Table S1. *B. thetaiotaomicron* genes with altered expression *in vitro* during growth on plant and host glycans or *in vivo* in mono-associated gnotobiotic mice fed a plant glycan rich diet
Genes are separated according to the Venn diagram sectors delineated in Figure S1. Values shown are the mean fold differences compared to expression during growth in MM-G; only fields with values ≥10-fold are shown.

Gene	gene are shown in green; downregulated ge Gene description	arabinan	arabino	pectic	homogal	rhamnogal	rhamnogal acturonan II	neutral O- glycans	α-manna	n chondroitin sulfate	heparin	hyaluronan	adult plant	adult simple su	uckling
			gaiactan	galactan	acturonan	acturonan i	acturonan II	giycans		Suitate			ricn	sugar	
Upregulated	:														
Sector 1															
BT0292	hypothetical protein												15.4		42.
BT0294	hypothetical protein												94.1		43.
BT0317	susC-like												116.3		39.
BT0318	susD-like												18.7		
BT0483	susC-like		40.			40	•		4.0		45.0		14.5		40
BT0484	susD-like		10.	1		19.	2		16	.9	15.2		11.7		48.
BT0683 BT0693	Glycoside hydrolase family 97 hypothetical protein												16.0 59.2		40.
BT0722	conserved hypothetical protein, putative												10.4		40.
BT0754	surface protein, function unknown susC-like												13.8		
BT0754	hypothetical protein												23.9		
BT0764	hypothetical protein												18.9		
BT0765	putative protease												23.3		116.
BT0765	Carbohydrate binding module family 32												42.5		246.
BT0866	susD-like												21.4		145.
BT0867	susC-like												10.1		140.
BT0901	putative universal stress protein UspA												19.4		
BT1008	xylanase												66.0		
BT1009	dihydroorotate dehydrogenase							74.9	9		14.0		139.9		457.
BT1034	putative signal transducer							17.					75.1		104.
BT1047	susD-like												21.1		
BT1072	hypothetical protein												17.0		
BT1073	hypothetical protein												21.9	21.9	
BT1074	hypothetical protein												18.2	24.1	
BT1196	pyruvate carboxylase subunit B)												15.7		14.
BT1280	susC-like							22.7	7			13.0	176.7		18.
BT1283	hypothetical protein												17.2		20.
BT1287	hypothetical protein												22.9		40.
BT1486	hypothetical protein												41.0		59.
BT1487	hypothetical protein												43.7		82.
BT1488	hypothetical protein												26.2		26.
BT1489	vitamin B12 receptor, outer membrane												16.3		
BT1492	tyrosine phenol-lyase												68.1		
BT1530	putative outer membrane protein OprM												91.7		
BT1533	precursor hypothetical protein												12.0	93.8	38.
BT1619	susC-like												11.5		39.
BT1653	hypothetical protein												17.1		124.
BT1655	hypothetical protein												10.7		49.
BT1656	putative transcriptional regulator												14.3		152.
BT1718	putative 2-aminoethylphosphonate pyruvate aminotransferase												10.6		.02.
BT1904	transcriptional regulator, AraC-type												31.9	60.5	57.
BT1950	Fe3+ ABC transporter, ATP-binding protein												29.2		25.
BT1951	Fe3+ ABC transporter, permease												48.3	68.7	51.
BT1952	Fe3+ ABC transporter, periplasmic iron- binding protein												40.1		44.
BT1953	putative TonB-linked outer membrane receptor												31.0	53.2	35.
BT1954	putative surface layer protein												48.0	58.7	52.
BT1955	putative cell wall biogenesis protein												36.0		77.
BT1956	putative cell surface protein												21.4		
BT1973	NAD-specific glutamate dehydrogenase												12.5		11.
BT2038	cation efflux system protein												12.9)	
BT2040	hypothetical protein												16.2		
BT2087	hypothetical protein												17.2	14.2	12.
BT2094	TonB-dependent receptor												12.6		14.

BT2383	RNA polymerase ECF-type sigma factor				11.3	49.7	53.2
BT2395	hypothetical protein				19.9	19.8	11.9
BT2404	L-asparaginase I				17.2	21.3	
BT2551	phosphate butyryltransferase				20.8	19.1	
BT2552	putative butyrate kinase				18.4	69.1	22.8
BT2569	RNA polymerase ECF-type sigma factor				29.3	65.7	14.9
BT2690	histidine ammonia-lyase				14.8	30.5	12.2
BT2691	methenyltetrahydrofolate cyclohydrolase				35.1	36.3	
BT2692	imidazolonepropionase				31.0	63.9	19.6
BT2693	formiminotransferase-cyclodeaminase				23.4	28.8	
BT2694	putative urocanate hydratase				10.6	13.9	
BT2762	TonB				40.3	25.4	
BT2778	RNA polymerase ECF-type sigma factor				96.0	47.3	
BT2779	3-demethylubiquinone-9 3- methyltransferase				24.5	22.4	
BT2784	hypothetical protein				13.4	16.2	
BT2785	hypothetical protein				12.8	35.6	62.1
BT2804	ribokinase				34.4	00.0	02.1
BT2893	susD-like				14.2		
BT2894	susC-like	34.8	10.4	12.6	313.2		
BT2896	hypothetical protein				11.4		
BT2899	hypothetical protein				21.5		
BT3043	Glycoside hydrolase family 30				16.6		
BT3048	hypothetical protein				14.4		
BT3188	hypothetical protein				11.4		
BT3189	hypothetical protein				10.1		
BT3190	putative RNA polymerase ECF-type sigma factor				164.0	77.6	58.0
BT3259	hypothetical protein				18.9	37.6	
BT3436	hypothetical protein				25.1	53.4	
BT3437	hypothetical protein				27.3	138.7	
BT3438	hypothetical protein				139.3	201.8	
BT3441	hypothetical protein				18.3	16.1	
BT3475	susC-like				10.1		
BT3525	hypothetical protein				15.3		
BT3650	hypothetical protein				50.3		
BT3651	hypothetical protein				70.4		
BT3652	hypothetical protein				89.6		
BT3653	hypothetical protein				10.3		
BT3769 BT3822	hypothetical protein hypothetical protein				16.8 10.5		
BT3874	hypothetical protein				45.9	104.8	125.0
BT3983	susC-like				60.0	90.7	102.1
BT3984	susD-like				42.3	223.8	203.4
BT3985	hypothetical protein				102.8	243.8	270.0
BT3986	putative patatin-like protein				54.9	133.1	147.5
BT3987	Glycoside hydrolase family 18				43.3	103.9	136.4
BT3988	putative peptidoglycan bound protein				19.1	47.8	42.4
BT4038	susD-like				17.0	32.2	23.2
BT4040	Carbohydrate binding module family 32				16.3	50.4	10.4
