

Article title: *Lactobacillus paracasei* and *Lactobacillus plantarum* Strains Downregulate Proinflammatory Genes in an *Ex Vivo* System of Cultured Human Colonic Mucosa

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Online Resource 2: Differentially expressed genes in Cluster 1 to Cluster 11

CLUSTER 1			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
203518_at	LYST: lysosomal trafficking regulator	NM_000081	1,07	-1,41	-1,31	-1,36	-1,5	-1,41	-1,45
203882_at	ISGF3G: interferon-stimulated transcription factor 3, gamma 48kDa	NM_006084	1,15	-1,46	-1,32	-1,53	-1,68	-1,51	-1,76
204298_s_at	LOX: lysyl oxidase	NM_002317	-1,01	-1,5	-1,89	-1,69	-1,49	-1,88	-1,68
204523_at	ZNF140: zinc finger protein 140	NM_003440	1,29	-1,32	-1,48	-1,25	-1,7	-1,91	-1,61
206118_at	STAT4: signal transducer and activator of transcription 4	NM_003151	-1,01	-1,41	-1,54	-1,56	-1,4	-1,53	-1,55
207651_at	GPR171: G protein-coupled receptor 171	NM_013308	2,12	-1,01	-1,61	-1,08	-2,13	-3,4	-2,29
208933_s_at	LGALS8: lectin, galactoside-binding, soluble, 8 (galectin 8)	A1659005	1,04	-1,55	-1,35	-1,25	-1,62	-1,41	-1,3
209012_at	TRIO: triple functional domain (PTPRF interacting)	AV718192	1,09	-1,5	-1,32	-1,51	-1,63	-1,43	-1,64
209884_s_at	SLC4A7: solute carrier family 4, sodium bicarbonate cotransporter, member 7	AF047033	-1,11	-1,92	-2,02	-1,65	-1,73	-1,81	-1,48
209941_at	RIPK1: receptor (TNFRSF)-interacting serine-threonine kinase 1	U50062	1,28	-1,29	-1,19	-1,3	-1,66	-1,53	-1,67
212689_s_at	JMJD1A: jumonji domain containing 1A	AA524505	1,06	-1,43	-1,35	-1,55	-1,52	-1,44	-1,64
213908_at	WHDC1L1: WAS protein homology region 2 domain containing 1-like 1	A1824078	1,11	-1,23	-1,77	-1,26	-1,37	-1,97	-1,4
221094_s_at	ELP3: elongation protein 3 homolog (<i>S. cerevisiae</i>)	NM_018091	1,1	-1,36	-1,03	-1,32	-1,5	-1,14	-1,46

Online Resource 2 - Differentially expressed genes Cluster 1 to Cluster 11

221559_s_at	MIS12: MIS12, MIND kinetochore complex component, homolog (yeast)	BC000229	1,41	-1,33	-1,26	-1,22	-1,88	-1,78	-1,73
224260_at	CDNA clone IMAGE:4478733	AF062385	1,38	-2,82	-1,27	-2,26	-3,89	-1,75	-3,12
224872_at	DIP2B: DIP2 disco-interacting protein 2 homolog B (Drosophila)	AB040896	1,27	-1,22	1,03	-1,16	-1,55	-1,24	-1,48
225024_at	C20orf77: chromosome 20 open reading frame 77	AL117521	-1,02	-1,56	-1,19	-1,33	-1,53	-1,17	-1,31
225296_at	ZNF317: zinc finger protein 317	AB046808	1,12	-1,52	-1,49	-1,44	-1,69	-1,66	-1,61
226218_at	IL7R: interleukin 7 receptor	BE217880	1,18	-1,26	-1,9	-1,2	-1,49	-2,24	-1,41
226555_at	FLJ20309: hypothetical protein FLJ20309	BG026789	1,31	-1,28	-1,12	-1,21	-1,67	-1,46	-1,58
227892_at	PRKAA2: protein kinase, AMP-activated, alpha 2 catalytic subunit	AA855042	1,38	-1,13	-1,14	-1,1	-1,56	-1,57	-1,51
228230_at	PRIC285: peroxisomal proliferator-activated receptor A interacting complex 285	AL121829	1,45	-1,61	1,04	-1,87	-2,33	-1,39	-2,7
