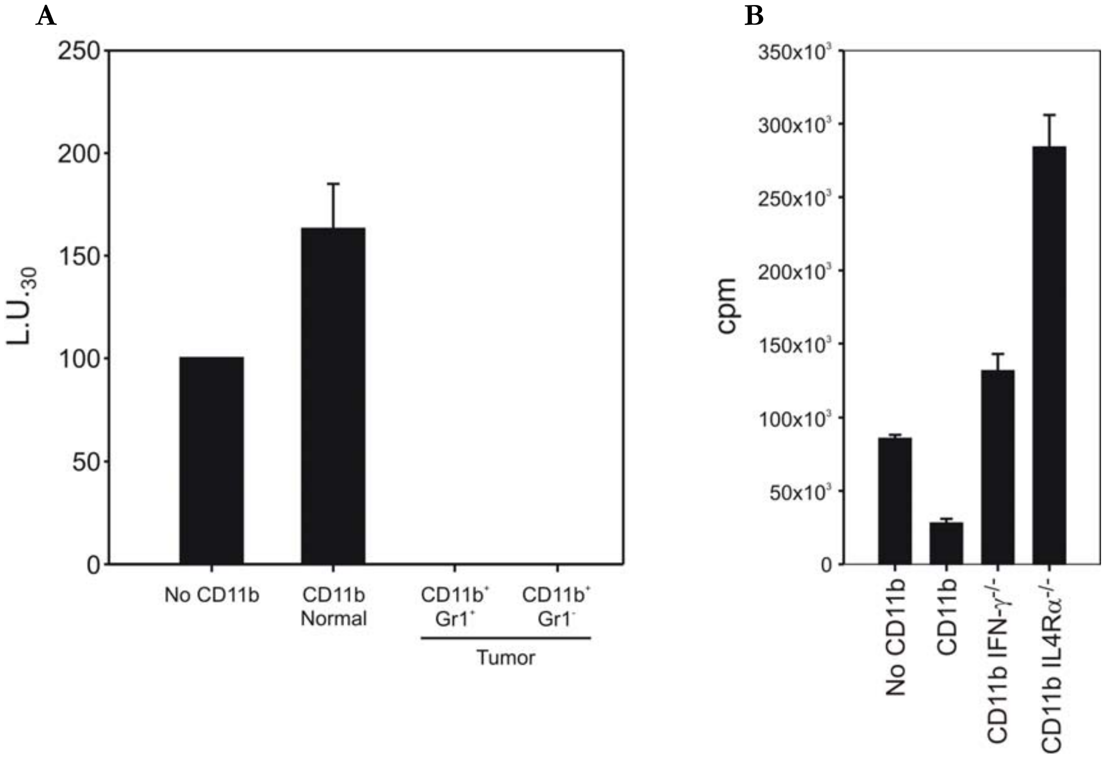
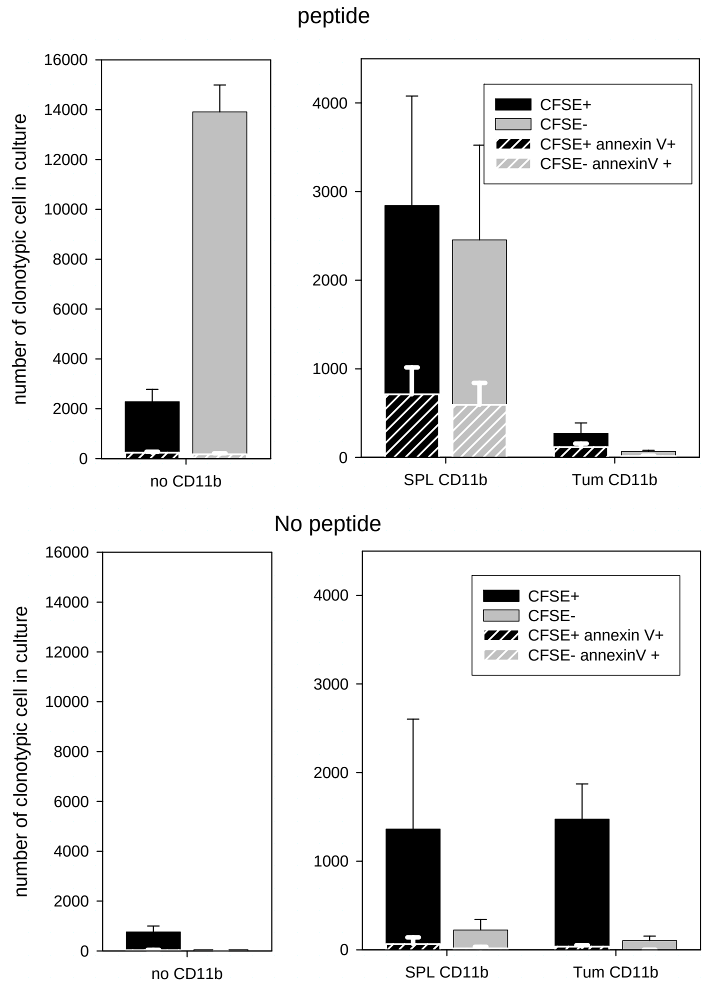