BT4356	putative anti-sigma factor				61.8	400.8	47.4
BT4358	susD-like				14.6	00.4	18.5
BT4404	susC-like				27.1	33.1 12.0	43.0 16.2
BT4405 BT4406	susD-like hypothetical protein				18.3 12.4	17.4	16.2
BT4465	conserved hypothetical protein, putative				30.9	13.1	
D17700	outer membrane protein				30.8	10.1	
BT4647	RNA polymerase ECF-type sigma factor				17.2		
BT4649	hypothetical protein				18.5	17.7	11.4
BT4689	Glycoside hydrolase family 13				20.6		
BT4708	susD-like				25.4		
BT4709	Glycoside hydrolase family 18				18.5		
BT4710	hypothetical protein				21.1		
BT4711	hypothetical protein				13.3		11.5
BT4712	hypothetical protein						

Sector 2														
BT0319	hypothetical protein											162.6	346.7	101.6
BT0348	Glycoside hydrolase family 51	41.2	12.6	25.6			31.8					18.1		
BT0349	hypothetical protein	49.2	11.6	31.3			47.6					16.0		19.1
BT0360	Glycoside hydrolase family 43	315.8		156.7								67.6		13.1
BT0361	susD-like	381.0		210.0								156.1	28.2	46.6
BT0362	susC-like	234.0		118.8								57.2		11.4
BT0365	hypothetical protein	1222.0		676.7								780.7	29.0	100.0
BT0366	hybrid two-component system (HTCS)	35.1		16.9	12.1						12.0	10.9		40.4
BT0367 BT0368	Glycoside hydrolase family 43 Glycoside hydrolase family 51	1723.0 52.5		944.6 30.7	12.1						12.0	200.7 20.3		16.1
BT0369	Glycoside hydrolase family 43	77.2		43.3								19.4		15.1
BT0565	putative heat shock protein	11.2		45.5								15.2	11.7	13.1
BT0787	succinyl-CoA synthetase alpha chain											15.3	30.4	
BT0788	succinyl-CoA synthetase beta chain											11.2	35.2	
BT0978	ECF-type sigma factor			17.9		146.2	251.3					22.3		15.4
BT1029	susC-like			14.8		551.4	495.0					61.0		
BT1142	hypothetical protein		10.2									37.4	16.9	
BT1448	biotin carboxyl carrier protein											26.8	58.1	15.6
BT1449	biotin carboxylase											36.4	52.9	18.6
BT1450	propionyl-CoA carboxylase beta chain											38.6	51.1	16.8
BT1491	hypothetical protein	40.0		44.0								24.6	12.2	26.0
BT1535 BT1757	ABC transporter ATP-binding protein fructokinase	12.0		11.6								134.0 23.1		16.6 10.5
BT1757	glucose/galactose transporter				16.9							96.9	19.2	38.9
BT1760	Glycoside hydrolase family 32				21.9							72.5	50.8	90.4
BT1761	hypothetical protein				22.9							83.0	21.9	36.1
BT1763	susC-like				13.7							42.2	14.5	24.4
BT1765	Glycoside hydrolase family 32				13.3							40.8	10.0	21.6
BT2131	hypothetical protein		10.6									19.8	278.8	273.3
BT2500	hypothetical protein											150.7	19.4	
BT3046	susC-like	22.2										43.6		
BT3047	hypothetical protein	184.1	41.8	33.6	30.2		28.8		10.8		24.3	365.2	22.0	61.0
BT3082	Glycoside hydrolase family 32					54.0	400.0					18.2		
BT3614	putative oxidoreductase		04.0			54.2	103.8					23.1		
BT3614 BT3655	putative oxidoreductase Glycoside hydrolase family 43		24.8			54.2	103.8					23.1 17.4		
BT3614 BT3655 BT3656	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43	88 3	20.9		58 Q					13.6		23.1 17.4 19.1		
BT3614 BT3655 BT3656 BT3681	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like	88.3			58.9	54.2 20.4	103.8	43.7		13.6		23.1 17.4 19.1 33.7		24.2
BT3614 BT3655 BT3656 BT3681 BT3699	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF	88.3	20.9		58.9			43.7 54.2		13.6		23.1 17.4 19.1 33.7 11.5	17.1	24.2 49.3
BT3614 BT3655 BT3656 BT3681	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like	88.3	20.9		58.9			43.7 54.2 29.2		13.6		23.1 17.4 19.1 33.7	17.1	24.2 49.3 17.6
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC, outer membrane protein involved in starch binding	88.3	20.9		58.9			54.2 29.2		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3	17.1	49.3 17.6
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC, outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97	88.3	20.9		58.9			54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3	17.1	49.3 17.6 23.1
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13	88.3	20.9		58.9			54.2 29.2		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3	17.1	49.3 17.6 23.1 16.5
BT3614 BT3655 BT3656 BT3681 BT3689 BT3700 BT3702 BT3703 BT3704 BT3735	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC, outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein		20.9	447.7		20.4	11.4	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9		49.3 17.6 23.1
BT3614 BT3655 BT3656 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC, outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase	88.3	20.9	147.7 53.0	55.0	20.4	11.4	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8	13.4	49.3 17.6 23.1 16.5 14.8
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like		20.9	53.0	55.0 92.6	20.4 245.6 49.3	11.4 263.4 50.7	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5	13.4 38.1	49.3 17.6 23.1 16.5 14.8
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like		20.9	53.0 68.2	55.0 92.6 136.1	20.4	11.4 263.4 50.7 73.7	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7	13.4	49.3 17.6 23.1 16.5 14.8
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC, outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein		20.9	53.0	55.0 92.6	20.4 245.6 49.3	11.4 263.4 50.7	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5	13.4 38.1	49.3 17.6 23.1 16.5 14.8
BT3614 BT3655 BT3656 BT3686 BT3689 BT3700 BT3702 BT3703 BT3704 BT3704 BT4113 BT4113 BT4114 BT4120	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like		20.9	53.0 68.2 61.0	55.0 92.6 136.1 187.9	20.4 245.6 49.3	263.4 50.7 73.7 148.2	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3	13.4 38.1	49.3 17.6 23.1 16.5 14.8