231876_at	TRIM56: tripartite motif-containing 56	AL512757	1,17	-1,45	-1,38	-1,41	-1,7	-1,62	-1,65
234725_s_at	SEMA4B: sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	AK026133	1,21	-1,5	-1,06	-1,52	-1,82	-1,28	-1,84
235157_at	Transcribed locus	AW297731	1,83	-1,46	-1,09	-1,31	-2,67	-2	-2,4
236026_at	GPATCH2: G patch domain containing 2	AA160529	1,3	-1,15	1,33	-1,49	-1,49	1,03	-1,93
236480_at	CDNA FLJ41489 fis, clone BRTHA2004582	AA543084	1,02	-1,78	-1,4	-2,33	-1,8	-1,42	-2,36
238493_at	ZNF506: zinc finger protein 506	AI559570	1,16	-1,33	-1,36	-1,24	-1,55	-1,57	-1,43
242052_at	CDNA FLJ31445 fis, clone NT2NE2000864	AW979272	1,58	1,02	-1,17	1,02	-1,56	-1,85	-1,55
1562275_at	MRNA; cDNA DKFZp667P1024 (from clone DKFZp667P1024)	AL832835	1,3	-2,71	-2,16	-2,31	-3,53	-2,81	-3
CLUSTER 2			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
213265_at	PGA3 /// PGA4 /// PGA5: pepsinogen 5, group I (pepsinogen A) /// pepsinogen 3, group I (pepsinogen A) /// pepsinogen 4, group I (pepsinogen A)	AI570199	-1,14	-1,46	-1,58	-1,05	-1,28	-1,38	1,08
227229_at	CDNA clone IMAGE:5303499	BE467416	-1,39	-1,55	-1,41	-1,03	-1,11	-1,01	1,35
CLUSTER 3			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
214972_at	MGEA5: Meningioma expressed antigen 5 (hyaluronidase)	AU144791	-1,78	-1,6	-1,21	-1,92	1,12	1,48	-1,08
244871_s_at	USP32: ubiquitin specific peptidase 32	AW268357	-1,44	-1,29	-1,42	-1,55	1,11	1,01	-1,08

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236930_at	NUMB: Numb homolog (Drosophila)	AW167424	-1,66	-1,3	-1,15	-1,41	1,28	1,45	1,18
217620_s_at	PIK3CB: phosphoinositide-3-kinase, catalytic, beta polypeptide	AA805318	-1,62	-1,61	-1,34	-1,53	1	1,21	1,06
1555523_a_at	FYCO1: FYVE and coiled-coil domain containing 1	BC007218	-4,03	-5,18	-1,86	-3,83	-1,29	2,16	1,05
226125_at	CDNA clone IMAGE:4346813	BF346665	-2,72	-2,48	-2,53	-2,29	1,1	1,07	1,18
232628_at	CDNA FLJ13464 fis, clone PLACE1003478	AI740629	-1,9	-1,61	-1,39	-1,61	1,18	1,37	1,18
240081_at	Hs.272139.0	AA004803	-2,12	-1,78	-1,6	-1,85	1,19	1,32	1,15
239990_at	Transcribed locus	AI821426	-2,02	-1,64	-1,39	-1,34	1,23	1,46	1,51
210224_at	MR1: major histocompatibility complex, class I-related	AF031469	-2,13	-2,03	-2,19	-1,38	1,05	-1,03	1,54
208386_x_at	DMC1: DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	NM_007068	-1,91	-1,4	-1,98	-1,65	1,36	-1,04	1,16
223975_at	SPRYD5: SPRY domain containing 5	BC005014	-2,88	-2,63	-3,28	-2,24	1,1	-1,14	1,29
205448_s_at	MAP3K12: mitogen-activated protein kinase kinase kinase 12	NM_006301	-1,43	-1,76	-1,23	-1,44	-1,24	1,16	-1,01
211884_s_at	CIITA: class II, major histocompatibility complex, transactivator	U31931	-1,75	-1,94	-1,19	-1,67	-1,11	1,47	1,05
204348_s_at	AK3L1 /// AK3L2 /// LOC645619: adenylate kinase 3-like 1 /// adenylate kinase 3-like 2 /// similar to Adenylate kinase isoenzyme 4, mitochondrial (ATP-AMP transphosphorylase)	NM_013410	-1,27	-1,65	-1,29	-1,81	-1,29	-1,01	-1,42