Supplemental Figure 1. (A) Evaluation of inhibitory activity of tumor-induced CD11b^{+}/Gr-1^{+} and CD11b^{+}/Gr-1^{-} cells CD11b^{+} splenocytes were sorted from tumor-free (normal) mice and from mice bearing a subcutaneous C26-GM tumor. These last cells were separated into CD11b^{+}/Gr-1^{+} and CD11b^{+}/Gr-1^{-} fractions. CD11b^{+} cells were then added at final concentration of 3% to alloantigen-stimulated cultures of syngeneic T lymphocytes to evaluate the ability to inhibit generation of alloreactive CTL, as described in the Material and Methods **(B)** Tumor-induced CD11b^{+} cells inhibit proliferation of CD8^{+} T cells. CD11b^{+} cells sorted from wild type and knockout BALB/c mice were added at final concentration of 20% to 200,000 CD8^{+} T cells enriched from BALB/c spleen and stimulated with anti-CD3 and anti-CD28 antibodies to induce T lymphocyte proliferation. Differences between "No CD11b" group (control without tumor-derived CD11b^{+} cells) and other groups were significant ($p<0.05$). Data are expressed as cpm (mean ± SE) of triplicate cultures.



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Supplemental Figure 2. Apoptosis of antigen-activated CD8$^+$ T cells induced by tumor-conditioned CD11b$^+$ splenocytes. CFSE-labeled splenocytes derived from mice transferred with HA-specific CD8$^+$ (CL4) T cells and primed with HA-encoding vaccinia virus were stimulated with the HA peptide in the absence (No CD11b) or in the presence of CD11b$^+$ cells magnetically purified from either the spleen (SPL CD11b) or the tumor infiltrate (Tum CD11b) of tumor-bearing mice and admixed at 1/10 ratio. The cultures were stimulated for 60 h with the relevant peptide and number of AnnexinV$^+$ (apoptotic) cells was evaluated within the divided (CFSE$^+$) or undivided (CFSE$^-$) clonotypic T cells recovered from the culture. Unstimulated cultures (No peptide) were included as control. The cultures contained 1,980 clonotypic T cells at the beginning. While in the absence of CD11b$^+$ cells a total of 18,000 clonotypic T cells were recovered (16,000 divided + 2,000 undivided cells) from the culture, the recovery in the presence of splenic CD11b$^+$ cells was 1/3 (total cells recovered 5,000: 2,800 divided + 2,400 undivided cells) and was dramatically impaired with tumor-infiltrating CD11b$^+$ cells (total cells recovered 330: 270 undivided + 60 divided). Annexin V analysis revealed that while, in the absence of CD11b$^+$ cells, the number of apoptotic clonotypic T cells is negligible (400 apoptotic cell every 18,000 clonotypic, 2%), in the presence splenic CD11b$^+$ cells this number increased (1,300/5,000 = 26%) to became important in the presence of tumor-derived CD11b$^+$ cells (130/330 40%).

Supplemental Results

Tumors induce a subset of inflammatory monocytes with immunosuppressive activity on CD8$^+$ T cells

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The data analysis consists of the following steps:

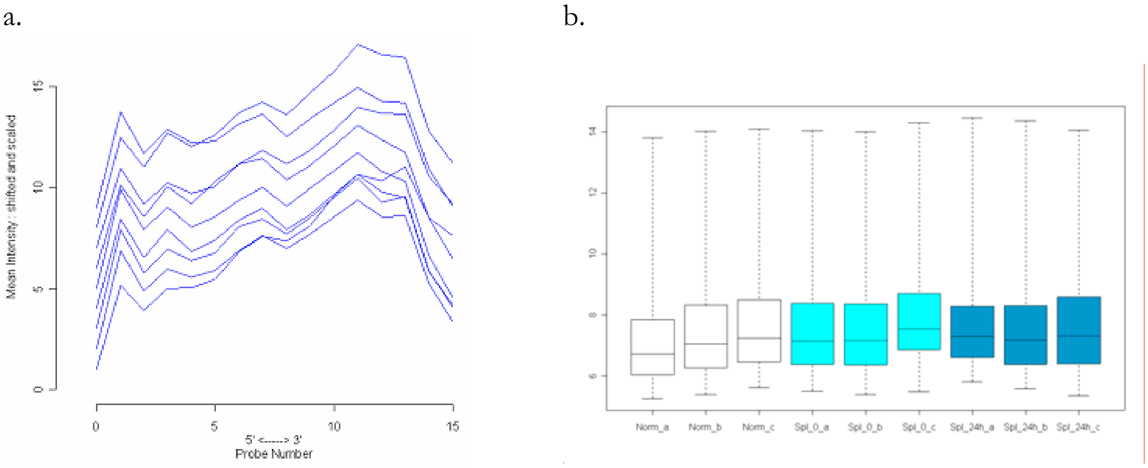
1. quality control of raw data
2. normalization, intensity calculation, and filtering
3. supervised comparative analysis and clustering
4. functional annotation of relevant genes

1. Quality control of raw data

The quality of raw data has been assessed through MAS5.0 control parameters. RNA quality has been inspected using the functions *AffyRNAdeg*, *summaryAffyRNAdeg*, and *plotAffyRNAdeg* in Bioconductor. Individual probes in a probeset are ordered by location relative to the 5' end of the targeted RNA molecule. Since RNA degradation typically starts from the 5' end of the molecule, it should be expected that probe intensities be systematically lowered at that end of a probeset when compared to the 3' end. On each chip, probe intensities are averaged by location in probeset, with the average taken over probe sets. Table 1 reports MAS5.0 quality and control parameters of raw data, indicating the overall high quality of the data set. Figure 2a shows a side-by-side plot of probe intensities averaged by location in probeset. The RNA digestion plot gives a qualitative idea of the amount of RNA degradation that occurred during RNA preparation (due presumably to RNAases) and of the quality of the second strand synthesis in the sample preparation. The absence in Figure 2 of any particular trend confirms the good data quality. Figure 2b reports a boxplot representation of raw intensities.

Supplemental Table 1 - Quality and control parameters of raw data.

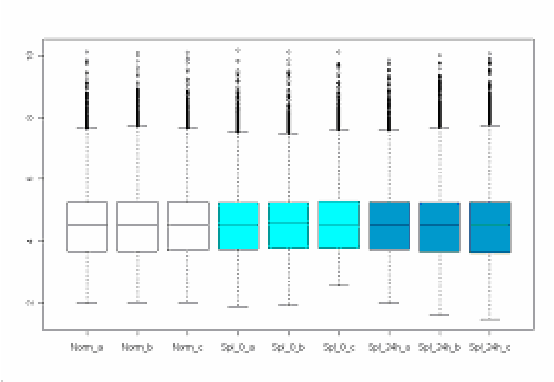
Sample ID	Background	Noise	Signal P	Signal A	Signal M	% Present	% Absent	% Marginal	Scaling Factor	Noise (RawQ)	TGT	3'/5'_actin	3'/5'_GAPDH
Norm_a	44.55	1.82	382.96	32.25	86.82	37.88	60.14	1.87	1.83	1.81	100	2.57	1.63
Norm_b	49.58	2.07	340.28	26.58	94.85	41.72	56.25	1.91	1.14	1.98	100	0.99	0.92
Norm_c	56.59	2.41	354.04	34.57	95.05	37.72	60.12	2.03	1.23	2.22	100	1.19	1.11
Spl_0_a	52.74	2.32	422.09	41.26	122.25	31.29	66.58	2.02	1.5	2.12	100	1.59	1.07
Spl_0_b	51.29	2.39	428.7	46.48	128.85	28.92	68.87	2.09	1.67	2.16	100	1.58	0.99
Spl_0_c	70.62	3.99	364.08	26.76	84.29	38.20	59.98	1.70	0.88	3.1	100	1.35	1.69
Spl_24h_a	62.55	2.95	429.33	39.32	118.46	32.46	65.32	2.10	1.65	2.49	100	2.27	0.98
Spl_24h_b	51.71	2.33	382.73	32.62	92.13	37.48	60.60	1.80	1.31	2.1	100	2.36	1.26
Spl_24h_c	47.56	2.3	337	28.94	78.96	40.80	57.28	1.80	0.98	1.9	100	1.16	0.84



Supplemental Figure 3 - a. Side-by-side plot of probe intensities averaged by location in probe sets; b. Boxplot representation of raw log intensities.