BT3614 BT3655 BT3656 BT3686 BT3689 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like	163.7	20.9	53.0 68.2 61.0 53.6 187.5 45.3	55.0 92.6 136.1 187.9 224.5 755.4 13.2	20.4 245.6 49.3 82.7	263.4 50.7 73.7 148.2 145.6 404.4 13.7	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 209.1 13.5	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT3686 BT3689 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4163	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein	163.7 52.9 101.3	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3	245.6 49.3 82.7 70.7 186.5	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 209.1	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4163 BT4164	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like susD-like susD-like	163.7 52.9 101.3 88.2	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0	245.6 49.3 82.7 70.7 186.5 135.7	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 209.1 13.5 20.7	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT36869 BT3700 BT3702 BT3703 BT3704 BT3704 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4163 BT4164 BT4164	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like	163.7 52.9 101.3 88.2 114.9	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6	245.6 49.3 82.7 70.7 186.5 135.7 128.0	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT36869 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4164 BT4165 BT4166	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like susD-like susD-like susD-like susD-like susD-like susD-like susD-like susD-like susD-like putative lipoprotein	52.9 101.3 88.2 114.9 69.0	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8	263.4 50.7 73.7 148.6 404.4 13.7 46.2 38.3 50.8	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 209.1 13.5 20.7 10.6 16.1	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4164 BT4165 BT4166 BT4166 BT4167	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusF outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like susD-like susD-like susD-like susD-like susD-like susD-like	52.9 101.3 88.2 114.9 69.0 68.6	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 209.1 13.5 20.7 10.6 16.1 10.9	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT36869 BT3700 BT3702 BT3703 BT3704 BT3704 BT4113 BT4114 BT4120 BT4121 BT4121 BT4122 BT4153 BT4163 BT4165 BT4166 BT4166 BT4166 BT4167 BT4169	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like susD-like putative lipoprotein hypothetical protein	52.9 101.3 88.2 114.9 69.0 68.6 77.1	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1 10.9 11.1 13.5	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT3689 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4164 BT4166 BT4166 BT4167 BT4169 BT4170	putative oxidoreductase Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like susD-like susD-like susD-like susD-like putative lipoprotein hypothetical protein susC-like susD-like putative lipoprotein hypothetical protein susC-like susD-like putative lipoprotein hypothetical protein susD-like	163.7 52.9 101.3 88.2 114.9 69.0 68.6 77.1 34.5	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4	263.4 50.7 73.7 148.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5 14.8	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1 10.9 11.4	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT3681 BT3699 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4164 BT4165 BT4166 BT4167 BT4169 BT4170 BT4170	putative oxidoreductase Glycoside hydrolase family 43 Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like susD-like susD-like susD-like putative lipoprotein hypothetical protein susD-like putative lipoprotein hypothetical protein susD-like	52.9 101.3 88.2 114.9 69.0 68.6 77.1 34.5 52.1	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1 45.4	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9 16.3	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4 65.4	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 238.3 50.8 29.0 27.1 38.5 14.8	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 209.1 13.5 20.7 10.6 16.1 10.9 11.4	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT3689 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4164 BT4166 BT4166 BT4167 BT4169 BT4170	putative oxidoreductase Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like susD-like susD-like susD-like susD-like putative lipoprotein hypothetical protein susC-like susD-like putative lipoprotein hypothetical protein susC-like susD-like putative lipoprotein hypothetical protein susD-like	163.7 52.9 101.3 88.2 114.9 69.0 68.6 77.1 34.5	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4	263.4 50.7 73.7 148.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5 14.8	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1 10.9 11.4	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT36869 BT3700 BT3702 BT3703 BT3704 BT3704 BT4113 BT4114 BT4120 BT4121 BT4122 BT4153 BT4163 BT4166 BT4166 BT4166 BT4166 BT4167 BT4172 BT4175	putative oxidoreductase Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like susD-like putative lipoprotein hypothetical protein susC-like putative lipoprotein hypothetical protein susD-like polysaccharide lyase family hypothetical protein	52.9 101.3 88.2 114.9 69.0 68.6 77.1 34.5 52.1 73.6	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1 45.4 57.0	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9 16.3 20.0	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4 65.4 140.7	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5 14.8 19.7 28.2	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1 10.9 11.4 16.6 10.7 10.9 11.4	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2
