	3.7E-03
		BT1805	Electron transfer flavoprotein alpha-subunit	1.7	1.8E-04
		BT1696	Oxaloacetate decarboxylase beta chain	1.7	3.4E-04
		BT1747	Pyruvate-flavodoxin oxidoreductase	1.6	1.2E-04
		BT0333	Hypothetical protein	1.6	1.1E-03
		BT1935	Hypothetical protein	1.5	4.7E-03
		BT0330	Ketoisovalerate oxidoreductase subunit vorA	1.5	7.4E-04
		BT1697	Pyruvate carboxylase subunit B	1.4	1.5E-03
		BT1680	Putative NADH dehydrogenase/NAD(P)H nitroreductase	1.3	8.6E-03
	18 down-regulated (162)	BT1316	Putative NADH dehydrogenase/NAD(P)H nitroreductase	-1.3	5.3E-03
		BT4445	Hypothetical protein	-1.5	1.1E-03
		BT3162	Glycerophosphoryl diester phosphodiesterase	-1.6	6.5E-03
		BT4359	Alpha-N-acetylglucosaminidase precursor	-1.6	7.3E-03
		BT0309	Dihydrolipoamide dehydrogenase	-1.7	4.3E-03
		BT3411	Pyrophosphate-energized vacuolar membrane proton pump	-1.8	7.6E-03
		BT1210	Cytochrome D ubiquinol oxidase subunit I	-1.8	6.3E-03
		BT0123	NADH-ubiquinone oxidoreductase subunit	-1.8	5.0E-04
		BT0313	Flavodoxin	-1.9	3.2E-03
		BT0442	Glycerophosphoryl diester phosphodiesterase	-1.9	1.4E-04
		BT1006	Putative nitroreductase	-2.0	6.9E-03
		BT2071	Isocitrate dehydrogenase [NADP]	-2.0	7.9E-03
		BT2552	Putative butyrate kinase	-2.0	5.8E-04
		BT2551	Phosphate butyryltransferase	-2.1	1.2E-03
		BT2072	Aconitate hydratase	-2.2	7.5E-03
		BT0787	Succinyl-CoA synthetase alpha chain	-2.8	5.6E-03
		BT0788	Succinyl-CoA synthetase beta chain	-2.8	7.9E-03
		BT1196	Pyruvate carboxylase subunit B)	-2.8	1.1E-03
<b>Function unknown [S]</b>	20 up-regulated (207)	BT4390	Hypothetical protein	4.2	8.9E-03
		BT0874	Hypothetical protein	3.9	3.1E-03
		BT0974	Conserved hypothetical protein, putative integral membrane protein	3.7	9.3E-03
		BT4389	Hypothetical protein	3.0	7.3E-03
		BT4561	Conserved hypothetical protein, putative integral membrane protein	2.6	6.4E-04
		BT0627	Conserved hypothetical protein, with a conserved domain of unknown function	2.5	7.2E-03
		BT1755	Putative exported 24-amino acid repeat protein	2.4	1.9E-03
		BT4459	Conserved hypothetical protein, putative transport protein	2.2	2.2E-03
		BT3250	Hypothetical protein	2.1	6.3E-03
		BT1949	Hypothetical protein	1.9	1.5E-03
		BT2008	Hypothetical protein	1.9	3.7E-03
		BT0579	Putative transcription regulator	1.9	3.0E-03
		BT4316	Hypothetical protein	1.8	3.4E-03
		BT1521	Hypothetical protein	1.8	5.4E-03
		BT2139	Hypothetical protein	1.7	7.3E-05
		BT3251	Conserved hypothetical protein, putative integral membrane protein	1.6	6.3E-03
		BT1208	Hypothetical protein	1.5	8.0E-03
		BT1678	Hypothetical protein	1.4	8.7E-03
		BT3378	Hypothetical protein	1.3	9.8E-03
		BT3647	Hypothetical protein	1.3	7.0E-03
	23 down-regulated (207)	BT2135	Hypothetical protein	-1.3	6.2E-03
		BT4608	Hypothetical protein	-1.4	4.2E-03
		BT1422	Hypothetical protein	-1.4	8.1E-03
		BT2080	Conserved hypothetical protein, putative inner membrane protein	-1.4	7.1E-03
		BT3180	Hypothetical protein	-1.4	4.7E-03
