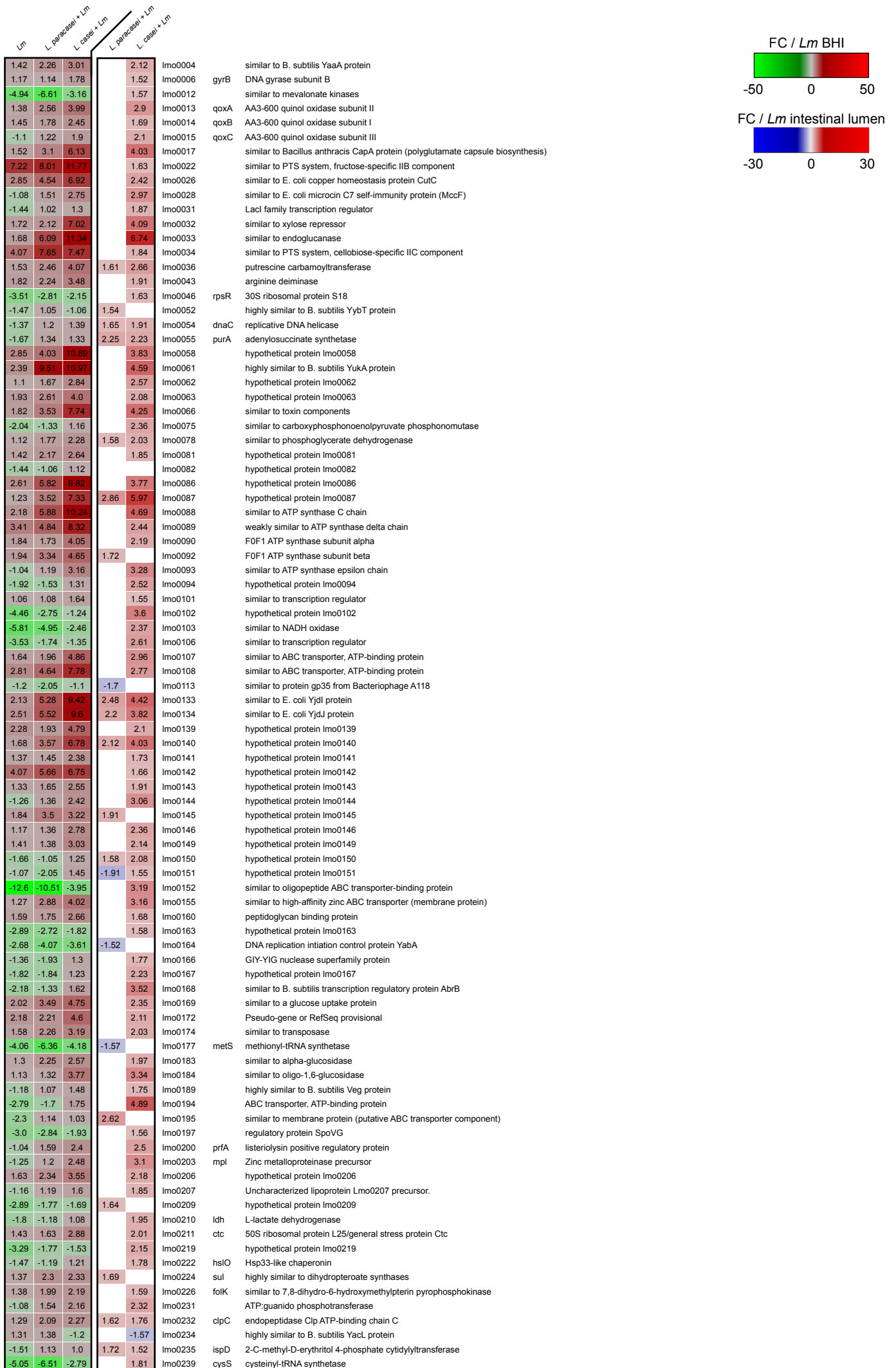


Figure S7 - Effect of treatment by *Lactobacillus* on *Lm* gene expression



Ln	L. paracasei + Ln	L. casei + Ln	L. paracasei + Ln	L. casei + Ln
-5.28	-5.87	-2.9	1.82	
-2.1	1.25	2.36	2.63	4.96
-1.08	1.29	2.37		2.56
-1.2	-1.86	-1.13	-1.55	
6.18	9.3	12.88		2.08
2.22	3.57	8.55	1.61	3.86
7.58	16.38	21.12		2.78
-1.02	1.21	3.13		3.2
2.79	5.44	4.11		1.47
-2.54	-2.35	-1.79		1.42
2.31	7.43	5.88		2.54
-1.06	1.48	2.07		2.18
-1.77	-1.23	1.5		2.65
-3.86	-2.04	-1.05		3.67
-2.27	-2.05	1.13		2.57
-1.88	-2.79	-2.98	-1.48	
-2.68	-3.67	-1.26		2.12
2.94	3.45	4.44		1.51
3.09	4.5	4.5	1.45	1.45
-1.71	-2.74	-1.18	-1.6	
-1.25	1.26	1.6		2.0
1.71	3.3	4.74	1.93	2.77
2.17	2.6	6.87		3.16
1.42	1.24	4.49		3.16
1.7	1.61	5.63		3.31
1.13	1.39	2.14		1.89
-3.96	-2.62	-1.95		2.03
1.17	1.72	3.01		2.57
1.37	1.39	2.32		1.69
1.12	1.59	2.57		2.3
1.18	1.37	2.71		2.29
1.23	3.16	3.93		3.18
1.66	2.92	4.13		2.49
1.07	1.88	2.8		2.6
2.9	3.48	5.77		1.99
-1.12	1.58	2.09	1.76	2.33
-2.11	-1.09	1.13	1.94	2.38
1.56	1.55	3.48		2.22
1.69	1.99	4.72		2.79
-1.63	-1.64	1.36		2.21
1.72	3.34	7.77		4.51
1.04	1.6	2.47		2.39
1.74	3.33	4.6	1.92	2.65
2.01	3.96	6.48	1.97	3.22
2.52	4.96	7.78	1.97	3.09
2.36	4.09	8.76		3.72
2.03	4.39	10.24	2.16	5.05
5.97	10.66	15.28		2.56
3.29	8.56	11.92		3.62
2.57	5.61	10.38	2.18	4.03
-1.63	1.16	1.27		2.07
-3.53	-3.09	-1.28		2.76
-1.08	1.0	2.34		2.53
-1.01	1.69	2.46	1.71	2.5
1.06	1.65	2.18		2.06
1.23	2.19	2.94		2.39
1.57	2.33	2.83		1.8
3.22	4.3	6.93		2.15
8.3	11.5	15.38		1.85
-1.71	-1.03	-1.07		1.6
1.09	1.41	2.28		2.09
1.15	1.5	1.94		1.68
1.29	1.54	2.1		1.63
-1.53	1.67	1.86	2.55	2.84
2.24	3.76	5.0		2.23
2.25	3.56	5.02		2.23
2.3	4.63	4.19	2.02	1.82
1.23	1.85	2.42		1.97
1.45	4.05	6.7		4.62
1.65	-1.18	1.45	-1.95	
1.06	1.58	1.56	1.49	
-1.44	-1.49	1.5		2.16
1.17	-1.39	-1.23	-1.62	-1.44
-1.51	-1.11	1.35		2.04
-2.22	2.05	1.39	4.54	3.07
-1.28	2.18	2.75	2.79	3.51
4.28	6.59	9.61		2.25
1.05	1.61	1.97	1.54	1.88
31.51	53.6	53.42	1.7	
19.35	27.39	46.1		2.38
2.57	7.91	8.88	3.08	3.46
1.29	1.83	3.39		2.64
1.97	2.48	3.58		1.81
1.01	1.07	3.4		3.37
1.37	3.12	3.96		2.88
1.74	6.76	6.56		3.76
1.43	3.11	5.28		3.69
1.9	3.26	3.5		1.85
-2.57	-2.93	-1.21		2.13
-1.44	1.41	3.45		4.97
-1.09	1.41	3.13		3.4
1.16	1.7	2.3	1.47	

Imo0241 similar to conserved hypothetical proteins like to B. subtilis YacO protein
 Imo0247 hypothetical protein Imo0247
 Imo0255 hypothetical protein Imo0255
 Imo0257 hypothetical protein Imo0257
 Imo0263 inIH internalin H
 Imo0264 inIE internalin E
 Imo0265 succinyl-diaminopimelate desuccinylase
 Imo0267 similar to other proteins
 Imo0270 hypothetical protein Imo0270
 Imo0273 hypothetical protein Imo0273
 Imo0274 hypothetical protein Imo0274
 Imo0275 hypothetical protein Imo0275
 Imo0277 similar to oxidoreductase
 Imo0281 hypothetical protein Imo0281
 Imo0286 transaminase
 Imo0287 similar to two-component response regulator
 Imo0289 similar to B. subtilis YycH protein
 Imo0291 conserved hypothetical protein similar to B. subtilis YycJ protein
 Imo0292 similar to heat-shock protein htrA serine protease
 Imo0293 rRNA large subunit methyltransferase
 Imo0295 similar to FMN-containing NADPH-linked nitroflavin reductase
 Imo0296 hypothetical protein Imo0296
 Imo0297 similar to transcriptional antiterminator (BglG family)
 Imo0298 similar to PTS beta-glucoside-specific enzyme IIC component
 Imo0301 similar to PTS beta-glucoside-specific enzyme IIA component
 Imo0305 similar to low specificity L-allo-threonine aldolase
 Imo0306 hypothetical protein Imo0306
 Imo0308 Pseudo-gene or RefSeq provisional
 Imo0310 hypothetical protein Imo0310
 Imo0311 hypothetical protein Imo0311
 Imo0313 hypothetical protein Imo0313
 Imo0315 similar to thiamin biosynthesis protein
 Imo0316 hydroxyethylthiazole kinase
 Imo0318 thiE thiamine-phosphate pyrophosphorylase
 Imo0320 similar to surface protein (peptidoglycan bound, LPXTG motif)
 Imo0321 hypothetical protein Imo0321
 Imo0322 hypothetical protein Imo0322
 Imo0326 similar to transcriptional regulators
 Imo0327 similar to cell surface proteins (LPXTG motif)
 Imo0332 hypothetical protein Imo0332
 Imo0333 similar to internalin proteins, putative peptidoglycan bound protein (LPXTG motif)
 Imo0335 hypothetical protein Imo0335
 Imo0339 weakly similar to inorganic pyrophosphatase
 Imo0340 hypothetical protein Imo0340
 Imo0342 similar to transketolase
 Imo0343 putative transaldolase
 Imo0344 short chain dehydrogenase
 Imo0347 similar to dihydroxyacetone kinase
 Imo0348 similar to dihydroxyacetone kinase
 Imo0350 hypothetical protein Imo0350
 Imo0359 similar to D-fructose-1,6-biphosphate aldolase
 Imo0362 similar to conserved hypothetical protein
 Imo0367 conserved hypothetical protein similar to B. subtilis YwbN protein
 Imo0378 hypothetical protein Imo0378
 Imo0379 hypothetical protein Imo0379
 Imo0380 hypothetical protein Imo0380
 Imo0381 hypothetical protein Imo0381
 Imo0383 highly similar to B. subtilis methylmalonate-semialdehyde dehydrogenase lolA
 Imo0386 similar to B. subtilis lolD protein, to acetolactate synthase
 Imo0389 itrA low temperature requirement protein A
 Imo0391 hypothetical protein Imo0391
 Imo0392 highly similar to B. subtilis YqfA protein
 Imo0393 hypothetical protein Imo0393
 Imo0398 similar to phosphotransferase system enzyme IIA
 Imo0401 alpha-mannosidase
 Imo0405 similar to phosphate transport protein
 Imo0406 similar to B. subtilis YyaH protein
 Imo0408 hypothetical protein Imo0408
 Imo0409 similar to internalin, peptidoglycan bound protein (LPxTG motif)
 Imo0411 phosphoenolpyruvate synthase
 Imo0412 hypothetical protein Imo0412
 Imo0414 hypothetical protein Imo0414
 Imo0415 similar to endo-1,4-beta-xylanase
 Imo0416 similar to putative transcription regulator
 Imo0420 hypothetical protein Imo0420
 Imo0424 similar to Staphylococcus xylosus glucose uptake protein
 Imo0428 similar to PTS fructose-specific enzyme IIC component
 Imo0431 similar to acetyltransferase
 Imo0433 inIA internalin A
 Imo0434 inIB internalin B
 Imo0435 peptidoglycan binding protein
 Imo0437 hypothetical protein Imo0437
 Imo0439 weakly similar to a module of peptide synthetase
 Imo0444 hypothetical protein Imo0444
 Imo0446 similar to penicillin acylase and to conjugated bile acid hydrolase
 Imo0447 similar to glutamate decarboxylase
 Imo0448 similar to amino acid antiporter
 Imo0450 hypothetical protein Imo0450
 Imo0454 conserved hypothetical protein similar to B. subtilis YeaC
 Imo0456 similar to permeases
 Imo0458 similar to hydantoinase
 Imo0462 hypothetical protein Imo0462

Ln	L. paracasei + Ln	L. casei + Ln	L. paracasei + Ln	L. casei + Ln	Imo	Protein Name
1.02	1.53	2.8		2.73	Imo0463	hypothetical protein Imo0463
1.83	4.19	6.14		2.29	Imo0466	hypothetical protein Imo0466
-2.2	-1.59	1.28		2.82	Imo0470	weakly similar to site-specific DNA-methyltransferase
11.93	20.74	26.74		1.74	Imo0471	hypothetical protein Imo0471
2.3	2.83	4.8		2.09	Imo0473	Pseudo-gene or RefSeq provisional
1.27	-1.32	1.12		-1.68	Imo0477	putative secreted protein