BT3614 BT3655 BT3656 BT36869 BT3700 BT3702 BT3703 BT3704 BT3704 BT4113 BT4114 BT4120 BT4121 BT4121 BT4122 BT4153 BT4163 BT4166 BT4166 BT4166 BT4167 BT4169 BT4170 BT4172 BT4175 BT4176 BT4667 BT46667 BT4668	putative oxidoreductase Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like putative lipoprotein hypothetical protein susD-like Polysaccharide lyase family phypothetical protein susD-like Polysaccharide lyase family Glycoside hydrolase family 11 Glycoside hydrolase family 105 Glycoside hydrolase family 2 Glycoside hydrolase family 2 Glycoside hydrolase family 2 Glycoside hydrolase family 53	163.7 52.9 101.3 88.2 114.9 69.0 68.6 77.1 34.5 52.1 73.6 35.2	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1 45.4 57.0 25.6 123.4 140.7	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9 16.3 20.0	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4 65.4 140.7	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5 14.8 19.7 28.2	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1 10.9 11.4 16.6 10.7 10.9 11.4 16.6 10.7 10.9 18.3 10.0 10.9 11.9	13.4 38.1 20.4	49.3 17.6 23.1 16.5 14.8 74.4 34.2 14.4
BT3614 BT3655 BT3656 BT3681 BT3689 BT3700 BT3702 BT3703 BT3704 BT3735 BT3764 BT4113 BT4114 BT4120 BT4121 BT4121 BT4122 BT4153 BT4164 BT4166 BT4166 BT4167 BT4167 BT467	putative oxidoreductase Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like susD-like susD-like pyothetical protein susC-like susD-like pyothetical protein susC-like susD-like pyothetical protein susC-like susD-like putative lipoprotein hypothetical protein susD-like Polysaccharide lyase family hypothetical protein susD-like Polysaccharide lyase family 11 Glycoside hydrolase family 11 Glycoside hydrolase family 2 Glycoside hydrolase family 3 susD-like	52.9 101.3 88.2 114.9 69.0 68.6 77.1 73.6 35.2 13.8 13.7	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1 45.4 57.0 25.6 123.4 140.7	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9 16.3 20.0 11.4 25.9 21.4	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4 65.4 140.7	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5 14.8 19.7 28.2	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 11.0 10.9 11.4 10.9 11.4 10.9 11.4 10.9 11.4 10.9 11.9	13.4 38.1 20.4 28.7	49.3 17.6 23.1 16.5 14.8 74.4 34.2 14.4
BT3614 BT3655 BT3656 BT36869 BT3700 BT3702 BT3703 BT3704 BT3704 BT4113 BT4114 BT4120 BT4121 BT4121 BT4122 BT4153 BT4163 BT4166 BT4166 BT4166 BT4167 BT4169 BT4170 BT4172 BT4175 BT4176 BT4667 BT46667 BT4668	putative oxidoreductase Glycoside hydrolase family 43 susD-like outer membrane protein SusF outer membrane protein SusE susC , outer membrane protein involved in starch binding susB, Glycoside hydrolase family 97 susA, Glycoside hydrolase family 13 hypothetical protein L-rhamnose isomerase susD-like susC-like hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like susD-like Glycoside hydrolase family 28 hypothetical protein susC-like putative lipoprotein hypothetical protein susD-like Polysaccharide lyase family phypothetical protein susD-like Polysaccharide lyase family Glycoside hydrolase family 11 Glycoside hydrolase family 105 Glycoside hydrolase family 2 Glycoside hydrolase family 2 Glycoside hydrolase family 2 Glycoside hydrolase family 53	52.9 101.3 88.2 114.9 69.0 68.6 77.1 34.5 52.1 73.6 35.2 13.8	20.9	53.0 68.2 61.0 53.6 187.5 45.3 72.9 68.0 83.3 48.7 53.3 67.0 26.1 45.4 57.0 25.6 123.4 140.7	55.0 92.6 136.1 187.9 224.5 755.4 13.2 36.3 34.0 37.6 29.5 26.3 35.9 12.9 16.3 20.0 11.4 25.9	245.6 49.3 82.7 70.7 186.5 135.7 128.0 92.8 71.3 93.8 47.4 65.4 140.7	263.4 50.7 73.7 148.2 145.6 404.4 13.7 46.2 38.3 50.8 29.0 27.1 38.5 14.8 19.7 28.2	54.2 29.2 26.4		13.6		23.1 17.4 19.1 33.7 11.5 15.9 11.3 10.9 11.2 13.9 33.8 12.5 11.7 36.3 14.5 20.7 10.6 16.1 10.9 11.4 16.6 10.7 10.9 11.4 16.6 10.7 10.9 18.3 10.0 10.9 11.9	13.4 38.1 20.4 28.7	49.3 17.6 23.1 16.5 14.8 74.4 34.2 14.4

Sector 3										
BT0111	hypothetical protein		16.6							
BT0112	putative permease		13.6							
BT0113	hypothetical protein		10.0							
BT0115	arsenate reductase		24.7							
BT0116	arsenical pump-driving ATPase		14.4							
BT0117	arsenical resistance operon trans-acting		15.2							
BT0118	repressor putative cytochrome c biogenesis protein		27.5							
BT0119	hypothetical protein		16.9							
BT0120	hypothetical protein		29.3							
BT0121	transcriptional regulator, ArsR family		10.6							
BT0198	hypothetical protein	10.8								
BT0262	hypothetical protein		66.1							
BT0263	hypothetical protein		42.0							
BT0264	Glycoside hydrolase family 43		1860.0							
BT0265	Glycoside hydrolase family 43		465.4							
BT0266	hypothetical protein		225.2					13.1		17.4
BT0268	susC-like		72.7							
BT0269	susD-like		222.6							
BT0270	hypothetical protein		214.8							
BT0271 BT0272	hypothetical protein susC-like		121.0 123.1							
BT0272 BT0273	susC-like susD-like		130.9							
BT0274	hypothetical protein		144.8							
BT0275	hypothetical protein		242.6							
BT0276	hypothetical protein		145.0							
BT0277	hypothetical protein		133.0							
BT0278	hypothetical protein		109.4							
BT0279	hypothetical protein		155.3						11.3	
BT0280	transposase for insertion sequence element ISRM3		11.7							
BT0284	putative peptidoglycan binding protein (LPXTG motif)		17.0							
BT0285	putative tolQ-type transport protein		17.2							
BT0286	hypothetical protein		16.5							
BT0287	putative biopolymer transmembrane		21.4							
BT0288	protein hypothetical protein		22.4							
BT0290	Glycoside hydrolase family 35		93.7							
BT0338	hypothetical protein		33.1			76.5	33.8			
BT0339	Glycoside hydrolase family 31					107.5	142.6	10.6		
BT0340	trimethylamine corrinoid protein 2 (TCP					42.4	68.9	15.6		
	2)									
BT0341	Na+/glucose cotransporter					211.6	360.8	11.3		
BT0342	hypothetical protein					47.6	143.2	10.7		
BT0343	methylcobamide:CoM methyltransferase mtbA					82.1	154.5	10.1		
BT0350	xylulose kinase (xylulokinase)	22.0		14.7			21.0			
BT0352	hypothetical protein	11.7								
BT0353	putative sugar epimerase/aldolase	10.2					10.7			
BT0354	hypothetical protein	12.9					14.7			
BT0355 BT0356	Na+/glucose cotransporter	12.9 11.7		10.2 10.7			13.7 12.6			
BT0363	aldose 1-epimerase precursor susD-like	471.2		256.2			12.0	98.6	13.6	26.9