1558430_at	CDNA FLJ36648 fis, clone UTERU1000138	R08650	-1,4	-1,28	-1,12	-1,68	1,09	1,24	-1,2
CLUSTER 4			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
202052_s_at	RAI14: retinoic acid induced 14	NM_015577	-1,01	-1,62	-1,78	-1,6	-1,61	-1,77	-1,59
202973_x_at	FAM13A1: family with sequence similarity 13, member A1	NM_014883	-1,52	-1,74	-1,48	-1,71	-1,14	1,03	-1,13
203282_at	GBE1: glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	NM_000158	-1,37	-2,19	-1,99	-1,97	-1,59	-1,45	-1,44
204422_s_at	FGF2: fibroblast growth factor 2 (basic)	NM_002006	-2,54	-4,08	-4,11	-3,55	-1,61	-1,62	-1,4
204614_at	SERPINB2: serpin peptidase inhibitor, clade B (ovalbumin), member 2	NM_002575	-3,43	-5,14	-5,23	-4,99	-1,5	-1,53	-1,46
204994_at	MX2: myxovirus (influenza virus) resistance 2 (mouse)	NM_002463	-1,55	-2	-1,85	-1,93	-1,29	-1,19	-1,24
205258_at	INHBB: inhibin, beta B	NM_002193	-1,2	-2,53	-2,53	-1,84	-2,11	-2,11	-1,53
206172_at	IL13RA2: interleukin 13 receptor, alpha 2	NM_000640	-1,43	-3,57	-3,6	-5,29	-2,5	-2,53	-3,71
206336_at	CXCL6: chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993	-1,98	-3,53	-3,38	-2,56	-1,78	-1,71	-1,29
206924_at	IL11: interleukin 11	NM_000641	-2,63	-3,75	-5,31	-5,03	-1,42	-2,02	-1,91

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207078_at	MED6: mediator complex subunit 6	NM_005466	-1,27	-1,24	-2,13	-1,51	1,02	-1,69	-1,2
211559_s_at	CCNG2: cyclin G2	L49506	-1,26	-1,86	-1,86	-1,95	-1,47	-1,47	-1,54
211743_s_at	PRG2: proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	BC005929	-3,15	-3,26	-3,08	-4,37	-1,04	1,02	-1,39
212942_s_at	KIAA1199: KIAA1199	AB033025	-1,66	-3,83	-6,08	-3,77	-2,31	-3,67	-2,28
214476_at	TFF2: trefoil factor 2 (spasmolytic protein 1)	NM_005423	-1,66	-3,37	-2,53	-2,59	-2,03	-1,52	-1,56
214974_x_at	CXCL5: chemokine (C-X-C motif) ligand 5	AK026546	-2,67	-9,88	-6,07	-7,85	-3,7	-2,27	-2,94
215446_s_at	LOX: lysyl oxidase	L16895	-1,18	-1,85	-2,15	-1,8	-1,57	-1,82	-1,52
218898_at	FAM57A: family with sequence similarity 57, member A	NM_024792	-1,3	-2,04	-2,46	-2,09	-1,57	-1,89	-1,61
219163_at	ZNF562: zinc finger protein 562	NM_017656	-1,07	-1,51	-1,42	-1,51	-1,41	-1,33	-1,42
219911_s_at	SLCO4A1: solute carrier organic anion transporter family, member 4A1	NM_016354	-1,22	-1,74	-1,71	-1,96	-1,43	-1,4	-1,61
225750_at	CDNA FLJ14162 fis, clone NT2RM4002504	BE966748	-1,02	-1,61	-1,48	-1,63	-1,57	-1,45	-1,59
226347_at	Hs.268231.0	AI754928	-1,18	-2,04	-1,84	-1,86	-1,73	-1,56	-1,57
226348_at	Hs.268231.0	AK026764	-1,16	-1,71	-1,49	-1,5	-1,48	-1,29	-1,3
226695_at	PRRX1: paired related homeobox 1	AA775472	-1,31	-3,76	-1,96	-2,28	-2,86	-1,5	-1,73
226705_at	FGFR1: fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	BE467261	-1,33	-1,56	-1,43	-1,45	-1,17	-1,07	-1,09
227919_at	UCA1: urothelial cancer associated 1	AA702248	-1,43	-2,07	-2,01	-2,46	-1,45	-1,4	-1,71
228082_at	ASAM: adipocyte-specific adhesion molecule	BF056275	-1,93	-1,81	-2,29	-1,91	1,07	-1,18	1,01