		BT0167	Hypothetical protein	-1.5	9.8E-03
		BT1393	4-carboxymuconolactone decarboxylase	-1.5	4.5E-03
		BT3536	Hypothetical protein	-1.6	5.8E-03
		BT0447	S-layer related protein precursor, sialic acid-specific 9-O-acetyltransferase	-1.6	1.8E-03
		BT1425	Hypothetical protein	-1.6	3.7E-03

		BT3863	Hypothetical protein	-1.6	2.5E-03
		BT3669	Hypothetical protein	-1.7	2.1E-03
		BT2760	Hypothetical protein	-1.7	2.1E-04
		BT4450	Hypothetical protein	-1.7	1.6E-03
		BT4272	Hypothetical protein	-1.8	9.1E-04
		BT0542	Hypothetical protein	-1.8	2.0E-03
		BT3528	Hypothetical protein	-1.8	2.8E-03
		BT4484	Hypothetical protein	-1.8	5.1E-04
		BT4299	Hypothetical protein	-1.9	8.3E-05
		BT2606	Hypothetical protein	-1.9	2.0E-03
		BT0449	Conserved hypothetical protein, putative S-layer related protein precursor	-2.1	4.9E-04
		BT4349	Hypothetical protein	-2.4	3.9E-03
		BT0284	Putative peptidoglycan binding protein (LPXTG motif)	-2.6	3.9E-03
<b>Transcription [K]</b>	7 up-regulated (231)	BT3762	Arginine repressor, transcriptional regulator of arginine metabolism	2.5	2.4E-04
		BT4366	Putative transcription regulator	2.1	9.0E-03
		BT4591	Putative nitrogen utilization substance protein	2.1	6.1E-03
		BT2116	Hypothetical protein	1.7	3.1E-03
		BT3122	Transcriptional regulator	1.6	7.8E-03
		BT2340	Hypothetical protein	1.6	4.4E-03
		BT4534	Hypothetical protein	1.5	7.9E-03
	27 down-regulated (231)	BT0582	Hypothetical protein	-1.3	9.9E-03
		BT1258	Putative acetyltransferase	-1.3	2.7E-03
		BT1568	Hypothetical protein	-1.4	7.1E-03
		BT1540	Transcriptional regulator	-1.4	8.1E-03
		BT1963	Putative transcriptional regulator	-1.4	9.9E-03
		BT1404	Putative transcriptional regulator	-1.5	9.1E-03
		BT0583	Hypothetical protein	-1.5	6.9E-03
		BT4402	RNA polymerase ECF-type sigma factor	-1.5	1.5E-03
		BT1797	Putative transcriptional regulator	-1.5	7.5E-04
		BT3899	Transcriptional regulator	-1.5	9.1E-04
		BT1587	Hypothetical protein	-1.6	8.7E-04
		BT4722	RNA polymerase ECF-type sigma factor	-1.6	1.8E-03
		BT2492	RNA polymerase ECF-type sigma factor	-1.6	2.7E-04
		BT0797	Transcriptional regulator, ArsR family	-1.6	2.4E-03
		BT3613	LacI family transcriptional regulator	-1.6	4.1E-03
		BT0824	Transcriptional regulator (LacI family)	-1.6	5.2E-04
		BT2463	RNA polymerase ECF-type sigma factor	-1.6	4.1E-03
		BT0636	Putative transcriptional regulator	-1.7	2.6E-03
		BT1078	Putative transcriptional regulator	-1.7	8.7E-03
		BT2435	MarR family transcriptional regulator	-1.7	3.1E-03
		BT2886	Putative transcriptional regulator	-1.7	3.5E-03
		BT4035	Hypothetical protein	-1.9	5.1E-03
		BT2792	AraC/XylS family transcriptional regulator	-1.9	1.8E-03
		BT4696	Hypothetical protein	-2.0	5.7E-04
		BT0433	Putative xylose repressor	-2.0	7.9E-05
		BT4643	RNA polymerase ECF-type sigma factor	-2.1	4.9E-04
		BT4647	RNA polymerase ECF-type sigma factor	-2.4	3.0E-03