BT0364	susC-like	297.4		151.6				177.0	13.0	18.4
BT0434	hypothetical protein	201.4		101.0		10.4		111.0		10.4
BT0435	hypothetical protein					10.1				
BT0437	N-acylglucosamine 2-epimerase					10.1			11.0	
BT0438	Glycoside hydrolase family 89					14.1			10.6	
BT0442	glycerophosphoryl diester					10.9			10.0	
	phosphodiesterase									
BT0622	Na+-transporting NADH:ubiquinone				11.2					
	oxidoreductase, Electron transport complex protein rnfA									
BT0823	uronate isomerase					20.5				
BT0824	transcriptional regulator (Lacl family)				19.9	10.4	14.3			

BT0854	hypothetical protein												11.3
BT0977	hypothetical protein					59.9	167.5						
BT0978	ECF-type sigma factor						251.3						
BT0979	hypothetical protein						14.1						
BT0980	Polysaccharide lyase family 1						11.5						
BT0982	hypothetical protein					20.5	62.1						
BT0983	Glycoside hydrolase family 2					14.2	24.0						
BT0984	hypothetical protein						22.9						
BT0985	putative sialic acid-specific					12.3	36.7						
BT0986	acetylesterase II Glycoside hydrolase family 106					11.2	17.5						
BT0980	Glycoside hydrolase family 2					77.9	115.6				35.4		
BT0992	Glycoside hydrolase family 2 Glycoside hydrolase family 2					22.7	66.6				10.2		10.3
BT0996	Glycoside hydrolase family 2					171.1	262.3				10.2		10.0
BT0997	hypothetical protein					47.6	63.9						
BT1001	Glycoside hydrolase family 78					24.8	64.4				36.9		
BT1002	hypothetical protein					55.8	83.7						
BT1003	hypothetical protein					35.6	56.4						
BT1010	Glycoside hydrolase family 95					68.7	147.7				15.8		
BT1011	Glycoside hydrolase family 105					140.4	210.7				16.4		
BT1012	hypothetical protein					82.6	165.1				17.1		
BT1013	Glycoside hydrolase family 78					77.0	118.0						
BT1017	hypothetical protein						28.2						
BT1018	Glycoside hydrolase family 28						24.1						
BT1019	Glycoside hydrolase family 78					13.8	33.4						
BT1020	hypothetical protein					105.8 23.0	264.8 60.0				11.4 15.5		
BT1021 BT1022	Glycoside hydrolase family 43 hypothetical protein					25.1	36.8				15.5		
BT1022 BT1023	Polysaccharide lyase family 1					31.9	49.8						
BT1025	hypothetical protein					31.3	36.4						
BT1020	hypothetical protein						22.8						
BT1028	susD-like					78.1	120.8						
BT1029	susC-like						495.0						
BT1030	hypothetical protein			13.8		676.1	457.3				14.4		
BT1031	hypothetical protein					84.5	123.1						
BT1230	hypothetical protein		19.1			25.1	77.1	11.1	15.4		50.2	15.7	
BT1415	cytochrome c biogenesis protein ccsA				11.4		16.0						
BT1417	cytochrome C552 precursor				14.4		16.5						14.1
BT1418	quinol oxidase				13.6		16.4						20.3
BT1518	hypothetical protein												15.3
BT1519	N-acetylmuramoyl-L-alanine amidase											14.1	17.8
BT1682	susD-like					182.2	115.6						13.4
BT1683	susC-like				04.7	148.2	106.8				00.0	00.4	12.1
BT1759 BT1762	Glycoside hydrolase family 32 susD-like				24.7 70.0						92.3 396.7	29.1 61.9	56.5 80.2
BT1884	cold shock protein, putative DNA-	15.2			70.0						390.7	01.9	00.2
D11004	binding protein	15.2											
BT1885	putative ATP-dependent RNA helicase	10.3											
BT1903	hypothetical protein											11.9	
BT2096	putative transcriptional regulator			10.1									
BT2097	hypothetical protein	17.9		32.5			11.6						
BT2118	transporter, AcrB/D/F family			10.0								15.4	
BT2254	Polysaccharide lyase family 10			10.2	30.1								
BT2680	Glycoside hydrolase family 2	31.2		22.8	10.4	50.7	12.8						
BT2813	sodium-dependent multivitamin					201.7	184.0				18.4		
DT0044	transporter					075.5	040.5				40.0		
BT2814 BT3044	dihydrodipicolinate synthase	32.6				275.5	219.5				13.0 88.3		14.7
BT3044	hypothetical protein susD-like	19.4									256.9	21.0	59.5
BT3045	Glycoside hydrolase family 31	10.4		13.9	17.4	17.0	10.3			14.5	200.8	21.0	58.5
BT3420	hypothetical protein		133.4	. 5.0			. 5.5			. 1.0	10.1		
BT3421	hypothetical protein		59.6										
BT3422	hypothetical protein		54.8										
BT3423	hypothetical protein		89.6										
BT3424	hypothetical protein		58.1										
BT3425	hypothetical protein		17.9										
BT3615	hypothetical protein					87.2	121.7				34.2		10.8
2.00.0													

BT3616	fucose permease					49.7	80.0								
BT3617	sorbitol dehydrogenase					42.2	111.0						12.6	10.9	
BT3654	Glycoside hydrolase family 35		23.7										25.1		
BT3657	Glycoside hydrolase family 51		20.9										29.6		15.0
BT3658	hypothetical protein	28.3	74.2		10.3								43.9		12.6
BT3662	Glycoside hydrolase family 43					13.0	21.3							29.7	
BT3665	Glycoside hydrolase family 29					11.5	23.9							28.7	
BT3669	hypothetical protein					18.5	53.1							45.6	
BT3672	hypothetical protein					75.0	123.1							65.8	
BT3674	hypothetical protein		19.7										16.4	10.8	22.6
BT3675	Glycoside hydrolase family 43	10.3	33.1												
BT3676	hypothetical protein		33.1												
BT3677	hypothetical protein	40.0	21.5		40.4								40.5		
BT3679	conserved hypothetical protein, with a conserved domain	10.9	110.5		10.4								13.5		
BT3680	susC-like	54.6	625.5		50.6								45.3		10.4
BT3682	hypothetical protein	33.4	170.8		19.8								77.0	22.4	44.8
BT3683	Glycoside hydrolase family 16	12.2	83.6		10.0								11.0	22.7	44.0
BT3685	Glycoside hydrolase family 43		12.2												
BT3686	hypothetical protein		13.9												
BT3698	alpha-amylase, susG							53.9							22.6
BT3701	susD							33.0							12.4
BT3747	hypothetical protein		36.6												
BT3763	rhamnulose kinase/L-fuculose kinase	497.1		523.4	184.0	602.2	827.6					11.2	28.7		
BT3765	L-rhamnose/H+ symporter	371.2		305.7	105.3	433.8	471.2						113.0	19.6	
BT3766	rhamnulose-1-phosphate aldolase	350.4		244.1	102.2	451.4	339.3						229.0	103.5	58.6
BT3767	lactaldehyde reductase	10.5				12.9	14.8								
BT4105	hexuronate transporter			10.1	17.1	16.1	12.4			40.4	40.0	40.0			
BT4109	Carbohydrate esterase family 8			117.0	374.2	51.8	140.9			19.4	18.2	12.0		40.0	40.7