1.05	-2.38	-3.44		-2.5	Imo0478	putative secreted protein
-1.89	-1.87	-1.15		1.64	Imo0482	ribosomal RNA large subunit methyltransferase N
-17.87	-5.99	-3.67		4.87	Imo0485	hypothetical protein Imo0485
-2.17	-1.33	1.34	1.63	2.92	Imo0491	aroD 3-dehydroquinate dehydratase
-1.72	-1.2	1.8		3.1	Imo0495	similar to transmembrane protein
2.57	5.17	10.5		4.08	Imo0498	similar to ribose 5-phosphate isomerase
3.73	2.93	8.7		2.33	Imo0499	similar to ribulose-5-phosphate 3 epimerase
4.14	5.85	11.32		2.73	Imo0502	similar to putative sugar-phosphate isomerase
9.72	10.38	20.97		2.16	Imo0503	similar to PTS fructose-specific enzyme IIA component
6.03	6.16	10.47		1.74	Imo0508	similar to PTS system, Galactitol-specific IIC component
-2.96	-1.26	1.09		2.35	Imo0513	weakly similar to transcription regulator
1.11	1.63	3.38		3.04	Imo0514	similar to internalin protein, putative peptidoglycan bound protein (LPXTG motif)
4.38	7.96	24.41		1.82	Imo0515	hypothetical protein Imo0515
-3.76	-2.07	-1.63		1.81	Imo0523	similar to B. subtilis YybC protein
1.41	2.32	2.57		1.82	Imo0524	similar to putative sulfate transporter
1.8	3.84	7.6		4.23	Imo0526	similar to transcription regulator (TipA from Streptomyces coelicolor)
-3.44	-1.82	-1.73		1.99	Imo0527	transmembrane protein
-1.66	-1.55	1.61		2.67	Imo0532	hypothetical protein Imo0532
-2.79	-2.39	-1.2		2.31	Imo0534	hypothetical protein Imo0534
-1.6	1.05	1.48	1.69	2.36	Imo0535	similar to transcription regulator (LacI family)
-1.57	-1.94	1.41		2.21	Imo0538	similar to N-acyl-L-amino acid amidohydrolase
2.26	3.92	4.45		1.97	Imo0539	tagatose 1,6-diphosphate aldolase
-2.78	-1.55	1.01		2.82	Imo0541	similar to ABC transporter (binding protein)
1.92	4.55	4.5		2.36	Imo0542	similar to PTS system, glucitol/sorbitol-specific enzyme IIA component
1.15	1.76	5.13		4.45	Imo0551	hypothetical protein Imo0551
1.77	4.09	5.38		2.31	Imo0552	hypothetical protein Imo0552
-1.53	-1.15	1.33		2.03	Imo0553	hypothetical protein Imo0553
1.28	2.18	1.68		1.7	Imo0555	similar to di-tripeptide transporter
1.28	1.61	2.43		1.89	Imo0556	similar to phosphoglycerate mutase
1.42	1.55	2.74		1.93	Imo0557	similar to phosphoglycerate mutase
1.39	3.42	6.07		2.45	Imo0563	hisF imidazole glycerol phosphate synthase subunit HisF
1.28	3.39	3.6		2.65	Imo0564	hisA 1-(5-phosphoribosyl)-5-
1.75	2.73	5.04		2.88	Imo0566	hisB imidazoleglycerol-phosphate dehydratase
1.04	1.74	4.08		3.91	Imo0567	hisD histidinol dehydrogenase
-1.59	-1.22	2.9		4.62	Imo0568	hisG ATP phosphoribosyltransferase catalytic subunit
1.37	1.94	2.21		1.61	Imo0570	hisJ histidinol-phosphatase
-2.21	-2.16	-1.1		2.0	Imo0572	hypothetical protein Imo0572
1.18	3.76	3.24		3.19	Imo0574	similar to beta-glucosidase
1.44	2.01	2.65		1.85	Imo0578	hypothetical protein Imo0578
1.25	2.59	4.42		2.06	Imo0579	hypothetical protein Imo0579
1.19	2.16	2.74		2.3	Imo0580	weakly similar to carboxylesterase
1.64	2.86	3.71		1.75	Imo0584	hypothetical protein Imo0584
1.86	3.08	6.85		3.67	Imo0585	putative secreted protein
1.39	5.39	5.29		3.87	Imo0587	putative secreted protein
1.18	1.25	1.67		1.42	Imo0593	similar to transport proteins (formate%3F)
-1.37	-1.04	1.86		2.54	Imo0594	metX homoserine O-acetyltransferase
-4.37	-2.03	-2.67		2.16	Imo0597	similar to transcription regulator CRP/FNR family
1.28	1.76	2.92		2.28	Imo0602	weakly similar to transcription regulator
-4.47	-3.33	-1.54		2.9	Imo0605	hypothetical protein Imo0605
1.75	1.91	2.64		1.51	Imo0606	similar to transcription regulator MarR family
1.36	1.79	2.24		1.65	Imo0607	similar to ABC transporter, ATP-binding protein
1.16	1.59	2.77		2.38	Imo0608	similar to ABC transporter, ATP-binding protein
-2.92	-2.15	-1.82			Imo0609	similar to E. coli phage shock protein E
-2.15	-3.05	-1.12		1.92	Imo0613	similar to oxidoreductase
1.04	1.22	2.72		2.62	Imo0617	hypothetical protein Imo0617
-1.93	-1.62	1.03		1.98	Imo0622	hypothetical protein Imo0622
1.69	1.8	4.47		2.64	Imo0623	hypothetical protein Imo0623
1.03	1.18	1.74		1.69	Imo0624	hypothetical protein Imo0624
-2.49	-1.36	1.1		1.83	Imo0626	hypothetical protein Imo0626
2.75	3.17	8.74		3.17	Imo0627	peptidoglycan bound protein
1.97	3.76	3.42		1.74	Imo0628	hypothetical protein Imo0628
2.23	3.28	3.68		1.47	Imo0629	hypothetical protein Imo0629
1.52	2.07	2.71			Imo0630	similar to transcription antiterminator BglG family
2.44	6.07	11.31		4.63	Imo0634	similar to an E. coli putative tagatose 6-phosphate kinase
-2.73	-1.06	-1.35		2.57	Imo0637	weakly similar to methyltransferase
1.71	1.46	2.94		1.73	Imo0638	hypothetical protein Imo0638
1.31	1.34	1.96		1.5	Imo0639	similar to a transcription regulator (surface protein PAG negative regulator par)
-1.78	-1.16	1.14		2.04	Imo0642	hypothetical protein Imo0642
-4.12	-4.62	-2.42		1.7	Imo0646	hypothetical protein Imo0646
1.09	1.99	2.41		1.83	Imo0647	hypothetical protein Imo0647
4.27	7.89	9.52		1.85	Imo0648	similar to membrane proteins
4.96	9.68	10.86		2.19	Imo0649	similar to transcription regulators
-2.11	-1.03	1.78		2.06	Imo0652	hypothetical protein Imo0652
1.35	1.74	2.2		1.63	Imo0655	similar to phosphoprotein phosphatases
-2.08	-1.81	-1.44		1.45	Imo0656	hypothetical protein Imo0656
-1.08	1.07	2.07		2.22	Imo0657	hypothetical protein Imo0657
1.51	2.85	4.61		3.06	Imo0659	similar to transcription regulator (Rgg type)
1.11	2.15	3.24		2.91	Imo0661	hypothetical protein Imo0661
-1.98	-1.67	-1.16		1.71	Imo0662	thiD highly similar to phosphomethylpyrimidine kinase thiD
-1.26	-1.86	-1.71		-1.47	Imo0663	hypothetical protein Imo0663
-1.59	-1.47	1.13		1.81	Imo0664	similar to acetyl transferase
2.42	3.45	4.31		1.78	Imo0670	hypothetical protein Imo0670
-2.45	1.18	1.02		2.49	Imo0672	hypothetical protein Imo0672
2.07	6.79	12.59		6.09	Imo0676	fljP flagellar biosynthesis protein FljP
-1.43	2.29	3.71		5.32	Imo0677	fljQ flagellar biosynthesis protein FljQ
3.1	6.55	8.28		2.11	Imo0678	fljR flagellar biosynthesis protein FljR

Lm			L. paracasei + Lm			L. casei + Lm			L. paracasei + Lm			L. casei + Lm		
-1.01	1.38	2.63			2.65	Imo0679	flhB	flagellar biosynthesis protein FlhB						
1.81	4.17	7.92	2.31			Imo0683		similar to chemotactic methyltransferase CheR						
2.19	3.72	6.39			2.92	Imo0685		flagellar motor protein MotA						
1.93	3.28	8.25	1.7	4.28		Imo0688		hypothetical protein Imo0688						
1.22	2.66	7.39			6.05	Imo0693		flagellar motor switch protein						
1.95	3.5	5.85			3.0	Imo0696	figD	flagellar basal body rod modification protein						
1.55	4.66	8.36	3.01	5.39		Imo0697	figE	flagellar hook protein FigE						
2.61	5.68	6.4			2.45	Imo0698		flagellar motor switch protein						
1.33	1.73	3.1			2.34	Imo0704		hypothetical protein Imo0704						
1.69	3.39	5.52			3.27	Imo0705	figK	flagellar hook-associated protein FigK						
1.26	1.53	1.8			1.43	Imo0706	figL	flagellar hook-associated protein FigL						
-1.35	1.75	2.42	2.35	3.26		Imo0707	fliD	flagellar capping protein						
2.07	1.35	4.17			2.01	Imo0711	figC	flagellar basal body rod protein FigC						
1.18	1.88	2.16			1.82	Imo0714	fliG	flagellar motor switch protein G						