228748_at	CD59: CD59 molecule, complement regulatory protein	AI653117	-1,17	-1,98	-1,47	-1,64	-1,69	-1,25	-1,4
229414_at	PITPNC1: phosphatidylinositol transfer protein, cytoplasmic 1	AI676095	1,02	-2,15	-2,24	-2,29	-2,19	-2,28	-2,34
238649_at	PITPNC1: phosphatidylinositol transfer protein, cytoplasmic 1	AA815089	-1,22	-2,4	-2,88	-2,31	-1,96	-2,36	-1,89
229795_at	Transcribed locus	AI701591	-1,59	-2,65	-3,21	-2,66	-1,67	-2,02	-1,68
230748_at	SLC16A6: solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	AI873273	-1,11	-1,91	-2,18	-2,02	-1,71	-1,96	-1,82
231751_at	ABCG8: ATP-binding cassette, sub-family G (WHITE), member 8 (sterolin 2)	NM_022437	-2,92	-1,43	-3,11	-4,06	2,04	-1,06	-1,39
232113_at	CDNA FLJ38472 fis, clone FEBRA2022148	N90870	-1,95	-2,02	-2,11	-2,04	-1,03	-1,08	-1,04
236474_at	Transcribed locus	AI797677	-1,29	-1,73	-1,8	-1,84	-1,34	-1,4	-1,43
236599_at	Hs.38449.0	AA703280	-1,58	-3,25	-2,73	-2,66	-2,06	-1,74	-1,69
240072_at	ASXL2: Additional sex combs like 2 (Drosophila)	N75937	-1,46	-1,39	-1,96	-1,66	1,05	-1,34	-1,13
243020_at	Transcribed locus	R06738	-1,91	-2,12	-1,77	-1,99	-1,11	1,08	-1,04
1555514_a_at	PIAS2: protein inhibitor of activated STAT, 2	AF361054	-1,66	-1,58	-1,67	-2,06	1,05	-1	-1,24
1555875_at	Homo sapiens, clone IMAGE:3604678, mRNA	BU733713	-1,3	-2,18	-1,69	-1,72	-1,68	-1,3	-1,33

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1556806_at	Clone TEA5 Cri-du-chat critical region mRNA	BM684993	-1,24	-1,51	-1,34	-1,51	-1,21	-1,08	-1,22
CLUSTER 5			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
217505_at	KLHL23: kelch-like 23 (Drosophila)	BG403790	2,27	1,27	1,5	2,63	-1,79	-1,51	1,16
243792_x_at	PTPN13: Protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	AI281371	2,07	1,21	1,42	2,7	-1,72	-1,46	1,3
1564996_at	CDNA FLJ20017 fis, clone ADSE00552	AK000024	1,07	-1,02	-2,33	7,77	-1,09	-2,49	7,27
CLUSTER 6			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
202531_at	IRF1: interferon regulatory factor 1	NM_002198	2,43	2,33	2,62	2,27	-1,04	1,08	-1,07
238725_at	Hs.180559.0 (IRF1: interferon regulatory factor 1)	AW392551	3,15	2,53	2,94	2,43	-1,25	-1,07	-1,3
202748_at	GBP2: guanylate binding protein 2, interferon-inducible	NM_004120	1,71	1,59	1,61	1,43	-1,08	-1,06	-1,2
242907_at	Hs.160628.0 (GBP2: guanylate binding protein 2, interferon-inducible)	BF509371	2,47	2,15	2,3	2,22	-1,15	-1,07	-1,11
203915_at	CXCL9: chemokine (C-X-C motif) ligand 9	NM_002416	9,91	3,02	3,49	2,37	-3,28	-2,84	-4,17
204121_at	GADD45G: growth arrest and DNA-damage-inducible, gamma	NM_006705	1,81	2,01	2,06	2,15	1,11	1,14	1,19
205249_at	EGR2: early growth response 2 (Krox-20 homolog, Drosophila)	NM_000399	2,56	2,1	2,3	2,02	-1,22	-1,11	-1,27
205890_s_at	UBD: ubiquitin D	NM_006398	2,87	2,19	2,43	1,87	-1,31	-1,18	-1,54
206256_at	CPN1: carboxypeptidase N, polypeptide 1	NM_001308	2	1,53	1,27	1,71	-1,31	-1,57	-1,17
206366_x_at	XCL2: chemokine (C motif) ligand 2	U23772	8,28	4,48	3,36	4,23	-1,85	-2,47	-1,96