BT4110 BT4112	Carbohydrate esterase family 8			37.5 64.5	90.5 138.2	21.1 46.3	56.9 57.9							10.2 12.0	13.7 28.8
BT4115	hypothetical protein Polysaccharide lyase family 1			36.5	73.6	11.0	24.4							12.0	20.0
BT4116	Polysaccharide lyase family 1			37.4	127.8	39.5	46.2								
BT4119	Polysaccharide lyase family 1			36.5	135.5	33.3	89.1						11.6		14.7
BT4123	Glycoside hydrolase family 28			37.6	150.8		42.0						11.0		14.1
BT4124	hybrid two-component system (HTCS)			01.0	24.2		12.0								
BT4145	Glycoside hydrolase family 106	14.0		13.9		20.7									
BT4146	Glycoside hydrolase family 28	21.5		17.5		29.8									
BT4147	hypothetical protein	21.2		19.1		19.2									
BT4148	hypothetical protein	22.5		18.5		34.9									
BT4149	Glycoside hydrolase family 28	46.7		38.4	16.0	64.3	20.1								
BT4150	Carbohydrate esterase family 12	37.5		33.8	15.4	73.3	13.1								
BT4151	Glycoside hydrolase family 2	242.3		219.9	91.1	568.6	75.0						26.3	17.6	23.4
BT4152	Glycoside hydrolase family 42	212.2		151.8	44.3	178.7	60.2						33.6		
BT4154	Carbohydrate esterase family 4	22.7		17.8		16.5									
BT4155 BT4156	Glycoside hydrolase family 28 Glycoside hydrolase family 2	10.2				11.0 10.7									
BT4158	hypothetical protein	70.2		52.7	24.8	132.5	36.6								
BT4159	hypothetical protein	24.8		23.2	24.0	88.9	19.7								
BT4160	beta-galactosidase precursor	31.7		36.3	12.4	77.6	51.2						12.7		
BT4168	susC-like	39.8		28.8	19.6	60.3	17.4						12.7		
BT4171	hypothetical protein	49.6		36.2	24.2	77.5	15.7								
BT4173	Carbohydrate esterase family 12	19.9		14.8		64.0	10.6								
BT4174	Glycoside hydrolase family 105	31.0		22.3		62.2	13.7								
BT4177	hypothetical protein	64.6		48.6	20.2	68.1	23.2								
BT4181	Glycoside hydrolase family 2	17.4													
BT4183	Polysaccharide lyase family 9	53.9		27.6	13.5	55.5	21.2								
BT4185	Glycoside hydrolase family 43			12.8	33.0		12.1								
BT4187	Glycoside hydrolase family 28			35.2	75.1	37.4	40.6								
BT4227	hypothetical protein	400.6		004.0	1100	04.0		10.4			40.4	40.0	11.2	53.2	19.3
BT4669	hypothetical protein	130.9		881.2	140.3	24.8					13.1	12.6	404.4	34.4	144.9
BT4671	susC-like	27.5		192.0	19.2								56.2		20.2
Sector 4															
BT0506	Glycoside hydrolase family 20								11.2				18.2	34.8	52.9
BT0791	hypothetical protein						18.5			13.4			13.8		
BT1036	hypothetical protein								37.7				35.4	153.4	39.5

BT1037 BT1038 BT1039 BT1040 BT1042 BT1043 BT1044 BT1045 BT1046	hypothetical protein hypothetical protein susD-like susC-like susC-like susD-like Glycoside hydrolase family 18 hypothetical protein susC-like							54.4 62.0 37.2 48.0 20.4 17.8 20.7 13.1 78.3					50.1 79.5 62.4 39.3 19.2 16.8 22.0 10.8 288.2	202.3 271.1 198.8 190.7 127.6 98.1 161.8 51.0	29.4 51.8 42.7 39.4 238.0 182.3 275.4 100.3 82.1
BT1048 BT1534 BT1554 BT2559 BT2561 BT2818 BT2820	Glycoside hydrolase family 18 hypothetical protein alanine dehydrogenase susD-like putative anti-sigma factor susC-like susC-like							11.5 22.6 368.2 4216.0	11.9 11.2		10.8		43.2 132.7 33.5 16.2 20.7 22.6 230.1	36.0 20.5 12.7 37.5 46.8	96.1 14.7
BT2821 BT2822 BT2823 BT3778 BT3790 BT3860 BT4294	susD-like hypothetical protein						17.0	433.0 139.5 3671.0 24.3 30.8	113.5 139.3 21.7			40.5	32.5 11.6 206.2 14.2 11.5 36.8 12.1 23.9	87.3 30.1 508.4 34.0 16.0 92.9 406.3	16.5 81.9 10.7
BT4295 BT4296 BT4297 BT4298 BT4299 BT4407 BT4648	putative chitobiase hypothetical protein susD-like susC-like hypothetical protein hypothetical protein hypothetical protein							30.8 32.8 37.3 33.5 38.0 12.6			11.8	13.5 17.9 16.1 16.5 19.0	23.9 21.8 23.9 23.4 20.6 34.1 55.3	406.3 109.2 77.9 472.6 126.4 37.6 13.4	488.3 126.3 76.8 415.8 176.8 92.1
Sector 5 BT1536 BT2167 BT3221 BT3222 BT3223 BT3572	ABC transporter permease elongation factor G hypothetical protein hypothetical protein hypothetical protein hypothetical protein	33.6	15.1 14.6	32.7 11.6 86.3 94.8 52.5	16.8 20.1	12.6 17.6	10.1	31.6 27.0 15.9 10.4 182.1	11.7		37.0	11.5	207.2 79.2 171.9 219.9 123.4 17.5	45.6 186.5	15.6 101.1
BT3573 BT3793 BT4108 BT4384	hypothetical protein hypothetical protein Glycoside hydrolase family 105 hypothetical protein	19.1	15.5	131.6	300.3	103.2	146.7	297.4	15.9	28.2	30.1 13.6	16.2	18.1 56.7 16.7 20.2	22.5 112.8 12.9 10.0	31.3 10.3
Sector 6 BT0489 BT1211 BT1572 BT1604 BT3231	putative gluconate aldolase hypothetical protein RNA polymerase ECF-type sigma factor hypothetical protein 4-deoxy-L-threo-5-hexosulose-uronate	10.7 31.7 12.2		51.1 21.4	11.7 58.4 10.4 10.9	13.7	10.9 54.3 10.6			54.7 15.9 13.3	11.2 12.7 52.8 11.7 19.7	14.0 15.4			
BT3571 BT3574 BT3575 BT4106	ketol- isomerase hypothetical protein hypothetical protein hypothetical protein 4-deoxy-L-threo-5-hexosulose-uronate		21.7 17.8		12.2	21.7	11.9	203.9 75.6 54.7		15.3	23.7	35.8	13.2		
BT4107 BT4393 BT4715	ketol- isomerase putative phosphotransferase enzyme II, C component hypothetical protein non-specific DNA-binding protein Dps	10.3		12.3	14.9 21.6	14.2 11.5	14.1 33.0	14.9		30.0 27.8	26.3 14.7 22.1	38.2		27.8	14.7
Sector 7 BT0215 BT0459	iron uptake regulatory protein Glycoside hydrolase family 20	25.7		21.1	21.0		55.0	11.2		21.0	10.3			22.3	15.5
BT0488 BT1049 BT1273 BT1274	2-dehydro-3-deoxygluconokinase putative patatin-like protein L-fucose isomerase L-fuculose-1-phosphate aldolase							20.5 21.6 15.6				11.2	83.4	269.7	119.0

BT1275	L-fuculose kinase			20.3							
BT1276	hypothetical protein			25.4						14.1	17.5
BT1277	L-fucose permease			33.2						11.4	13.3
BT1532	ABC transporter permease			14.2					181.0		21.2
BT1596	putative sulfatase yidJ					11.7	40.9				
BT1626	Glycoside hydrolase family 2			12.1							
BT1627	Glycoside hydrolase family 20			20.0							
BT1628	putative sulfatase yidJ			17.2							
BT1629	hypothetical protein						15.0			18.1	
BT1631	susC-like					10.7	11.7	11.4		14.3	