2. Normalization, intensity calculation, and filtering

Probe level data has been converted to expression values using the default parameters of Affymetrix MAS5.0 algorithm. Detection calls were calculated using the same software package. Intensity levels have been normalized using the Global Scaling option to target value (i.e., TGT=100, Figure 3). Probes with Absent calls in all arrays have been filtered out while no filtering procedure has been applied on the intensity signals. The filtered data set consists of 9 samples and 6341 probe sets which have been used in further analyses.



Supplemental Figure 4 - Boxplot representation of MAS5.0 scaled data (TGT=100).

3. Supervised comparative analysis and clustering

Differentially expressed genes have been identified using dChip Compare Sample procedure (Li and Wong, 2001). Supervised analyses have been carried out to identify expression signatures of CD11b^{+} splenocytes freshly isolated from tumor-bearing mice at time 0 and after 24 h as compared to the normal counterparts. Briefly, the comparison criterions utilized in dChip require the fold change and the absolute difference between two group means to exceed user defined thresholds (in the present study, 2 and 100 respectively). The "Use lower 90% confidence bound" has been selected to use the lower confidence bound of fold changes for filtering. The computation of confidence intervals of fold changes and the application of using lower bound as filtering criterion are described in Li and Wong (2001). The lower confidence bound is intended as a conservative estimate of the real underlying fold change. False Discovery Rate (FDR) has been used to adjust p-value for multiple comparisons. In particular, dChip estimates FDR by random permutations of the groups labels.

The supervised comparison of CD11b$^+$ splenocytes freshly isolated from tumor-bearing mice with normal splenocyte samples allowed the identification of 145 differentially expressed probe sets (67 over-expressed and 78 under-expressed in tumor specimens) with a median FDR of 0.7% over 100 permutations (Table 2). Similarly, the supervised comparison of CD11b$^+$ splenocytes freshly isolated from tumor-bearing mice and cultured for 24 hours with normal splenocyte samples selected 140 differentially expressed transcripts (57 over-expressed and 83 under-expressed in tumor specimens) with a median FDR of 3.6% over 100 permutations (Table 3). Finally a comparison between freshly isolated and cultured CD11b$^+$ splenocytes led to the identification of 220 differentially expressed probe sets (98 over-expressed and 122 under-expressed in cultured samples) with a median FDR of 2.3% over 100 permutations (Table 4).

Supplemental Table 2 - Differentially expressed transcripts in CD11b+ sorted from the spleen of tumor-bearing mice as compared to normal counterparts.

Probe ID	Gene Name	Gene Symbol	Accession number	Fold Change	Lower Bound of FC
A. Over-expressed probe sets					
95786_at	regenerating islet-derived 2	*Reg2*	19693	799.11	614.85
161890_f_at	pancreatitis-associated protein	*Pap*	18489	464.34	207.56
97523_i_at	amylase 2, pancreatic	*Amy2*	11723	423.92	178.87
161642_f_at	regenerating islet-derived 3 alpha	*Reg3a*	19694	277.01	134.54
97524_f_at	amylase 2, pancreatic	*Amy2*	11723	246.09	99.89
98041_at	ribonuclease, RNase A family, 1 (pancreatic)	*Rnase1*	19752	127.38	57.22
96009_s_at	pancreatitis-associated protein	*Pap*	18489	88.01	47.86
103954_at	regenerating islet-derived 3 alpha	*Reg3a*	19694	86.48	46.04
92601_at	pancreatic lipase related protein 1	*Pnliprp1*	18946	74.52	40.01
92873_f_at	protease, serine, 2	*Prss2*	22072	73.85	37.05
101043_f_at	trypsin 4		22074	59.11	28.27
160145_at	RIKEN cDNA 1810010M01 gene	*1810010M01Rik*	69036	43.3	33.03
99479_at	deleted in malignant brain tumors 1	*Dmbt1*	12945	41.91	22.02
96064_at	regenerating islet-derived 3 gamma	*Reg3g*	19695	40.97	18.18
160213_at	regenerating islet-derived 1	*Reg1*	19692	28.74	18.09
160421_r_at	chymotrypsinogen B1	*2200008D09Rik*	66473	26.57	21.35
94755_at	interleukin 1 alpha	*Il1a*	16175	24.51	12.79
161637_f_at	kallikrein 6	*Klk5*	16612	22.89	12.75
101338_f_at	trypsin 4		22074	22.81	12.04
100061_f_at	kallikrein 6		16612	21.19	14.63
160132_at	colipase, pancreatic	*Clps*	109791	19.06	9.28
104658_at	leukemia inhibitory factor receptor	*Lifr*	16880	15.77	8.37
160744_r_at	chymotrypsin-like	*Ctrl*	109660	14.3	5.84
100319_at	interleukin 10		16153	13.56	6.59
99864_at	adenosine A2b receptor	*Adora2b*	11541	12.85	8.7
100103_f_at	RIKEN cDNA 2210010C04 gene		67373	11.65	5.57
97733_at	adenosine A2b receptor	*Adora2b*	11541	10.33	5.12
99915_at	amphiregulin	*Areg*	11839	9.93	3.66