2.55	6.03	12.64			4.95	Imo0716	fliI	flagellum-specific ATP synthase						
1.84	2.65	6.83			3.71	Imo0717		similar to transglycosylase						
1.37	1.52	3.32			2.43	Imo0718		hypothetical protein Imo0718						
-1.32	1.56	2.4	2.06	3.16		Imo0719		hypothetical protein Imo0719						
-1.61	1.19	2.03	1.92	3.26		Imo0720		hypothetical protein Imo0720						
-1.42	-4.05	-2.1	-2.85			Imo0727		glucosamine--fructose-6-phosphate aminotransferase						
1.29	2.16	2.55			1.97	Imo0728		similar to riboflavin kinase / FAD synthase						
-14.55	-11.02	-6.3			2.31	Imo0731		hypothetical protein Imo0731						
1.18	2.13	2.02	1.8			Imo0733		similar to transcription regulator						
2.04	5.08	8.9	2.5	4.37		Imo0736		ribose-5-phosphate isomerase B						
4.18	6.79	11.62			2.78	Imo0737		hypothetical protein Imo0737						
4.77	12.52	19.88	2.62	4.17		Imo0738		similar to phosphotransferase system (PTS) beta-glucoside-specific enzyme IIABC component						
5.13	13.04	16.69	2.54	3.25		Imo0739		similar to 6-phospho-beta-glucosidase						
1.9	2.07	6.49			3.42	Imo0741		similar to transcriptional regulator (GntR family)						
1.84	2.93	4.85			2.64	Imo0742		similar to ABC transporter, ATP-binding protein						
1.51	3.06	4.3			2.84	Imo0743		hypothetical protein Imo0743						
1.72	2.7	6.78			3.94	Imo0744		similar to ABC transporter, ATP-binding protein						
1.34	2.24	2.41			1.8	Imo0747		hypothetical protein Imo0747						
-1.82	-1.07	1.05			1.92	Imo0748		hypothetical protein Imo0748						
-1.42	-1.57	1.4			2.0	Imo0749		hypothetical protein Imo0749						
-2.27	-1.6	1.07	1.42	2.42		Imo0751		hypothetical protein Imo0751						
-2.13	-1.25	1.21	1.7			Imo0755		hypothetical protein Imo0755						
-2.8	-1.3	-1.01			2.77	Imo0756		Similar to ABC transporter (ATP-binding protein)						
1.34	2.98	5.21	2.22	3.88		Imo0758		hypothetical protein Imo0758						
1.12	3.06	3.94	2.73	3.52		Imo0759		hypothetical protein Imo0759						
1.12	2.24	2.72	2.0	2.43		Imo0760		hypothetical protein Imo0760						
-1.57	-1.49	1.35			2.13	Imo0762		similar to ATP/GTP-binding protein						
1.06	1.88	2.02	1.78			Imo0772		similar to transcription regulator						
1.35	2.41	3.63	1.79	2.7		Imo0774		hypothetical protein Imo0774						
1.43	3.52	4.71	2.47	3.3		Imo0775		hypothetical protein Imo0775						
1.91	2.32	5.03			2.64	Imo0776		similar to transcription regulator (repressor)						
-1.14	1.44	2.19			2.49	Imo0780		hypothetical protein Imo0780						
-1.67	-1.18	-1.51	1.42			Imo0786		similar to acyl-carrier protein phosphodiesterase and to NAD(P)H dehydrogenase						
-1.29	-1.18	1.81			2.32	Imo0790		similar to transcription regulator (EbsC from Enterococcus faecalis)						
-1.39	1.63	1.88	2.26	2.6		Imo0798		similar to lysine-specific permease						
-5.52	-4.09	-1.37			4.04	Imo0800		similar to B. subtilis YqkB protein						
1.33	1.95	4.4			3.31	Imo0801		similar to internalin, putative peptidoglycan bound protein (LPXTG motif)						
1.35	1.85	2.78			2.07	Imo0807		similar to spermidine/putrescine ABC transporter, ATP-binding protein						
-13.45	-28.25	-13.36	-2.1			Imo0811		similar to carbonic anhydrase						
-1.51	-1.03	1.05			1.58	Imo0816		similar to B. subtilis regulatory protein PaiA						
2.7	3.96	3.69	1.47			Imo0818		similar to cation transporting ATPase						
-1.48	-1.3	1.28			1.89	Imo0820		some similarity to acetyltransferases						
-1.7	1.35	1.27	2.3	2.16		Imo0821		hypothetical protein Imo0821						
-2.31	-5.7	-2.52	-2.47			Imo0823		similar to oxidoreductases						
1.91	1.55	3.34			1.75	Imo0825		similar to 3-hydroxy-3-methylglutaryl-coenzyme a reductase						
-1.04	-2.15	-1.51	-2.07			Imo0826		similar to transport protein						
-1.13	1.34	2.94			3.34	Imo0833		similar to transcriptional regulator						
1.46	2.95	4.35			2.97	Imo0835		peptidoglycan binding protein						
-6.97	-4.03	-1.47			4.76	Imo0837		Pseudo-gene or RefSeq provisional						
-1.01	2.17	3.61	2.19	3.64		Imo0839		similar to Tetracycline resistance protein						
1.84	2.79	3.92			2.13	Imo0842		peptidoglycan binding protein						
2.3	2.76	5.29			2.3	Imo0849		amidase						
4.37	1.83	2.03			-2.15	Imo0850		hypothetical protein Imo0850						
-4.71	-2.98	-2.41	1.58			Imo0854		similar to E. coli SugE protein (transmembrane chaperone)						
5.75	7.81	15.98			2.78	Imo0860		similar to sugar ABC transporter, permease protein						
-4.45	-3.71	-2.94			1.51	Imo0866		similar to ATP-dependent RNA helicase						
1.41	1.7	4.77			3.39	Imo0869		hypothetical protein Imo0869						
-1.14	1.44	3.28	1.64	3.76		Imo0870		hypothetical protein Imo0870						
1.52	-1.11	-1.38	-1.69	-2.1		Imo0871		similar to B. subtilis YtcD protein						
1.14	1.8	3.14			2.75	Imo0872		similar to antibiotic resistance protein						
1.13	1.89	3.17			2.8	Imo0873		Similar to transcriptional regulator (antiterminator)						
2.05	4.72	5.78	2.3			Imo0877		similar to B. subtilis NagB protein (glucosamine-6-phosphate isomerase)						
2.82	2.83	5.6			1.98	Imo0878		similar to oxidoreductases						
3.97	4.06	9.44			2.38	Imo0879		hypothetical protein Imo0879						
-1.45	1.03	1.5			2.17	Imo0880		similar to wall associated protein precursor (LPXTG motif)						
2.04	2.5	3.86			1.89	Imo0881		hypothetical protein Imo0881						
-2.63	-3.42	-1.46			1.8	Imo0886	dal	similar to alanine racemase						
-4.32	-5.46	-2.82			1.53	Imo0896	rsbX	indirect negative regulation of sigma B dependant gene expression (serine phosphatase)						
1.57	2.43	3.32			2.11	Imo0897		similar to transport proteins						
1.09	2.36	4.63			4.26	Imo0901		similar to PTS system, cellobiose-specific IIC component						
-1.09	1.33	1.88	1.45	2.06		Imo0902		similar to transcription regulator (GntR family)						
-16.71	-9.58	-4.41			3.79	Imo0903		hypothetical protein Imo0903						
-1.13	1.19	1.58				Imo0906		glutathione reductase						
-3.37	-2.49	-1.38			2.44	Imo0908		similar to membrane proteins						
-1.22	1.11	1.87			2.28	Imo0910		hypothetical protein Imo0910						
2.13	2.69	5.96			2.8	Imo0911		hypothetical protein Imo0911						
-1.13	1.61	1.73	1.82			Imo0912		similar to transporters (formate)						
2.64	3.63	4.7			1.78	Imo0913		similar to succinate semialdehyde dehydrogenase						

	Lm	L. paracasei + Lm	L. casei + Lm	L. paracasei + Lm	L. casei + Lm				
	1.68	16.19	3.97	9.63	2.36	lmo1152		similar to Salmonella typhimurium PduB protein	
	1.44	19.38	5.3	13.46	3.68	lmo1153		highly similar to propanediol dehydratase, alpha subunit	
	1.13	27.18	6.8	24.09	6.03	lmo1154		similar to diol dehydratase (diol dehydratase) gamma subunit	
	2.57	12.69	6.96	4.93	2.71	lmo1155		similar to diol dehydratase (diol dehydratase) gamma subunit (pddC)	
	2.3	9.18	10.71		4.66	lmo1156		similar to diol dehydratase-reactivating factor large subunit	
	1.19	5.43	4.2	4.58	3.55	lmo1157		similar to diol dehydratase-reactivating factor small chain	
	3.7	8.88	11.47	2.4	3.1	lmo1158		similar to Salmonella enterica PduK protein	
	1.4	11.16	10.07	7.96	7.19	lmo1159		similar to carboxysome structural protein	
	1.73	5.68	4.63	3.28	2.67	lmo1160		similar to Salmonella enterica PduL protein	