BT2119	transmembrane protein precursor,	10.0	10.1					10.4		11.0	
	possibly involved in transport										
BT2451	putative pyrogenic exotoxin B			12.2	40.0				04.0	05.0	
BT2560	susC-like				13.8				21.3	25.0	
BT2615	reverse transcriptase				50.0						
BT2617	reverse transcriptase		40.7		95.0						
BT2618	two-component system response regulator		12.7		232.3						
BT2619	two-component system sensor histidine				39.8						
D12010	kinase				00.0						
BT2620	Glycoside hydrolase family 97		11.3		84.4						
BT2621	hypothetical protein				75.3						
BT2622	Glycoside hydrolase family 67				78.7						
BT2623	Glycoside hydrolase family 76		18.8		168.8				14.6	20.0	17.0
BT2624	hypothetical protein		12.3		93.2						
BT2625	susD-like		17.8		128.8					12.3	
BT2626	susC-like		16.4		128.2					33.4	23.8
BT2627	putative cell surface protein, have		18.7		104.7					23.2	14.9
	conserved domain										
BT2628	hybrid two-component system (HTCS)				55.7						
BT2629	Glycoside hydrolase family 92		15.6		99.0					12.9	
BT2630	conserved hypothetical protein with				16.6						
	endonuclease/exonuclease/phosphatas										
BT2631	e family domain Glycoside hydrolase family 76				13.1						
BT2632	hypothetical protein				15.6						
BT2633	hypothetical protein				14.3						
BT2812	alkyl hydroperoxide reductase C22				14.5		10.5				
DIZOIZ	protein						10.0				
BT2819	susD-like			416.8					27.9	45.8	17.0
BT2824	Glycoside hydrolase family 16			1264.0					79.3	66.5	26.5
BT2825	Glycoside hydrolase family 18			77.7						18.6	12.0
BT2919	susD-like						20.7			10.7	
BT2920	susC-like			14.5			51.8	14.4	44.0	45.3	
BT3233	hypothetical protein						10.1				
BT3324	Polysaccharide lyase family 8					78.5		100.3			
BT3328	hypothetical protein					57.2		71.9			
BT3329	hypothetical protein					160.8		456.4			
BT3330	hypothetical protein					184.7		433.3			
BT3331	susD-like					94.6		171.3			
BT3332	susC-like					120.6		314.6			
BT3333	arylsulfatase A precursor (ASA)					115.2		55.7			
BT3348	Glycoside hydrolase family 88					28.5		74.3 79.2			
BT3349	putative sulfatase yidJ					23.0					
BT3350	Polysaccharide lyase family 8			132.0		44.1		52.9	26.4	22.6	12.4
BT3750 BT3751	susC-like			152.0					36.1	23.6	12.4
BT3752	outer membrane protein susD-like			19.1							
BT3753	endo-beta-N-acetylglucosaminidase F2			12.7							
013/33	precursor			12.7							
BT3754	hypothetical protein			13.1						10.1	
BT3773	Glycoside hydrolase family 92				10.7						
BT3774	Glycoside hydrolase family 38				20.0						
BT3775	hypothetical protein				52.0				41.4	14.7	
BT3776	hypothetical protein				34.1				12.3	16.1	
BT3777	hypothetical protein				70.6				54.2	86.6	27.9
BT3779	hypothetical protein		10.5		41.4				50.1	43.0	
BT3780	hypothetical protein		10.3		88.5						

	hypothetical protein							14.0						
BT3781 BT3782	Glycoside hydrolase family 76							23.0						
BT3784	Glycoside hydrolase family 92					20.2		140.1					66.7	44.1
BT3786	hybrid two-component system (HTCS)							28.5						
BT3787	hypothetical protein					12.9		119.5						
BT3788	susC-like					19.3		161.8						11.4
BT3789	susD-like					12.2		96.7						
BT3791	hypothetical protein					40.0		56.6						
BT3792 BT3854	Glycoside hydrolase family 76 susC-like					12.6		86.6 41.2						
BT3855	susD-like							44.5				18.7	29.3	10.5
BT3856	hypothetical protein							24.2				10.7	25.5	10.5
BT3857	hypothetical protein							25.2						
BT3858	Glycoside hydrolase family 92				12.9			62.6				12.1	13.6	16.6
BT3859	hypothetical protein							38.5						
BT3861	hypothetical protein							46.2						
BT3862	Glycoside hydrolase family 99							50.5				25.6	12.0	10.6
BT3958 BT4132	susC-like Carbohydrate binding module family 32						11.6 100.7					12.4		
BT4133	hypothetical protein						395.8							
BT4134	susD-like						303.6					11.1		
BT4135	susC-like						723.8						22.0	
BT4136	Glycoside hydrolase family 29						1136.0					24.7	26.3	17.6
BT4244	Carbohydrate binding module family 32						49.3						187.0	19.3
BT4245	hypothetical protein						36.0						178.8	24.6
BT4246	susD-like						38.9						95.6	11.9
BT4247 BT4248	susC-like						36.7 34.6						86.4 105.7	14.3 10.6
BT4249	putative anti-sigma factor hypothetical protein						12.9						20.2	10.6
BT4394	Glycoside hydrolase family 20						10.7						14.1	
BT4410	hypothetical protein								40.9		54.1			
BT4411	hypothetical protein								37.3		91.2			
BT4631	putative arylsulfatase precursor						12.4							
BT4632	Carbohydrate binding module family 32						13.9							
BT4633	susD-like						12.4							13.8
BT4634 BT4652	susC-like Polysaccharide lyase family 15						17.1			88.9				12.4
BT4653	glucose/galactose transporter									123.1				
BT4654	ROK family transcriptional repressor,									51.1				
	with glucokinase domain													
BT4655	hypothetical protein									93.8				
BT4656														
	N-acetylglucosamine-6-sulfatase									158.1				
BT/1657	precursor													
BT4657 BT4658	precursor Polysaccharide lyase family 12									115.8				
BT4658	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88									115.8 88.5				
	precursor Polysaccharide lyase family 12									115.8				
BT4658 BT4659 BT4660 BT4661	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein									115.8 88.5 134.7 165.3 142.1				
BT4658 BT4659 BT4660 BT4661 BT4662	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12									115.8 88.5 134.7 165.3 142.1 120.5				
BT4658 BT4659 BT4660 BT4661	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein									115.8 88.5 134.7 165.3 142.1				
BT4658 BT4659 BT4660 BT4661 BT4662	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13									115.8 88.5 134.7 165.3 142.1 120.5				
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13									115.8 88.5 134.7 165.3 142.1 120.5				
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated:					24.5				115.8 88.5 134.7 165.3 142.1 120.5		14.0		