214567_s_at	XCL1 /// XCL2: chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	NM_003175	7,02	4,14	3,12	3,89	-1,7	-2,25	-1,8
206914_at	CRTAM: cytotoxic and regulatory T cell molecule	NM_019604	3,2	2,3	1,69	2,13	-1,39	-1,89	-1,5
207315_at	CD226: CD226 molecule	NM_006566	2,96	1,36	1,55	1,46	-2,18	-1,91	-2,03
207536_s_at	TNFRSF9: tumor necrosis factor receptor superfamily, member 9	NM_001561	3,9	2,49	2,44	1,9	-1,56	-1,59	-2,05
211786_at	TNFRSF9: tumor necrosis factor receptor superfamily, member 9	BC006196	4,99	1,2	2,15	1,28	-4,15	-2,31	-3,9
207849_at	IL2: interleukin 2	NM_000586	9,52	2,18	2,24	2,84	-4,38	-4,25	-3,36
207986_x_at	CYB561: cytochrome b-561	NM_001915	1,92	1,27	1,88	1,44	-1,51	-1,02	-1,33
210029_at	INDO: indoleamine-pyrrole 2,3 dioxygenase	M34455	4,46	1,79	1,34	1,55	-2,49	-3,34	-2,88
210056_at	RND1: Rho family GTPase 1	U69563	1,77	1,42	1,4	1,44	-1,24	-1,26	-1,23

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210163_at	CXCL11: chemokine (C-X-C motif) ligand 11	AF030514	8,74	3,81	5,86	3,11	-2,29	-1,49	-2,81
211122_s_at	CXCL11: chemokine (C-X-C motif) ligand 11	AF002985	12,95	4,6	7,15	3,01	-2,81	-1,81	-4,31
210164_at	GZMB: granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	J03189	6,5	2,32	3,18	2,61	-2,8	-2,05	-2,49
210354_at	IFNG: interferon, gamma	M29383	10,51	5,93	4,81	4,41	-1,77	-2,18	-2,38
211269_s_at	IL2RA: interleukin 2 receptor, alpha	K03122	2,66	2,07	1,69	2,02	-1,29	-1,58	-1,32
211597_s_at	HOP: homeodomain-only protein	AB059408	1,71	1,1	-1,09	1,4	-1,55	-1,87	-1,23
212005_at	C1orf144: chromosome 1 open reading frame 144	AL582808	4,93	1,45	1,37	-1,07	-3,4	-3,6	-5,28
214228_x_at	TNFRSF4: tumor necrosis factor receptor superfamily, member 4	AJ277151	2,69	1,78	1,52	1,59	-1,51	-1,76	-1,69
214447_at	ETS1: v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	NM_005238	2,65	1,62	-1,12	1,59	-1,63	-2,98	-1,67
216876_s_at	IL17A: interleukin 17A	Z58820	14,3	6,86	5,61	5,88	-2,08	-2,55	-2,43
218723_s_at	C13orf15: chromosome 13 open reading frame 15	NM_014059	1,68	1,56	1,53	1,64	-1,08	-1,09	-1,02
219359_at	ATHL1: ATH1, acid trehalase-like 1 (yeast)	NM_025092	1,89	1,4	1,36	1,33	-1,36	-1,39	-1,42
219597_s_at	DUOX1: dual oxidase 1	NM_017434	2,09	1,33	1,4	1,75	-1,57	-1,5	-1,2
219836_at	ZBED2: zinc finger, BED-type containing 2	NM_024508	3,68	2,39	1,65	1,9	-1,54	-2,24	-1,94
36019_at	STK19: serine/threonine kinase 19	L26260	2,13	1,29	1,15	1,43	-1,65	-1,85	-1,49
36564_at	RNF19B: ring finger protein 19B	W27419	4,19	1,28	2,18	1,61	-3,28	-1,92	-2,6
40687_at	GJA4: gap junction protein, alpha 4, 37kDa	M96789	2,29	1,96	2,67	2,09	-1,17	1,17	-1,1
222694_at	MGC2752: hypothetical protein MGC2752	AI015612	2,26	1,67	1,32	1,75	-1,36	-1,71	-1,29
223913_s_at	C19orf30: chromosome 19 open reading frame 30	AB058892	2,18	-2,05	-1,33	2,12	-4,47	-2,9	-1,03
225945_at	ZNF655: zinc finger protein 655	BF219240	1,58	-1,07	-1,02	-1,01	-1,7	-1,62	-1,6