<b>Carbohydrate transport and metabolism [G]</b>	19 up-regulated (372)	BT1765	Levanase precursor (2,6-beta-D-fructofuranosidase)	19.6	4.5E-03
		BT1758	Glucose/galactose transporter	8.8	6.2E-03
		BT1759	Levanase precursor (2,6-beta-D-fructofuranosidase)	6.3	5.2E-03
		BT1527	Hypothetical protein	5.3	4.0E-03
		BT3419	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	3.4	7.3E-03
		BT3773	Hypothetical protein	3.2	3.0E-03
		BT3082	2,6-beta-D-fructofuranosidase precursor	3.0	4.3E-03
		BT1872	Periplasmic beta-galactosidase precursor	2.7	4.5E-03
		BT0307	Phosphofructokinase	2.5	5.0E-03
		BT2799	Putative PfkB family carbohydrate kinase	2.4	8.5E-03
		BT1670	Putative transmembrane transport protein	2.2	1.7E-03
		BT1672	Phosphoglycerate kinase	1.8	4.7E-03
		BT1883	Putative alpha-1,6-mannanase	1.8	9.8E-03
		BT3929	Triosephosphate isomerase	1.8	3.6E-03
		BT4263	Glyceraldehyde 3-phosphate dehydrogenase	1.7	8.1E-03
		BT1663	Pullulanase precursor	1.7	6.0E-03
		BT1228	Fructose-1,6-bisphosphatase	1.6	6.0E-03
		BT3950	Phosphoglucomutase/phosphomannomutase	1.4	5.0E-03

45 down-regulated (372)	BT4379	Putative oxalate:formate antiporter	1.4	5.0E-03		
	BT4330	Xanthosine permease	-1.3	8.0E-03		
	BT3094	Putative secreted xylosidase	-1.4	9.8E-03		
	BT0825	Altronate oxidoreductase	-1.4	7.9E-03		
	BT0443	Thermostable beta-glucosidase B	-1.4	6.0E-03		
	BT3231	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	-1.4	5.6E-03		
	BT3774	Alpha-mannosidase	-1.4	6.3E-03		
	BT3085	Alpha-xylosidase	-1.5	5.9E-03		
	BT1780	Periplasmic beta-glucosidase precursor	-1.5	4.8E-03		
	BT3299	Alpha-glucosidase II	-1.5	2.2E-03		
	BT3659	Alpha-xylosidase	-1.5	5.3E-03		
	BT0757	Beta-galactosidase	-1.5	7.1E-03		
	BT2104	ROK family member transcriptional repressor	-1.5	3.7E-03		
	BT0823	Uronate isomerase	-1.5	8.0E-03		
	BT3132	Sialic acid-specific 9-O-acetylerase	-1.5	5.5E-03		
	BT4305	Putative alpha-amylase	-1.5	5.3E-03		
	BT1873	Endo-arabinase	-1.5	5.1E-04		
	BT4423	Xylulose kinase	-1.5	2.1E-03		
	BT0486	Altronate hydrolase	-1.6	7.3E-03		
	BT2969	Beta-galactosidase	-1.6	8.8E-03		
	BT4110	Putative pectinesterase precursor	-1.6	2.7E-03		
	BT3868	Beta-N-hexosaminidase, glycosyl hyrolase family 20	-1.6	3.3E-03		
	BT3685	Hypothetical protein	-1.6	3.7E-03		
	BT1625	Hypothetical protein	-1.7	4.8E-03		
	BT2430	Hexokinase type III	-1.7	1.8E-03		
	BT4091	Sialic acid-specific 9-O-acetylerase	-1.7	6.1E-03		
	BT4109	Putative pectinesterase precursor	-1.7	1.1E-03		
	BT4157	Alpha-galactosidase precursor	-1.7	8.9E-03		
	BT3173	Hypothetical protein	-1.7	5.6E-03		
	BT0235	Hypothetical protein	-1.7	8.7E-04		
	BT0996	Beta-galactosidase	-1.7	5.0E-03		
	BT3527	Alpha-1,2-mannosidase	-1.7	2.5E-03		
	BT3529	Aldose 1-epimerase precursor	-1.7	5.7E-03		
	BT0487	Transcriptional regulator	-1.7	2.9E-04		
	BT4446	Sugar phosphate isomerase/epimerase	-1.7	5.4E-05		
	BT1626	Beta-galactosidase	-1.8	5.2E-05		
	BT1778	Beta-glucosidase (gentiobiase)	-1.8	1.3E-03		
	BT3028	Hypothetical protein	-1.8	6.9E-04		