	2.06	11.8	7.0	5.74	3.4	lmo1161		similar to ethanolamine utilization protein EutJ	
	2.75	6.22	7.84		2.85	lmo1162		hypothetical protein lmo1162	
	1.72	4.61	4.24	2.69	2.47	lmo1163		similar to carbon dioxide concentrating mechanism protein	
	1.61	3.88	4.76		2.96	lmo1165		similar to ethanolamine utilization protein EutE	
	1.25	9.85	7.23		5.8	lmo1167	glpF	similar to glycerol uptake facilitator protein	
	-2.13	-1.12	1.12		2.39	lmo1169	cobD	threonine-phosphate decarboxylase	
	6.8	13.09	25.59		3.76	lmo1174	eutA	reactivating factor for ethanolamine ammonia lyase	
	6.6	11.76	17.37		2.63	lmo1175	eutB	similar to ethanolamine ammonia-lyase, heavy chain	
	2.66	12.57	12.11		4.54	lmo1178		similar to putative carboxysome structural protein	
	9.88	25.73	10.04	2.61		lmo1180		similar to putative carboxysome structural protein	
	4.18	9.5	11.77	2.28	2.82	lmo1183		hypothetical protein lmo1183	
	3.37	9.62	9.67	2.92	2.87	lmo1186		similar to ethanolamine utilization protein EutH - Escherichia coli	
	5.44	11.86	5.77	2.18		lmo1187		similar to ethanolamine utilization protein EutQ	
	1.53	2.68	4.82		3.16	lmo1189		similar to transcriptional regulator	
	20.96	97.22	62.35	4.64	2.97	lmo1190		hypothetical protein lmo1190	
	1.84	4.45	2.92	2.42		lmo1191	cbiA	cobyrinic acid a,c-diamide synthase	
	2.52	9.05	5.89	3.59		lmo1192	cobD	cobalamin biosynthesis protein	
	2.55	5.68	11.73		4.6	lmo1193	cbiC	cobalt-precorrin-8X methylmutase	
	2.22	4.24	4.22	1.91	1.9	lmo1194	cbiD	cobalt-precorrin-6A synthase	
	2.53	7.92	4.7	3.13		lmo1196		cobalt-precorrin-6Y C(15)-methyltransferase	
	1.74	8.54	2.94	4.92	1.69	lmo1198	cbiG	cobalamin biosynthesis protein CbiG	
	1.66	4.73	5.31	2.84	3.19	lmo1200		similar to cobalamin biosynthesis J protein CbiJ	
	2.54	5.68	6.68	2.24	2.63	lmo1203	cbiL	cobalt-precorrin-2 C(20)-methyltransferase	
	-1.04	2.09	2.62		2.73	lmo1208	cbiP	cobyrinic acid synthase	
	-1.55	1.0	1.65		2.56	lmo1209		hypothetical protein lmo1209	
	-5.8	-4.9	-3.5		1.66	lmo1211		hypothetical protein lmo1211	
	1.37	-1.2	1.27	-1.65		lmo1215		similar to N-acetylmuramoyl-L-alanine amidase (autolysin)	
	-4.49	-5.07	-1.59		2.81	lmo1216		similar to N-acetylmuramoyl-L-alanine amidase (autolysin)	
	-1.29	-1.2	1.57		2.02	lmo1219		hypothetical protein lmo1219	
	-1.27	-1.58	2.15		2.73	lmo1220		hypothetical protein lmo1220	
	-2.78	-2.14	-1.11		2.5	lmo1221	pheS	phenylalanyl-tRNA synthetase subunit alpha	
	-1.12	1.32	2.04		2.28	lmo1231		similar to DNA polymerase beta, to B. subtilis YshC protein	
	-6.66	-3.39	-2.68		2.48	lmo1233	trxA	thioredoxin	
	-1.54	-1.31	1.24		1.91	lmo1236		similar to B. subtilis YslB protein	
	4.12	8.0	6.41	1.94		lmo1241		hypothetical protein lmo1241	
	1.04	1.53	2.65		2.56	lmo1242		similar to B. subtilis YdeI protein	
	1.05	1.86	2.05		1.94	lmo1244		weakly similar to phosphoglycerate mutase 1	
	-1.21	2.2	3.23	2.66	3.91	lmo1249		hypothetical protein lmo1249	
	-1.26	2.65	2.98	3.33	3.74	lmo1251		similar to regulator of the Fnr CRP family (including PrfA)	
	-5.03	-2.14	-2.44	2.35		lmo1252		similar to B. subtilis YxkD protein	
	3.61	5.32	7.75		2.15	lmo1253		similar to transcription regulator GntR family	
	-13.54	-14.01	-5.23		2.59	lmo1255		similar to PTS system trehalose specific enzyme IIBC	
	1.61	3.44	6.62	2.13	4.1	lmo1256		hypothetical protein lmo1256	
	-1.61	-1.18	1.24		1.99	lmo1257		hypothetical protein lmo1257	
	-3.25	-3.86	-1.74		1.87	lmo1260	proB	gamma-glutamyl kinase	
	2.62	3.24	4.17		1.59	lmo1261		hypothetical protein lmo1261	
	1.3	1.66	6.38		4.9	lmo1263		similar to transcriptional regulator	
	1.69	1.65	4.34		2.56	lmo1264		hypothetical protein lmo1264	
	1.9	2.62	5.62		2.95	lmo1265		weakly similar to oligopeptide ABC transporter AppA (binding protein)	
	1.74	-1.03	1.15	-1.78		lmo1271		similar to signal peptidase I	
	1.12	-1.43	-1.35	-1.6		lmo1276	gid	tRNA (uracil-5-)-methyltransferase Gid	
	1.74	2.09	3.4		1.95	lmo1281		similar to B. subtilis YneP protein	
	1.05	1.41	2.13		2.04	lmo1282		similar to B. subtilis YneQ protein	
	1.25	1.94	2.66		2.13	lmo1284		conserved hypothetical protein, similar to B. subtilis YneS protein	
	1.57	3.45	4.94		3.15	lmo1289		similar to internalin proteins, putative peptidoglycan bound protein (LPXTG motif)	
	1.57	1.25	-1.04		-1.64	lmo1291		similar to acyltransferase (to B. subtilis YrhL protein)	
	7.74	9.4	15.03		1.94	lmo1293	glpD	similar to glycerol 3 phosphate dehydrogenase	
	-1.0	-1.17	2.12		2.13	lmo1295		similar to host factor-1 protein	
	-4.94	-2.35	-1.85	2.11	2.66	lmo1296		conserved hypothetical protein similar to B. subtilis YrnA protein	
	1.43	2.57	3.54		1.79	lmo1301		hypothetical protein lmo1301	
	1.76	3.06	3.91		1.74	2.23	lmo1302		LexA repressor
	-1.67	-1.33	-2.59		-1.55	lmo1318		Putative zinc metalloprotease lmo1318	
	-2.33	-4.65	-2.63	-2.0		lmo1319	proS	prolyl-tRNA synthetase	
	-2.12	-1.5	-1.3	1.42		lmo1322	nusA	transcription elongation factor NusA	
	2.8	4.09	5.44		1.94	lmo1340		similar to B. subtilis YqgU protein	
	1.14	1.55	2.7		2.37	lmo1344		similar to comG operon protein 4 (comGD)	
	1.22	1.56	2.97		2.43	lmo1346	comGB	similar to B. subtilis comG operon protein 2	
	14.2	7.85	15.24	-1.81		lmo1349		glycine dehydrogenase subunit 1	
	-1.79	-2.23	-2.9		-1.62	lmo1354		similar to aminopeptidase P	
	-1.26	-1.24	1.17		1.48	lmo1362		exodeoxyribonuclease VII small subunit	
	-1.7	-1.19	-1.0		1.69	lmo1363		similar to geranyltransferase	
	-1.74	-1.59	-1.21		1.44	lmo1364	cspL	similar to cold shock protein	
	1.14	1.11	2.18		1.91	lmo1368	recN	DNA repair and genetic recombination	
	1.32	2.74	3.36		2.07	2.54	lmo1370		butyrate kinase
	1.32	2.48	2.15		1.63	lmo1371		dihydroliipoamide dehydrogenase	
	1.36	1.6	2.03		1.5	lmo1372		similar to branched-chain alpha-keto acid dehydrogenase E1 subunit (2-oxoisovalerate dehydrogenase alpha subunit)	
	3.63	6.34	5.88		1.62	lmo1375		similar to aminotripeptidase	
	-1.21	1.06	1.17		1.42	lmo1376		6-phosphogluconate dehydrogenase	
	-1.32	1.08	1.21		1.61	lmo1379		OxaA-like protein precursor	
	1.56	2.22	2.74		1.43	1.76	lmo1380		hypothetical protein lmo1380
	1.46	3.01	2.62			1.8	lmo1381		acylphosphatase
	-3.39	-2.4	-1.21			2.8	lmo1387		pyrroline-5-carboxylate reductase
	1.53	1.04	1.11	-1.46		lmo1395		hypothetical protein lmo1395	

Ln	L. paracassi + Lm	L. casapi + Lm	L. paracassi + Lm	L. casapi + Lm	Imo	Gene	Description
1.09	1.44	4.22		3.89	Imo1397	cinA	competence damage-inducible protein A
-1.37	-1.0	1.75		2.4	Imo1398	recA	recombinase A
1.78	-1.0	1.17	-1.78		Imo1403	mutS	DNA mismatch repair protein MutS
-1.39	1.14	1.8		2.5	Imo1409		similar to multidrug-efflux transporter
-1.37	1.67	1.56		2.29	2.14	Imo1413	peptidoglycan binding protein
2.1	2.6	2.98		1.42	Imo1415		similar to hydroxy-3-methylglutaryl coenzyme A synthase
-5.56	-3.78	-2.0		2.77	Imo1416		hypothetical protein Imo1416
-1.42	1.07	1.73	1.51		Imo1423		hypothetical protein Imo1423
-3.79	-1.07	-1.09	3.55	3.49	Imo1429		hypothetical protein Imo1429
-4.22	-2.05	-2.68	2.06		Imo1430		hypothetical protein Imo1430
8.17	18.33	22.26		2.24	2.72	Imo1433	similar to glutathione reductase