230453_s_at	ATP2A3: ATPase, Ca++ transporting, ubiquitous	AW188009	2,74	-2,84	2,33	1,43	-7,79	-1,18	-1,91
231578_at	GBP1: guanylate binding protein 1, interferon-inducible, 67kDa	AW014593	3,47	1,97	1,58	2,03	-1,76	-2,19	-1,71
232593_at	LINCR: likely ortholog of mouse lung-inducible Neutralized-related C3HC4 RING domain protein	AL389981	2,32	1,39	1,54	1,1	-1,67	-1,5	-2,12
235042_at	XIRP1: xin actin-binding repeat containing 1	AW755250	4,4	2,76	2,66	2,2	-1,59	-1,65	-2
235175_at	GBP4: guanylate binding protein 4	BG260886	2,9	1,58	1,57	1,3	-1,83	-1,85	-2,22
237104_at	CTSS: cathepsin S	BE675415	1,95	1,3	1,26	1,12	-1,5	-1,55	-1,74
237487_at	Transcribed locus	N69685	3,94	1,08	3,8	1,86	-3,64	-1,03	-2,11
238950_at	Transcribed locus	BF056988	4,35	2,21	2,64	2,85	-1,97	-1,65	-1,53
239931_at	MYC: v-myc myelocytomatosis viral oncogene homolog (avian)	BF512882	2,87	1,77	1,26	2,23	-1,62	-2,28	-1,29
244029_at	CDNA FLJ42228 fis, clone THYMU2041252	AW967768	1,91	-1,05	-1,01	1,36	-2,01	-1,92	-1,4
244044_at	ENPP3: Ectonucleotide pyrophosphatase/phosphodiesterase 3	AV691872	3,02	1,42	1,89	1,57	-2,12	-1,6	-1,92
1566303_s_at	PPP1R11: protein phosphatase 1, regulatory (inhibitor) subunit 11	AV755778	1,83	-1,01	1,24	1,14	-1,84	-1,47	-1,6

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CLUSTER 7									
probe set	gene	Accession	inflamed vs Control fold-change	iLP vs Control fold-change	iLP (A-) vs Control fold-change	iBL23 vs Control fold-change	iLP vs inflamed fold-change	iLP (A-) vs inflamed fold-change	iBL23 vs inflamed fold-change
210225_x_at	LILRB3: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	AF009635	-1,79	1,05	-1,33	-2,67	1,89	1,35	-1,49
225238_at	MSI2: musashi homolog 2 (Drosophila)	BF435123	-2,37	1,14	-1,1	-3,04	2,69	2,15	-1,29
CLUSTER 8									
probe set	gene	Accession	inflamed vs Control fold-change	iLP vs Control fold-change	iLP (A-) vs Control fold-change	iBL23 vs Control fold-change	iLP vs inflamed fold-change	iLP (A-) vs inflamed fold-change	iBL23 vs inflamed fold-change
206823_at	L3MBTL: l(3)mbt-like (Drosophila)	NM_015478	-1,26	2,06	1,2	-1,07	2,6	1,51	1,17
207823_s_at	AIF1: allograft inflammatory factor 1	NM_004847	1,04	3,01	-1,09	1,03	2,9	-1,14	-1,01
215151_at	DOCK10: dedicator of cytokinesis 10	AB014594	1,26	1,44	-1,24	1,29	1,14	-1,56	1,03
216328_at	SIGLEC8: sialic acid binding Ig-like lectin 8	AF287892	-2,15	3,91	1,26	1,51	8,43	2,72	3,26
216948_at	Hs.247878.0	AL049545	1,2	9,26	3,42	-1,42	7,72	2,85	-1,7
219521_at	B3GAT1: beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	NM_018644	4,43	23,26	2,64	1,18	5,26	-1,68	-3,74
220698_at	MGC4294: hypothetical protein MGC4294	NM_024314	-1,04	1,63	-1,2	1,06	1,7	-1,15	1,1
220824_at	CCDC37: coiled-coil domain containing 37	NM_017674	-1,07	1,6	-1,65	1,23	1,72	-1,54	1,32
229079_at	EHMT2: Euchromatic histone-lysine N-methyltransferase 2	AI828004	-1,91	1,87	1,06	1,11	3,57	2,02	2,13