	BT1013	Putative alpha-rhamnosidase	-2.0	1.5E-03		
	BT1764	Hypothetical protein	-2.0	7.1E-03		
	BT0436	Arabinose-proton symporter	-2.0	1.1E-03		
	BT1658	Transaldolase	-2.1	2.6E-03		
	BT4718	Putative aquaporin	-2.2	1.5E-03		
	BT0453	N-acylglucosamine 2-epimerase	-2.3	2.3E-04		
	BT1986	Putative ribose 5-phosphate isomerase	-2.3	3.3E-04		
BT3673	TonB	-2.4	2.4E-04			
Inorganic ion transport and metabolism [P]	8 up-regulated (265)	BT2541	Putative calcium-transporting ATPase	3.5	2.5E-03	
		BT3944	Putative chloride channel protein	2.1	7.4E-03	
		BT4098	Trk system K <sup>+</sup> uptake protein trkA	1.9	1.5E-03	
		BT0633	Putative Na <sup>+</sup> /H <sup>+</sup> exchange protein	1.9	5.0E-03	
		BT3248	Putative metal ABC transporter, ATP-binding protein	1.8	1.1E-03	
		BT2099	Fe <sup>3+</sup> ABC transporter, permease	1.7	5.2E-03	
		BT1736	Chromate transport protein	1.7	3.1E-04	
		BT1052	Putative anti-sigma factor	1.3	9.6E-03	
		39 down-regulated (265)	BT2789	Chromate transport protein	-1.4	7.0E-04
			BT4665	K <sup>+</sup> uptake protein	-1.4	4.5E-03
BT3670	Putative outer membrane protein, probably involved in nutrient binding		-1.4	8.4E-03		
BT1918	Choline-sulfatase		-1.4	4.9E-03		
BT4679	Mg <sup>2+</sup> /Co <sup>2+</sup> transport protein		-1.5	5.1E-03		
BT4635	Putative anti-sigma factor		-1.5	4.3E-03		
BT4644	Putative anti-sigma factor		-1.5	4.6E-03		
BT2626	Putative outer membrane protein, probably involved in nutrient binding		-1.5	9.2E-03		
BT3107	Arylsulfatase (aryl-sulfate sulphohydrolase)		-1.5	7.2E-03		
BT1373	Ferritin A		-1.5	5.3E-03		
BT3093	Arylsulfatase (aryl-sulfate sulphohydrolase)		-1.5	2.8E-03		
BT1876	Putative anti-sigma factor		-1.5	3.9E-03		



		BT2511	Putative transcription regulator	-1.5	2.7E-03
		BT3346	Putative outer membrane protein, probably involved in nutrient binding	-1.5	5.0E-03
		BT1624	Putative secreted sulfatase	-1.5	5.6E-03
		BT2462	Putative anti-sigma factor	-1.5	6.5E-04
		BT2914	Iduronate 2-sulfatase precursor	-1.5	3.0E-04
		BT1279	Putative anti-sigma factor	-1.6	9.3E-03
		BT2560	Putative outer membrane protein, probably involved in nutrient binding	-1.6	1.1E-03
		BT2512	Cation-transporting ATPase, P-type, putative zinc-transporting ATPase	-1.7	2.8E-03
		BT4081	Putative outer membrane protein, probably involved in nutrient binding	-1.7	9.4E-03
		BT1046	Putative outer membrane protein, probably involved in nutrient binding	-1.7	6.3E-03
		BT3518	Putative anti-sigma factor	-1.7	1.2E-03
		BT0756	Iduronate 2-sulfatase precursor	-1.7	1.8E-03
		BT3788	Putative outer membrane protein, probably involved in nutrient binding	-1.7	4.4E-04
		BT3749	Putative anti-sigma factor	-1.9	6.1E-04
		BT1875	Putative outer membrane protein, probably involved in nutrient binding	-1.9	3.7E-04
		BT2019	Polyphosphate kinase	-1.9	2.1E-03
		BT0268	Putative outer membrane protein, probably involved in nutrient binding	-2.0	1.2E-03