1.5	1.05	1.39	-1.43		Imo1434		hypothetical protein Imo1434
-1.34	-1.34	1.15		1.53	Imo1441	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
1.83	2.66	3.55		1.95	Imo1453		hypothetical protein Imo1453
1.63	2.25	4.82		2.95	Imo1454	rpoD	RNA polymerase sigma factor RpoD
1.99	3.36	2.86	1.69	1.44	Imo1463		similar to cytidine deaminase
3.28	3.34	5.22		1.59	Imo1464		similar to diacylglycerol kinase
3.29	4.49	4.78			Imo1465		putative metalloprotease
-1.77	-1.85	1.24		2.19	Imo1470		16S ribosomal RNA methyltransferase RsmE
-1.69	-1.89	-1.08		1.56	Imo1472	dnaJ	chaperone protein DnaJ
1.85	2.74	3.54		1.91	Imo1484	comEA	similar to integral membrane protein ComEA
-3.05	-2.38	-1.16		2.63	Imo1491		GTP-binding protein YqeH
1.29	1.37	2.41		1.87	Imo1501		hypothetical protein Imo1501
1.85	2.42	2.89		1.57	Imo1502		Holliday junction resolvase-like protein
1.72	2.26	3.03		1.77	Imo1503		hypothetical protein Imo1503
-3.64	-2.38	-1.81		2.01	Imo1504	alaS	alanyl-tRNA synthetase
1.66	3.3	7.14		4.3	Imo1505		similar to ABC transporter, ATP-binding protein
1.92	1.9	4.17		2.17	Imo1507		similar to two-component response regulators
-13.86	-6.48	-3.19		4.34	Imo1516		similar to ammonium transporter NrgA
-10.63	-5.72	-5.1		2.08	Imo1520	hisS	histidyl-tRNA synthetase
2.32	1.38	1.94	-1.67		Imo1522		D-tyrosyl-tRNA(Tyr) deacylase
1.97	2.86	2.24	1.45		Imo1534		similar to L-lactate dehydrogenase
2.08	2.01	3.0		1.44	Imo1535		hypothetical protein Imo1535
2.19	3.05	4.77		2.17	Imo1538	glpK	glycerol kinase
9.03	10.18	16.88		1.87	Imo1539		similar to glycerol uptake facilitator
-2.28	-1.64	-1.46		1.56	Imo1551	folC	similar to Folyl-polyglutamate synthetase
-1.58	-2.37	-3.05	-1.5		Imo1558	engB	ribosome biogenesis GTP-binding protein YsxC
1.99	1.05	1.96	-1.89		Imo1561	dnaB	chromosome replication initiation / membrane attachment protein DnaB
1.2	1.5	1.92		1.61	Imo1570	pykA	pyruvate kinase
1.91	3.71	4.05	1.95		Imo1575		hypothetical protein Imo1575
2.4	3.44	5.21	1.44	2.17	Imo1577		metal-dependent hydrolase
-2.82	-1.84	1.04		2.93	Imo1579		similar to alanine dehydrogenase
3.18	6.03	8.13	1.89	2.55	Imo1580		hypothetical protein Imo1580
1.17	2.16	9.08		7.75	Imo1588	argD	acetylornithine aminotransferase
-1.01	4.01	7.38		7.44	Imo1589	argB	acetylglutamate kinase
1.0	1.59	2.79		2.79	Imo1590	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein
2.97	6.65	10.1		3.4	Imo1591	argC	N-acetyl-gamma-glutamyl-phosphate reductase
-1.92	-1.95	1.04		1.99	Imo1595		hypothetical protein Imo1595
1.55	2.78	3.62		2.35	Imo1601		similar to general stress protein
2.43	3.25	4.28		1.76	Imo1602		hypothetical protein Imo1602
1.09	-1.7	1.16	-1.86		Imo1612		hypothetical protein Imo1612
-2.87	-1.35	1.66	2.13	4.78	Imo1613		hypothetical protein Imo1613
1.26	1.08	2.86		2.26	Imo1618		similar to transcription regulator MarR family
-16.47	-10.78	-6.91		2.38	Imo1619	daaA	D-amino acid aminotransferase
-1.42	-2.08	-2.02	-1.46		Imo1621		weakly similar to E. coli MutT protein (dGTP pyrophosphohydrolase
-2.92	-2.17	-1.46		2.0	Imo1627	trpA	tryptophan synthase subunit alpha
1.8	2.39	3.4		1.89	Imo1629	trpF	N-(5'-phosphoribosyl)anthranilate isomerase
2.15	2.36	5.99		2.79	Imo1631	trpD	anthranilate phosphoribosyltransferase
-1.15	1.37	3.1		3.57	Imo1633	trpE	anthranilate synthase component I
1.07	3.12	2.39	2.91	2.23	Imo1634		bifunctional acetaldehyde-CoA/alcohol dehydrogenase
1.38	1.81	3.28			Imo1638		hypothetical protein Imo1638
1.02	1.57	1.91	1.54	1.87	Imo1639		similar to dna-3-methyladenine glycosidase
1.32	1.51	3.99		3.03	Imo1640		hypothetical protein Imo1640
-1.84	1.04	1.06		1.95	Imo1641	citB	aconitate hydratase
2.28	3.04	3.52		1.54	Imo1642		similar to putative sigma factor regulator
1.82	2.0	3.9		2.15	Imo1646		similar to putative exonucleases SbcD
6.44	8.04	11.58		1.8	Imo1659		hypothetical protein Imo1659
-2.84	-6.73	-4.1	-2.37		Imo1660	leuS	leucyl-tRNA synthetase
-1.08	-1.47	1.39		1.51	Imo1662		similar to conserved hypothetical protein
1.96	2.72	3.26			Imo1666		peptidoglycan linked protein (LPXTG)
-1.12	1.0	1.85		2.08	Imo1674		similar to prolyl aminopeptidases
-1.11	1.36	1.19	1.52		Imo1675	menD	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase
-8.58	-3.05	-2.88		2.98	Imo1682		similar to transmembrane transport proteins
1.49	3.27	3.02	2.2	2.03	Imo1684		similar to glycerate dehydrogenases
1.44	2.81	5.56		3.88	Imo1694		similar to CDP-abequose synthase
-1.02	1.27	2.43		2.47	Imo1698		similar to ribosomal-protein-alanine N-acetyltransferase
1.16	2.09	3.01	1.79	2.58	Imo1699		some similarities to methyl-accepting chemotaxis proteins
1.33	1.66	2.14		1.6	Imo1703		similar to similar to RNA methyltransferases
-12.21	-22.19	-5.45		2.24	Imo1707		hypothetical protein Imo1707
1.75	2.09	2.74		1.57	Imo1708		similar to aminoglycoside N3'-acetyltransferases
1.02	1.65	2.18		2.14	Imo1716		similar to putative transcription regulators
-2.1	-1.32	1.45		1.59	3.05	Imo1718	similar to putative outer surface protein
-1.57	1.33	3.02	2.09	4.73	Imo1719		similar to phosphotransferase system (PTS) lichenan-specific enzyme IIA component
-1.12	2.17	5.5	2.42	6.15	Imo1720		similar to phosphotransferase system (PTS) lichenan-specific enzyme IIB component
1.79	1.39	2.56		1.43	Imo1725		similar to transcriptional regulator (GntR family)
1.22	-1.48	-1.36		-1.66	Imo1726		hypothetical protein Imo1726
1.83	2.53	5.89		3.22	Imo1731		similar to sugar ABC transporter, permease protein
1.29	2.99	7.62		5.93	Imo1732		similar to sugar ABC transporter, permease protein
-3.05	-2.73	-1.24		2.47	Imo1735	gltC	transcription activator of glutamate synthase operon GltC
1.27	3.24	3.39		2.67	Imo1739		similar to amino acid (glutamine) ABC transporter (ATP-binding protein)
1.05	3.84	2.59		2.46	Imo1740		similar to amino acid (glutamine) ABC transporter, permease protein
-2.28	-2.07	1.13		2.58	Imo1744		hypothetical protein Imo1744

Lm			L. paracasei + Lm			L. casei + Lm			L. paracasei + Lm			L. casei + Lm		
-5.26	-3.2	-1.57			3.35	lmo1751		Uncharacterized RNA methyltransferase lmo1751						
-6.15	-3.05	-1.65			3.72	lmo1752		hypothetical protein lmo1752						
-1.32	-1.92	-1.68	-1.46			lmo1755	gatA	aspartyl/glutamyl-tRNA amidotransferase subunit A						
1.19	1.25	-1.54		-1.83		lmo1756	gatC	aspartyl/glutamyl-tRNA amidotransferase subunit C						
-1.18	-1.83	-1.72	-1.55	-1.45		lmo1759	pcrA	ATP-dependent DNA helicase						
-2.24	-1.74	-1.06		2.1		lmo1761		similar to putative sodium-dependent transporter						
-1.33	1.55	1.43	2.07	1.91		lmo1765	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase						
-1.3	-1.14	1.34		1.74		lmo1767	purM	phosphoribosylaminoimidazole synthetase						
-1.28	1.41	1.51	1.81			lmo1769	purQ	phosphoribosylformylglycinamide synthase II						
-1.82	1.14	1.01		1.84		lmo1771		phosphoribosylformylglycinamide synthase subunit PurS						
1.25	2.29	1.66	1.84			lmo1777		hypothetical protein lmo1777						
-1.99	1.02	-1.22	2.02	1.63		lmo1778		similar to ABC transporter (ATP-binding protein)						
1.47	3.38	4.51	2.29	3.06		lmo1781		hypothetical protein lmo1781						
-3.48	-3.24	-2.23		1.56		lmo1787	rplS	50S ribosomal protein L19						