233081_at	receptor accessory protein 5, CDNA FLJ12305 fis, clone MAMMA1001890,	AV712346	1,39	1,69	1,12	-1,09	1,21	-1,25	-1,52
234858_at	LOC646693: similar to Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin)	AL008639	1,53	4,29	1,25	1,22	2,8	-1,23	-1,25
234881_at	Hs.248020.0	L33988	1,24	2,02	1,69	-1,09	1,63	1,36	-1,35
236005_at	KLF12: Kruppel-like factor 12	AI807987	-1,79	2,03	-1,32	1,12	3,63	1,35	1,99
237448_at	Transcribed locus	AI216576	-2,31	1,55	-1,78	-1,33	3,57	1,3	1,73
237878_at	MAP2K2: mitogen-activated protein kinase kinase 2 pseudogene; mitogen-activated protein kinase kinase 2	H69555	-1,22	1,81	1,74	-1,08	2,21	2,12	1,13
238837_at	PHF8: PHD finger protein 8	BE676640	5,62	20,76	3,23	1,15	3,69	-1,74	-4,88
243955_at	Transcribed locus	AI934364	-1,71	1,92	-1,05	-1,29	3,28	1,63	1,33
1554492_at	THADA: thyroid adenoma associated	BC037990	1,55	41,67	2,02	1,91	26,96	1,31	1,23
1555605_x_at	BAGE: B melanoma antigen	AF527551	-1,5	2,93	-1,34	-2,49	4,39	1,12	-1,67
1558648_at	CCDC32: coiled-coil domain containing 32	AL832032	1,73	2,74	1,5	1,04	1,58	-1,16	-1,66

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1569338_at	PAPLN: papilin, proteoglycan-like sulfated glycoprotein	BC044305	1,2	1,14	-1,72	-1,04	-1,05	-2,06	-1,25
CLUSTER 9			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
202911_at	MSH6: mutS homolog 6 (E. coli)	NM_000179	1,24	1,7	1,79	1,71	1,37	1,44	1,37
209808_x_at	ING1: inhibitor of growth family, member 1	AW193656	1,32	1,41	1,66	1,67	1,06	1,25	1,26
210933_s_at	FSCN1: fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	BC004908	1,15	1,68	1,66	1,85	1,46	1,44	1,6
213931_at	ID2 /// ID2B: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	A1819238	1,09	1,45	1,43	1,77	1,32	1,31	1,62
218032_at	SNN: stannin	AF070673	1,35	1,91	1,75	1,84	1,41	1,29	1,36
219566_at	PLEKHF1: pleckstrin homology domain containing, family F (with FYVE domain) member 1	NM_024310	1,44	2,78	3	2,71	1,93	2,08	1,88
223129_x_at	MYLIP: myosin regulatory light chain interacting protein	T63512	1,17	1,54	1,6	1,6	1,32	1,37	1,37
223130_s_at	MYLIP: myosin regulatory light chain interacting protein	AF212221	1,09	1,49	1,52	1,5	1,37	1,4	1,38
228098_s_at	MYLIP: myosin regulatory light chain interacting protein	AW292746	1,14	1,39	1,46	1,56	1,23	1,28	1,37
225005_at	PHF13: PHD finger protein 13	AL039384	1,04	1,75	1,72	1,72	1,68	1,65	1,64
225977_at	PCDH18: protocadherin 18	BF062943	1,93	3,53	2,41	2,22	1,82	1,25	1,15
226552_at	IER5L: immediate early response 5-like	BF110608	1,19	1,41	1,62	1,84	1,19	1,37	1,55
230477_at	MUC16: mucin 16, cell surface associated	A1588962	1,29	1,77	2	2,02	1,37	1,54	1,56
230508_at	DKK3: dickkopf homolog 3 (Xenopus laevis)	AL569601	1,12	1,54	1,15	1,59	1,37	1,03	1,42
1561619_at	LINGO-1: leucine rich repeat and Ig domain containing 1	BI463387	2,16	2,84	1,74	2,51	1,31	-1,24	1,16
1569376_s_at	CDNA clone IMAGE:4297546	BC029435	-1,2	3,04	2,69	1,72	3,66	3,23	2,07
CLUSTER 10			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