		BT0439	Putative outer membrane protein, probably involved in nutrient binding	-2.0	7.8E-03
		BT1683	Putative outer membrane protein, probably involved in nutrient binding	-2.0	1.1E-03
		BT3176	Hypothetical protein	-2.1	2.7E-04
		BT1109	Ferritin A	-2.1	5.7E-03
		BT4248	Putative anti-sigma factor	-2.1	1.7E-03
		BT0452	Putative outer membrane protein, probably involved in nutrient binding	-2.4	5.8E-05
		BT4247	Putative outer membrane protein, probably involved in nutrient binding	-2.5	3.0E-03
		BT2461	Putative outer membrane protein, probably involved in nutrient binding	-2.7	2.5E-05
		BT0317	Putative outer membrane protein, probably involved in nutrient binding	-2.7	2.8E-04
		BT0483	Putative outer membrane protein, probably involved in nutrient binding	-2.7	1.3E-04
<b>Signal transduction mechanisms [T]</b>	3 up-regulated (161)	BT4218	Phosphate starvation-inducible protein, PhoH	2.0	3.7E-03
		BT3805	Two-component system sensor histidine kinase	1.8	3.1E-03
		BT3154	Hypothetical protein	1.7	1.7E-04
	26 down-regulated (161)	BT0729	Transcriptional regulator	-1.3	5.3E-03
		BT1123	Transcriptional regulator	-1.3	6.5E-03
		BT3786	Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')	-1.4	4.7E-03
		BT2750	Putative protein-tyrosine-phosphatase	-1.4	5.7E-03
		BT0688	CAMP-binding domain (catabolite gene activator) transcriptional regulator	-1.5	8.5E-03
		BT1482	Two-component system response regulator	-1.5	1.7E-03
		BT1117	Conserved hypothetical protein, with a cAMP-binding domain	-1.5	3.5E-03
		BT2574	Two-component system sensor histidine kinase	-1.5	3.8E-03
		BT2923	Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')	-1.5	2.6E-03
		BT0989	Two-component system sensor histidine kinase	-1.5	7.6E-03
		BT1483	Two-component system sensor histidine kinase	-1.6	1.2E-04
		BT3172	Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')	-1.6	9.7E-04
		BT0732	Two-component system response regulator	-1.6	4.3E-03
		BT0990	Two-component system response regulator	-1.6	2.7E-03
		BT1318	Signaling protein without kinase domain	-1.6	6.8E-03
		BT0324	Hypothetical protein	-1.6	9.1E-03
		BT3645	Two-component system sensor histidine kinase	-1.6	6.5E-03
		BT1183	Two-component system sensor histidine kinase/response regulator, hybrid ('one component system')	-1.7	6.7E-03

	BT1802	Two-component system sensor histidine kinase	-1.7	1.7E-03
	BT4182	Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')	-1.8	6.2E-03
	BT4354	Two-component system sensor histidine kinase	-1.8	5.9E-04
	BT2204	Hypothetical protein	-1.9	1.3E-03
	BT1810	GAF domain-containing protein, involved in signal transduction	-1.9	1.2E-03
	BT0901	Putative universal stress protein UspA	-2.0	5.6E-03
	BT2628	Two-component system sensor histidine kinase/response regulator, hybrid ('one-component system')	-2.2	5.1E-04
	BT1334	PhoH-like protein	-2.3	2.1E-04

\* - number in parentheses refers to the total number of genes in the *B. thetaiotaomicron* genome belonging to the COG