2.69	2.7	4.24		1.58		lmo1789		weakly similar to Nad(P)h Oxidoreductase chain B						
1.47	1.4	3.06		2.08		lmo1790		hypothetical protein lmo1790						
1.68	2.81	5.04		3.01		lmo1791		hypothetical protein lmo1791						
2.12	3.07	3.73		1.76		lmo1792	trmD	tRNA (guanine-N(1)-)-methyltransferase						
2.8	4.6	4.93	1.64			lmo1795		hypothetical protein lmo1795						
3.81	2.67	7.29		1.91		lmo1798		hypothetical protein lmo1798						
-2.02	-2.31	-1.24		1.63		lmo1805	mc	ribonuclease III						
-1.7	-2.83	-2.27	-1.66			lmo1807	fabG	similar to 3-ketoacyl-acyl carrier protein reductase						
-1.11	1.45	-1.35	1.62			lmo1812		similar to L-serine dehydratase						
-1.19	1.02	1.45		1.73		lmo1813		similar to phosphoglycerate dehydrogenase						
-1.09	-1.71	-1.25	-1.57			lmo1821		similar to putative phosphoprotein phosphatase						
2.22	1.55	-1.2		-2.65		lmo1822		similar to RNA-binding Sun protein						
1.78	3.01	4.36		2.45		lmo1830		short chain dehydrogenase						
1.87	2.83	5.0		2.67		lmo1835	carB	carbamoyl phosphate synthase large subunit						
-1.14	1.81	2.74		3.12		lmo1837	pyrC	dihydroorotase						
-2.55	-1.19	1.99	2.13	5.07		lmo1839	pyrP	highly similar to uracil permease						
1.03	1.29	2.41		2.34		lmo1842		hypothetical protein lmo1842						
-1.66	1.03	1.25		2.07		lmo1845		hypothetical protein lmo1845						
101	-50.28	-28.39	2.02	3.58		lmo1847		similar to adhesion binding proteins and lipoproteins with multiple specificity for metal cations (ABC transporter)						
-31.24	-28.48	-10.32		3.03		lmo1848		similar metal cations ABC transporter (permease protein)						
1.14	1.51	2.41		2.12		lmo1851		similar to carboxy-terminal processing proteinase						
-1.12	1.11	2.08		2.33		lmo1854		hypothetical protein lmo1854						
1.94	3.79	3.85		1.99		lmo1858		similar to dehydrogenases and hypothetical proteins						
-3.91	1.14	1.56	4.44	6.09		lmo1865		hypothetical protein lmo1865						
-2.96	-1.24	1.7	2.4			lmo1866		hypothetical protein lmo1866						
1.82	6.41	11.49	3.52	6.3		lmo1867		pyruvate phosphate dikinase						
-1.01	-1.69	2.28		2.31		lmo1869		similar to conserved hypothetical proteins, putative integral membrane protein						
1.82	2.41	5.06		2.78		lmo1871		similar to phosphoglucomutases						
-1.88	-1.75	-1.19		1.57		lmo1873		similar to dihydrofolate reductases						
8.2	29.04	25.65		3.13		lmo1883		similar to chitinases						
-4.71	-4.49	-1.32		3.55		lmo1884		similar to xanthine permeases						
-1.62	-1.24	-1.14				lmo1892	pbpA	similar to penicillin-binding protein 2A						
2.4	4.89	4.1	2.03			lmo1895	dnaD	similar to chromosome replication initiation protein						
1.47	1.45	-1.11		-1.64		lmo1897	aspB	aspartate aminotransferase						
2.34	2.9	3.35		1.43		lmo1902	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase						
1.08	2.06	2.07		1.91		lmo1904	birA	similar to transcriptional regulator and biotin acetyl-CoA-carboxylase synthetase						
-1.61	-1.02	1.72		2.76		lmo1910		similar to oxidoreductases						
1.11	1.77	2.13	1.6	1.93		lmo1912		similar to unknown proteins (hypothetical sensory transduction histidine kinase)						
-4.27	-4.27	-2.99		1.43		lmo1922		hypothetical protein lmo1922						
-3.15	-2.96	-1.63		1.93		lmo1928	aroF	chorismate synthase						
-1.18	-1.09	1.68		1.98		lmo1930		similar to heptaprenyl diphosphate synthase component II (menaquinone biosynthesis)						
1.73	2.58	3.01		1.74		lmo1931	ubiE	ubiquinone/menaquinone biosynthesis methyltransferase						
1.81	3.28	3.29		1.81		lmo1932		similar to heptaprenyl diphosphate synthase component I						
1.1	2.21	2.56	2.01	2.34		lmo1933	folE	GTP cyclohydrolase I						
-11.3	-7.84	-6.83		1.66		lmo1936	gpsA	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase						
-1.12	1.39	1.36		1.52		lmo1941		hypothetical protein lmo1941						
1.06	1.24	1.61		1.52		lmo1943		hypothetical protein lmo1943						
-1.15	1.65	2.33	1.89	2.67		lmo1946		similar to similar to acyl-CoA hydrolase						
-1.6	-1.15	1.02		1.63		lmo1948	resD	similar to two-component response regulator (ResD)						
-2.38	-3.7	-2.12	-1.56			lmo1949		hypothetical protein lmo1949						
1.09	2.53	11.17		10.3		lmo1959		similar to ferrichrome binding protein						
-1.48	-1.46	1.78		2.64		lmo1960	fhuC	similar to ferrichrome ABC transporter (ATP-binding protein)						
-5.92	-4.11	-1.53		3.85		lmo1961		similar to oxidoreductases						
1.45	2.17	2.48		1.71		lmo1962		similar to transcription regulators (TetR family)						
1.83	2.29	3.37		1.84		lmo1963		hypothetical protein lmo1963						
2.01	2.91	4.29	1.45	2.14		lmo1964		similar to ABC transporter, ATP-binding protein						
-1.63	-1.21	1.65		2.69		lmo1965		hypothetical protein lmo1965						
2.13	2.29	5.0		2.35		lmo1968		similar to creatinine amidohydrolases						
1.83	3.2	7.92		4.33		lmo1971	ulaA	PTS system ascorbate-specific transporter subunit IIC						
1.11	-1.79	-1.76	-1.99	-1.96		lmo1980		hypothetical protein lmo1980						
-10.93	-2.77	-2.29		4.78		lmo1983	ilvD	dihydroxy-acid dehydratase						
-2.56	1.78	1.56		3.98		lmo1984	ilvB	similar to acetolactate synthase (acetohydroxy-acid synthase) (large subunit)						
-1.31	-1.92	1.44		1.88		lmo1985	ilvH	acetolactate synthase 3 regulatory subunit						
-4.11	-3.11	-1.77		2.32		lmo1986	ilvC	ketol-acid reductoisomerase						
1.66	5.31	7.02		4.22		lmo1987	leuA	2-isopropylmalate synthase						
1.23	2.06	3.63		2.95		lmo1988	leuB	3-isopropylmalate dehydrogenase						
-1.2	1.54	2.47		2.97		lmo1989	leuC	isopropylmalate isomerase large subunit						
1.0	1.95	3.83		3.82		lmo1991	ilvA	threonine dehydratase						
1.28	2.3	1.18	1.8			lmo1994		similar to transcription regulators (LacI family)						
1.46	2.72	1.59	1.87			lmo1995	dra	deoxyribose-phosphate aldolase						
2.05	8.23	7.81		3.81		lmo1997		similar to PTS mannose-specific enzyme IIA component						
3.49	5.32	5.7	1.53	1.64		lmo2000		similar to PTS mannose-specific enzyme IID component						
2.78	5.07	5.82	1.82			lmo2001		similar to PTS mannose-specific enzyme IIC component						
2.19	3.88	3.9		1.78		lmo2002		similar to PTS mannose-specific enzyme IIB component						
2.4	7.5	2.7	3.13			lmo2003		similar to transcription regulator GntR family						
1.8	4.06	2.95		2.25		lmo2004		similar to transcription regulator GntR family						
-1.05	1.01	2.57		2.7		lmo2005		similar to oxidoreductase						
2.81	3.42	6.84		2.43		lmo2008		similar to putative ABC transporter, permease protein						

Ln	L. parvasei + Ln	L. casei + Ln	L. parvasei + Ln	L. casei + Ln	Ln	Ln	Ln
2.86	5.93	6.64	2.07	2.33	Imo2009		similar to putative transport system integral membrane protein
1.13	1.19	2.22		1.96	Imo2011		similar to two-component sensor histidine kinase
1.15	1.97	3.36		2.93	Imo2013		hypothetical protein Imo2013
2.59	2.88	8.8		3.39	Imo2014		similar to putative sugar hydrolases
1.42	3.37	6.33		4.46	Imo2015		similar to alpha-mannosidase
1.25	1.8	2.45		1.95	Imo2016	cspB	similar to major cold-shock protein
-5.13	-7.62	-3.63		1.41	Imo2018	dapF	diaminopimelate epimerase
1.02	1.31	1.88		1.85	Imo2021		hypothetical protein Imo2021