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13					24.5				115.8 88.5 134.7 165.3 142.1 120.5		14.0 20.7		
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor					24.5				115.8 88.5 134.7 165.3 142.1 120.5		20.7		
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain					24.5				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0	56.0	88.3
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5'-					24.5				115.8 88.5 134.7 165.3 142.1 120.5		20.7	56.0	88.3
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain					24.5				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0	56.0	88.3 10.9
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527 BT0528 BT0529 BT0530	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5'- phosphoribosyl)anthranilate isomerase					24.5				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0 12.6 16.8 11.8		
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527 BT0528 BT0529 BT0530 BT0532	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5'- phosphoribosyl)anthranilate isomerase indole-3-glycerol phosphate synthase anthranilate phosphoribosyltransferase anthranilate synthase component I					24.5				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0 12.6 16.8 11.8 12.6		
BT4658 BT4659 BT4660 BT4661 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527 BT0528 BT0529 BT0530 BT0532 BT0533	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5'- phosphoribosyl)anthranilate isomerase indole-3-glycerol phosphate synthase anthranilate pynthase component I tryptophan synthase beta chain									115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0 12.6 16.8 11.8 12.6 12.2	23.2	10.9
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527 BT0528 BT0529 BT0530 BT0532 BT0533 BT0678	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5'- phosphoribosyl)anthranilate isomerase indole-3-glycerol phosphate synthase anthranilate phosphoribosyltransferase anthranilate synthase component I tryptophan synthase beta chain cation efflux system protein czcC	25.6	59.5	132.1	157.5	68.1				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0 12.6 16.8 11.8 12.6 12.2 116.6	23.2	
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0524 BT0527 BT0528 BT0529 BT0530 BT0532 BT0533 BT0678 BT0679	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5¹- phosphoribosyl)anthranilate isomerase indole-3-glycerol phosphate synthase anthranilate synthase component I tryptophan synthase beta chain cation efflux system protein czcC cation efflux system protein czcB	25.6 14.8	132.1	78.7	54.1	68.1 43.8				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0 12.6 16.8 11.8 12.6 12.2 116.6 29.6	23.2 204.0 24.0	10.9
BT4658 BT4659 BT4660 BT4661 BT4662 BT4675 Down regula Sector 1 BT0225 BT0504 BT0527 BT0528 BT0529 BT0530 BT0532 BT0533 BT0678	precursor Polysaccharide lyase family 12 Glycoside hydrolase family 88 susD-like susC-like hypothetical protein Polysaccharide lyase family 12 Polysaccharide lyase family 13 ated: hypothetical protein TonB-dependent outer membrane receptor tryptophan synthase alpha chain putative N-(5'- phosphoribosyl)anthranilate isomerase indole-3-glycerol phosphate synthase anthranilate phosphoribosyltransferase anthranilate synthase component I tryptophan synthase beta chain cation efflux system protein czcC					68.1				115.8 88.5 134.7 165.3 142.1 120.5		20.7 28.0 12.6 16.8 11.8 12.6 12.2 116.6	23.2	10.9

BT0988	Mg2+ transport ATPase protein B					30.6	16.0						56.2	96.9	33.2
BT1563	hypothetical protein												14.5	24.8	
BT1566	putative aluminum resistance protein												11.7	17.9	
BT1567	hypothetical protein												10.5	12.6	
BT1574	putative outer membrane protein												24.4		
DT4700	precursor												44.4	040.4	44.0
BT1798 BT1895	hypothetical protein												14.1 17.2	212.4 36.3	14.0 85.0
	hypothetical protein														
BT1896	putative cell surface antigen												17.5	59.8	20.4
BT2387	O-acetylhomoserine (thiol)-lyase												14.6	14.4	00.0
BT2409	putative TonB-dependent outer membrane protein												37.6	28.3	23.3
BT4037	hypothetical protein										50.8		10.3	16.0	
BT4693	cation efflux system protein					104.9	16.9				30.6		52.9	34.8	19.2
BT4694	cation efflux system protein					127.1	17.9						43.3	48.1	33.9
BT4695	outer membrane efflux protein precursor					11.3	17.9						21.9	15.7	33.9
B14093	outer membrane emux protein precursor					11.5							21.9	15.7	
Sector 2															
BT0226	hypothetical protein					11.9	17.8						12.7		
BT1564	hypothetical protein					11.0	17.0						15.5	21.5	
D11004	nypotriction protein												10.0	21.0	
Sector 3															
BT1573	hypothetical protein				10.3										
BT2157	hypothetical protein					10.2									
	, p														
Sector 4															
BT1419	hypothetical protein		12.0						73.5				23.5	31.4	11.5
Sector 6															
BT2156	putative sugar phosphate	11.9		13.7	10.7	15.1				15.6					
	isomerase/epimerase														
BT2158	putative dehydrogenases and related					11.0				10.9					
BT3113	proteins putative transmembrane efflux protein	10.3	12.9						11.9		29.4	16.4		25.9	10.8
BT3240	susC-like	12.9	11.8					11.2	11.9		29.4	10.4		25.9	10.6
BT3240	susD-like susD-like	13.2	11.8				13.0	15.1				10.1			
BT3241		15.4					17.4	18.7				18.1			
	hypothetical protein		17.3												
BT3243	hypothetical protein	10.7	10.7				10.9	11.0				11.9			
BT3244	hypothetical protein	13.5	15.1				14.8	16.4				16.4			
Sector 7															
BT1420	hypothetical protein								12.5						
BT2159	putative oxidoreductase								12.0	10.3		10.4			
BT3430	ribosomal protein S20									10.3	10.2	10.4			
BT4499	conserved hypothetical protein, putative					18.8			10.6		10.2	16.1			
014499	membrane protein					10.0			10.0		104.0	10.1			
	membrane protein														