212142_at	MCM4: minichromosome maintenance complex component 4	A1936566	-1,66	1,12	1,81	1,23	1,86	3	2,05
212964_at	HIC2: hypermethylated in cancer 2	A1912206	1,21	1,52	2,46	1,58	1,26	2,03	1,3
212981_s_at	FAM115A: family with sequence similarity 115, member A	BF030508	1,11	1,38	1,65	1,41	1,24	1,49	1,27
214245_at	RPS14: ribosomal protein S14	A1734124	1,43	-1,4	1,91	1,37	-2,01	1,33	-1,05
214651_s_at	HOXA9: homeobox A9	U41813	-1,3	1,08	1,49	1,29	1,41	1,93	1,68

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220987_s_at	C11orf17 /// NUA2: chromosome 11 open reading frame 17 /// NUA2 family, SNF1-like kinase, 2	NM_030952	1,24	1,29	1,64	1,4	1,04	1,32	1,12
34697_at	LRP6: low density lipoprotein receptor-related protein 6	AF074264	-1,57	-1,19	1,86	1,35	1,32	2,92	2,12
224958_at	NUFIP2: nuclear fragile X mental retardation protein interacting protein 2	AV728521	-1,13	1,18	1,36	1,21	1,33	1,53	1,37
229043_at	PAPD5: PAP associated domain containing 5	AI492902	1,09	1,49	1,81	1,62	1,36	1,66	1,48
229051_at	YPEL2: yippee-like 2 (Drosophila)	AW005748	1,17	1,77	2,84	1,09	1,52	2,44	-1,07
235823_at	ACSF3: acyl-CoA synthetase family member 3	AI763000	1,18	1,38	1,87	1,52	1,17	1,58	1,28
237019_at	Transcribed locus	AI479285	1,44	-1,37	2,13	1,58	-1,97	1,48	1,09
239115_at	MRNA full length insert cDNA clone EUROIMAGE 687685	AA670271	4,52	2,02	7,4	1,58	-2,24	1,64	-2,86
240744_at	CPA5: carboxypeptidase A5	AW184014	3,72	3,99	6,76	1,99	1,07	1,81	-1,87
242118_x_at	QRSL1:glutamyl-tRNA synthase (glutamine-hydrolyzing)-like 1	N80145	1,94	2,02	4,61	1,63	1,04	2,37	-1,19
1553875_s_at	ZSCAN10: zinc finger and SCAN domain containing 10	NM_032805	-1,26	-2,34	3,99	2,01	-1,85	5,04	2,54
1555529_at	RNH1: ribonuclease/angiogenin inhibitor 1	AY071904	1,24	1,26	1,6	1,28	1,02	1,29	1,03
1556851_at	CDNA FLJ33171 fis, clone ADRGL2000644	BE222476	1,35	2,9	8,11	1,69	2,14	5,98	1,24
1557257_at	BCL10: B-cell CLL/lymphoma 10	AA994334	1,42	1,81	2,64	2,03	1,27	1,86	1,43
1561041_at	TNRC6C: trinucleotide repeat containing 6C	BM459591	-1,11	-1,56	2,62	1,52	-1,4	2,91	1,69
1569905_at	HSD11B1L: hydroxysteroid (11-beta) dehydrogenase 1-like	BC018336	-1,51	1,14	2,6	1,25	1,73	3,92	1,89
CLUSTER 11			inflamed vs Control	iLP vs Control	iLP (A-) vs Control	iBL23 vs Control	iLP vs inflamed	iLP (A-) vs inflamed	iBL23 vs inflamed
probe set	gene	Accession	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change	fold-change
204323_x_at	NF1: neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	M61213	-1,59	1,09	-1,1	1,19	1,73	1,44	1,88
221088_s_at	PPP1R9A: protein phosphatase 1, regulatory (inhibitor) subunit 9A	NM_017650	-1,52	-1,23	1,03	-1,1	1,24	1,57	1,38
223072_s_at	WBP1: WW domain binding protein 1	U79457	-1,56	-1,1	1,03	1,26	1,41	1,6	1,96
223074_s_at	C9orf58: chromosome 9 open reading frame 58	AA205873	-1,37	-1,38	1,05	2,44	-1,01	1,43	3,34
235953_at	ZNF610: zinc finger protein 610	AA776810	-1,45	-1,33	1,29	1,03	1,09	1,86	1,48