1.49	2.12	3.31		2.21	Imo2022		similar to a NifS-like protein required for NAD biosynthesis
1.05	1.49	4.48		4.25	Imo2023	nadB	L-aspartate oxidase
1.26	1.37	4.34		3.43	Imo2024	nadC	nicotinate-nucleotide pyrophosphorylase
2.07	3.43	8.43		4.08	Imo2025	nadA	quinolinate synthetase
1.05	1.77	4.12		3.93	Imo2027		putative cell surface protein, internalin proteins
1.13	1.45	1.77		1.56	Imo2029		hypothetical protein Imo2029
2.65	1.92	1.48		-1.79	Imo2035	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
1.45	-1.05	-1.22		-1.77	Imo2036	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
1.96	1.57	1.29		-1.52	Imo2040	ftsL	similar to cell-division protein FtsL
-1.99	-1.35	1.37		2.72	Imo2043		similar to integral membrane proteins
-1.63	-1.31	1.74		2.83	Imo2049		hypothetical protein Imo2049
-1.32	-1.19	1.27		1.68	Imo2054		hypothetical protein Imo2054
1.04	1.35	2.25		2.16	Imo2057	ctaB	protoheme IX farnesyltransferase
-2.43	-1.81	-1.72		1.41	Imo2059		similar to potassium channel subunit
1.18	1.83	2.35		1.99	Imo2065		hypothetical protein Imo2065
4.27	5.87	9.99		2.34	Imo2066		hypothetical protein Imo2066
9.77	14.39	22.61	1.47	2.32	Imo2067		similar to conjugated bile acid hydrolase
-1.25	1.62	1.9	2.02	2.37	Imo2069	groES	co-chaperonin GroES
-1.21	1.6	2.11		2.56	Imo2074		hypothetical protein Imo2074
-2.2	-2.19	-1.28		1.72	Imo2075		putative DNA-binding/iron metalloprotein/AP endonuclease
-5.64	-3.79	-3.46	1.49	1.63	Imo2080		hypothetical protein Imo2080
-1.47	-1.27	1.19		1.75	Imo2082		camphor resistance protein CrcB
-1.25	1.02	1.31		1.64	Imo2084		hypothetical protein Imo2084
3.92	9.56	11.54	2.44	2.94	Imo2085		peptidoglycan binding protein
1.02	-1.67	1.08		-1.7	Imo2089		similar to lipases
-1.81	-1.12	1.58		2.86	Imo2091	argH	argininosuccinate lyase
-1.19	-1.2	1.22		1.45	Imo2092	betL	glycine betaine transporter BetL
1.71	5.16	4.54	3.01	2.65	Imo2093		hypothetical protein Imo2093
2.25	5.42	4.19	2.41		Imo2097		similar to PTS system galactitol-specific enzyme IIB component
3.99	6.19	13.13		3.29	Imo2098		similar to PTS system galactitol-specific enzyme IIA component
5.9	10.96	16.44	1.84	2.79	Imo2099		similar to transcription antiterminator
-1.27	1.24	1.45		1.84	Imo2105		similar to ferrous iron transport protein B
-1.06	-1.2	2.01		2.13	Imo2108		similar to N-acetylglucosamine-6-phosphate deacetylase
1.83	1.74	2.79		1.52	Imo2112		hypothetical protein Imo2112
-1.37	1.29	1.73	1.77	2.37	Imo2113		putative heme peroxidase
-1.39	1.28	2.51	1.78	3.48	Imo2115		similar to ABC transporter (permease)
-7.04	-3.24	-2.02		3.49	Imo2116		hypothetical protein Imo2116
-2.47	-1.69	-1.37		1.8	Imo2117		hypothetical protein Imo2117
2.16	3.09	9.39		4.35	Imo2121		maltose phosphorylase
7.88	8.81	15.31		1.94	Imo2122		similar to maltodextrin utilization protein MalA
-2.53	-1.43	-1.77	1.77	1.43	Imo2128		similar to transcription regulator, LacI family
1.17	2.27	3.14		2.68	Imo2131		hypothetical protein Imo2131
1.26	2.24	2.87	1.79	2.29	Imo2132		hypothetical protein Imo2132
4.32	7.3	11.91		2.76	Imo2134		similar to fructose-1,6-biphosphate aldolase type II
5.24	9.32	14.69		2.8	Imo2135		similar to PTS system, fructose-specific enzyme IIC component
2.29	3.56	7.71		3.36	Imo2137		similar to PTS system, fructose-specific enzyme IIA component
2.43	3.24	4.82		1.99	Imo2140		similar to ABC transporter (membrane protein)
-3.82	-2.68	-1.63		2.35	Imo2145		hypothetical protein Imo2145
3.38	2.69	1.56		-2.16	Imo2154	nrpF	ribonucleotide-diphosphate reductase subunit beta
2.66	3.61	4.74		1.78	Imo2157	sepA	hypothetical protein Imo2157
2.91	6.05	4.78	2.08		Imo2158		similar to B. subtilis YwmG protein
1.16	-1.53	-1.77		-2.06	Imo2165		similar to transcription regulator CRP/FNR family
5.7	6.93	8.42		1.48	Imo2170		hypothetical protein Imo2170
1.42	3.67	7.32	2.58	5.15	Imo2171		similar to antiporter proteins
2.31	2.69	5.06		2.19	Imo2172		similar to propionate CoA-transferase
2.86	3.65	5.69		1.99	Imo2174		hypothetical protein Imo2174
-1.72	1.2	1.36	2.07		Imo2177		hypothetical protein Imo2177
2.56	5.64	12.79	2.2	5.0	Imo2178		peptidoglycan binding protein
1.56	2.97	2.54		1.63	Imo2180		hypothetical protein Imo2180
-1.5	1.28	2.04		3.07	Imo2181		hypothetical protein Imo2181
-6.34	-1.98	-1.01		6.28	Imo2186		hypothetical protein Imo2186
-1.15	-1.13	1.37		1.58	Imo2187		hypothetical protein Imo2187
1.62	1.91	2.31		1.42	Imo2191	spxA	transcriptional regulator Spx
-3.84	-4.11	-1.51		2.54	Imo2197		hypothetical protein Imo2197
-4.96	-2.84	1.17		5.78	Imo2198	trpS	tryptophanyl-tRNA synthetase
-2.42	-1.01	-1.16	2.4		Imo2200		similar to transcription regulator
1.33	1.69	2.08		1.57	Imo2204		hypothetical protein Imo2204
2.56	3.93	5.9	1.54	2.31	Imo2205		similar to phosphoglyceromutase 1
3.33	5.2	7.06	1.56	2.12	Imo2206	clpB	similar to endopeptidase Clp ATP-binding chain B (ClpB)
-7.22	-5.02	-2.54		2.84	Imo2209		hypothetical protein Imo2209
-2.36	-1.51	-1.77	1.56		Imo2212	hemE	uroporphyrinogen decarboxylase
2.53	2.88	4.66		1.84	Imo2213		hypothetical protein Imo2213
-1.27	1.24	1.09	1.58		Imo2214		similar to ABC transporter (membrane protein)
-1.24	1.4	1.01	1.74		Imo2216		similar to histidine triad (HIT) protein
-2.43	-1.26	-1.58		1.54	Imo2217		hypothetical protein Imo2217
1.25	1.8	5.36		4.28	Imo2226		hypothetical protein Imo2226
-1.24	1.68	2.08		2.57	Imo2227		similar to ABC transporter (ATP-binding protein)
2.39	3.5	4.77		2.0	Imo2230		similar to arsenate reductase
1.18	1.44	2.53		2.15	Imo2233		similar to transcriptional regulators (LysR family)
3.16	6.96	12.36		3.91	Imo2236		shikimate 5-dehydrogenase
2.68	3.82	8.0		2.98	Imo2237		similar to transport system permease protein
2.37	-1.04	1.98	-2.46		Imo2239		hypothetical protein Imo2239
1.34	2.11	7.48		5.59	Imo2242		similar to O6-methylguanine-DNA methyltransferase
-3.5	-3.64	-1.62		2.16	Imo2245		hypothetical protein Imo2245

	Ln	L. paracasei + Ln	L. casei + Ln	L. paracasei + Ln	L. casei + Ln		
1.05	1.59	2.18			2.08	lmo2247	similar to oxidoreductase
-1.83	1.05	1.28		1.91	2.34	lmo2251	similar to amino acid ABC transporter (ATP-binding protein)
-2.05	-1.03	1.89		2.0	3.87	lmo2256	hypothetical protein lmo2256
1.11	1.17	1.66			1.49	lmo2257	hypothetical protein lmo2257
1.93	1.26	1.11			-1.73	lmo2258	hypothetical protein lmo2258
-3.31	-2.61	-1.85			1.78	lmo2261	hypothetical protein lmo2261
-2.66	-2.18	-1.39			1.91	lmo2262	hypothetical protein lmo2262
-3.22	-1.67	-1.56		1.93	2.06	lmo2263	similar to unknown proteins
1.59	2.63	1.89		1.66		lmo2266	hypothetical protein lmo2266
-1.18	-1.03	1.28			1.51	lmo2268	addB similar to ATP-dependent deoxyribonuclease (subunit B)
-1.88	-1.46	1.75			3.29	lmo2269	hypothetical protein lmo2269
-2.37	-1.36	-1.08			2.2	lmo2270	comK' similar to competence transcription factor ComK, N terminal part
-1.66	-1.09	1.71			2.83	lmo2272	hypothetical protein lmo2272
2.07	1.18	1.82		-1.75		lmo2274	protein gp29
2.05	2.78	4.89			2.38	lmo2275	protein gp28
-3.14	-2.01	-1.67			1.88	lmo2277	hypothetical protein lmo2277
3.82	5.81	7.71			2.02	lmo2278	lysA L-alanyl-D-glutamate peptidase
2.18	1.48	3.34			1.53	lmo2280	protein gp23
1.37	1.46	3.19			2.33	lmo2282	protein gp21
3.45	3.84	7.66			2.22	lmo2290	protein gp13
1.57	2.88	5.9			3.75	lmo2300	putative terminase large subunit from bacteriophage A118
1.55	1.85	3.36			2.17	lmo2304	bacteriophage A118 gp65 protein
-1.0	1.33	1.56			1.56	lmo2334	similar to transcriptional regulator
1.75	-2.43	1.08		-4.25		lmo2335	fruA highly similar to phosphotransferase system (PTS) fructose-specific enzyme IIA/B component
5.6	1.36	3.96		-4.11		lmo2336	fruB fructose-1-phosphate kinase
3.09	-1.86	1.62		-5.76		lmo2337	similar to regulatory protein DeoR family
-1.83	-1.21	1.25			2.28	lmo2338	pepC aminopeptidase C
-1.02	1.18	2.09			2.14	lmo2342	similar to 16S pseudouridylylase synthase
-2.68	-1.36	1.38			3.71	lmo2343	similar to nitrotriacetate monooxygenase
-2.41	1.21	1.76		2.9	4.23	lmo2345	hypothetical protein lmo2345
-1.75	1.8	3.68		3.16	6.45	lmo2346	similar to amino acid ABC-transporter, ATP-binding protein
-1.58	1.05	1.39		1.66	2.19	lmo2347	similar to amino acid ABC transporter (permease)
2.45	2.69	6.24			2.55	lmo2348	similar to amino acid ABC-transporter (permease)
-2.3	-1.06	3.02			8.95	lmo2350	similar to B. subtilis YtmI protein
-2.63	1.09	-1.09		2.85	2.41	lmo2351	similar to NADH-dependent FMN reductase
-1.14	-1.23	1.97			2.26	lmo2354	hypothetical protein lmo2354
-2.94	-2.93	-1.44			2.04	lmo2355	Similar to multidrug resistance protein
-1.07	1.61	2.69		1.73	2.89	lmo2356	hypothetical protein lmo2356
4.21	16.02	21.62			5.14	lmo2362	similar to amino acid antiporter (acid resistance)
4.39	5.77	10.1			2.3	lmo2363	similar to glutamate decarboxylase
1.66	1.31	2.62			1.58	lmo2370	similar to aminotransferase
1.11	1.59	1.61			1.45	lmo2373	similar to phosphotransferase system (PTS) beta-glucoside-specific enzyme IIB component
-2.86	-2.43	-1.77			1.62	lmo2376	similar to peptidyl-prolyl cis-trans isomerase
-1.16	1.29	1.79		1.5	2.07	lmo2379	putative monovalent cation/H+ antiporter subunit B
-1.21	1.08	1.5			1.83	lmo2382	putative monovalent cation/H+ antiporter subunit E
1.1	1.27	1.64			1.48	lmo2383	putative monovalent cation/H+ antiporter subunit F
-1.71	-1.36	1.47			2.51	lmo2384	putative monovalent cation/H+ antiporter subunit G
1.02	1.39	2.02			1.98	lmo2386	similar to B. subtilis YuiD protein
3.19	5.7	4.9		1.79	1.53	lmo2387	hypothetical protein lmo2387
-1.22	1.12	1.19			1.45	lmo2388	similar to B. subtilis YwqG protein
-9.85	-9.64	-4.96			1.99	lmo2390	similar to hypothetical thioredoxine reductase
2.32	6.89	10.42		2.97	4.49	lmo2391	conserved hypothetical protein similar to B. subtilis YhfK protein
-1.71	1.07	1.4		1.83	2.4	lmo2393	similar to B. subtilis YuzD protein
3.86	6.89	9.31			2.41	lmo2395	hypothetical protein lmo2395
1.31	3.15	3.37		2.41	2.57	lmo2396	similar to internalin proteins, putative peptidoglycan bound protein (LPXTG motif)
-1.12	1.22	1.38			1.54	lmo2398	ltrC hypothetical protein lmo2398
1.23	2.96	4.5		2.4	3.65	lmo2399	hypothetical protein lmo2399
-1.14	-1.17	1.42			1.61	lmo2401	similar to conserved hypothetical protein and to B. subtilis YutF protein
-1.16	1.26	1.58		1.46	1.84	lmo2403	similar to B. subtilis YunD protein
1.16	1.3	1.8			1.56	lmo2406	similar to B. subtilis YunF protein
-2.25	-2.32	1.27			2.84	lmo2408	similar to repressor protein
-1.48	-2.15	-2.13			-1.44	lmo2418	similar to ABC transporter, permease protein
-3.93	-3.16	-2.14			1.83	lmo2420	hypothetical protein lmo2420
1.17	1.54	2.04			1.75	lmo2424	similar to thioredoxin
-1.02	1.22	1.45			1.47	lmo2425	glycine cleavage system protein H
1.23	2.28	7.91		1.86	6.46	lmo2432	hypothetical protein lmo2432
7.96	-3.63	-1.47		2.19	5.41	lmo2433	similar to acetyltransferase
4.23	6.21	10.29			2.43	lmo2434	highly similar to glutamate decarboxylases
1.75	2.16	2.73			1.57	lmo2442	hypothetical protein lmo2442
-7.89	-3.21	-2.05			3.85	lmo2443	hypothetical protein lmo2443
2.05	2.47	4.82			2.35	lmo2445	similar to internalin
-1.04	1.29	2.14			2.23	lmo2447	similar to transcription regulator
1.34	2.78	2.79			2.09	lmo2448	smpB SsrA-binding protein
-1.16	1.53	1.55			1.8	lmo2449	similar to exoribonuclease RNase-R
-1.37	-1.52	1.26			1.73	lmo2450	similar to carboxylesterase
1.18	1.21	2.59			2.2	lmo2452	similar to carboxylesterase
2.4	6.11	8.06		2.55	3.36	lmo2453	similar to lipolytic enzyme
5.95	10.51	16.42			2.76	lmo2454	hypothetical protein lmo2454
-1.56	-1.16	1.18			1.84	lmo2455	eno phosphopyruvate hydratase
-1.94	-1.21	1.07		1.6	2.07	lmo2456	pgm phosphoglyceromutase
-1.81	-1.03	1.17		1.76	2.12	lmo2457	tpiA triosephosphate isomerase
-1.39	-1.04	1.44				lmo2458	pgk phosphoglycerate kinase
-2.61	-1.66	-1.35		1.58	1.94	lmo2459	gap glyceraldehyde-3-phosphate dehydrogenase
-2.71	-1.47	-1.4		1.85	1.94	lmo2460	similar to B. subtilis CggR hypothetical transcriptional regulator
1.49	2.47	4.87		1.65		lmo2463	similar to transport protein
-2.2	-1.81	-1.49			1.48	lmo2465	hypothetical protein lmo2465
-3.75	-1.42	1.08		2.64		lmo2466	hypothetical protein lmo2466
1.42	2.8	1.56		1.97		lmo2467	similar to chitinase and chitin binding protein
1.02	2.66	6.07		2.6	5.95	lmo2470	similar to internalin proteins
-1.03	1.12	1.4			1.44	lmo2485	similar to B. subtilis yvlC protein
-2.11	-3.24	-3.35		-1.59		lmo2489	uvrB excinuclease ABC subunit B
-4.29	-2.99	-2.42			1.77	lmo2490	similar to B. subtilis CsbA protein

	Lm	L. paracasei + Lm	L. casei + Lm	L. paracasei + Lm	L. casei + Lm			
	1.31	2.58	1.86	1.98		Imo2810	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA
	-1.81	-1.35	1.62		2.94	Imo2814		similar to transcriptional regulator
	2.29	2.94	5.01		2.19	Imo2817		similar to peptidases
	2.25	5.09	7.7	2.27	3.42	Imo2818		similar to transmembrane efflux protein
	3.17	4.44	6.21		2.59	Imo2819		similar to carboxypeptidase
	-8.39	-7.0	-5.03		1.67	Imo2822		hypothetical protein Imo2822
	-1.27	1.35	3.08		3.91	Imo2823		similar to an hypothetical protein from Thermotoga maritima
	-3.21	-5.26	-2.06	-1.64	1.56	Imo2824		similar to D-3-phosphoglycerate dehydrogenase
	-4.19	-2.47	-2.13		1.97	Imo2825	serC	phosphoserine aminotransferase
	-2.31	1.24	1.47	2.85	3.39	Imo2826		similar to efflux proteins
	-3.79	-2.31	-1.18		3.22	Imo2830		similar to thioredoxin
	1.34	2.27	2.7		2.02	Imo2833		similar to a maltose phosphorylase
	1.18	6.06	5.67	5.12	4.79	Imo2834		similar to oxidoreductases
	1.23	1.79	4.41		3.58	Imo2838		similar to sugar ABC transporter permease protein
	1.24	2.86	3.21		2.59	Imo2840		similar to Sucrose phosphorylase
	-3.02	-3.49	-1.81		1.67	Imo2844		hypothetical protein Imo2844
	4.45	10.4	15.93	2.34	3.58	Imo2846		highly similar to B. subtilis YulD protein
	6.39	8.46	16.67		2.61	Imo2848		L-rhamnose isomerase
	3.2	6.03	12.51		3.91	Imo2849		similar to rhamnulokinase
	4.94	8.33	11.99		2.43	Imo2850		similar to sugar transport proteins
	-1.51	1.43	2.65		4.0	Imo2852		hypothetical protein Imo2852
	1.6	-1.1	1.42	-1.76		Imo2853		highly similar to B. subtilis Jag protein
	-5.05	-5.26	-3.23		1.56	Imo2856	rpmH	50S ribosomal protein L34
	-2.12	-1.78	-1.16		1.83	Imo2857		hypothetical protein Imo2857