95775_f_at	kallikrein 1	*Klk1*	16623	9.83	7.02
104495_f_at	kallikrein 5	*Klk5*	16622	9.66	4.64
104659_g_at	leukemia inhibitory factor receptor	*Lifr*	16880	9.14	5.7
93444_at	basic leucine zipper transcription factor, ATF-like	*Batf*	53314	8.78	6.21
99835_at	fos-like antigen 1	*Fosl1*	14283	8.62	3.85
94186_at	Tnf receptor-associated factor 1	*Traf1*	22029	7.81	4.29
99939_at	carboxyl ester lipase	*Cel*	12613	6.59	4.11
95348_at	chemokine (C-X-C motif) ligand 1	*Cxcl1*	14825	6.59	3.22
102921_s_at	Fas (TNF receptor superfamily member)	*Tnfrsf6*	14102	6.56	2.26
103892_r_at	elongation factor RNA polymerase II 2	*Ell2*	192657	6.54	3.92
100104_r_at	RIKEN cDNA 2210010C04 gene		67373	6.49	4.07
94036_at	CDC42 effector protein (Rho GTPase binding) 4	*Cdc42ep4*	56699	5.92	3.68
103830_at	snail homolog 1 (Drosophila)	*Snai1*	20613	5.76	2.92
97105_at	RIKEN cDNA C230027N18 gene	*C230027N18Rik*	330940	5.44	4.55
94716_f_at	kallikrein 9	*Klk9*	13648	5.39	4.1
101289_f_at	kallikrein 22		13646	5.08	3.59
92768_s_at	aminolevulinic acid synthase 2, erythroid	*Alas2*	11656	5.05	4.38
102712_at	serum amyloid A 3	*Saa3*	20210	5.01	2.04
103891_i_at	elongation factor RNA polymerase II 2	*Ell2*	192657	4.58	2.77
92694_at	chitinase 3-like 3	*Chi3l3*	12655	4.57	3
96930_at	EH-domain containing 1	*Ehd1*	13660	4.46	2.77
103977_at	coagulation factor X	*F10*	14058	4.41	2.15
103416_at	mitogen-activated protein kinase 6	*Mapk6*	50772	4.35	2.12
100437_g_at	orosomucoid 1		18405	4.19	2.03
99387_at	formyl peptide receptor 1	*Fpr1*	14293	4.12	2.44
102198_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	*Kcnn4*	16534	4.09	3.49
100988_at	BCL2-like 11 (apoptosis facilitator)		12125	4.01	3.03
103697_at	RIKEN cDNA A230075M04 gene	*A230075M04Rik*	319661	3.93	2.72
94781_at	hemoglobin alpha, adult chain 1	*Hba-a1*	15122	3.59	2.11
103534_at	hemoglobin, beta adult minor chain	*Hbb-b2*	15130	3.49	2.18
102239_at	B-cell leukemia/lymphoma 3	*Bcl3*	12051	3.49	2.72
99592_f_at	retinol dehydrogenase 11	*Rdh11*	17252	3.22	2.5
93013_at	inhibitor of DNA binding 2	*Idb2*	15902	3.01	2.48
94341_at	jumonji, AT rich interactive domain 2	*Jarid2*	16468	3	2.42
104755_at	TNFAIP3 interacting protein 1	*Tnip1*	57783	2.99	2.21
103433_at	pleckstrin homology, Sec7 and coiled-coil domains 3	*Pscd3*	19159	2.8	2.44
160138_at	Max interacting protein 1	*Mxi1*	17859	2.66	2.2
93779_at	AA261092:mz65g04.r1 Mus musculus cDNA	*5830484A20Rik*		2.58	2.15
94037_at	elastase 2	*Ela2*	13706	2.46	2.16
B. Under-expressed probe sets					
93351_at	hydroxyprostaglandin dehydrogenase 15 (NAD)	*Hpgd*	15446	-40.37	-7.73
95024_at	ubiquitin specific protease 18	*Usp18*	24110	-32.73	-17.44
102906_at	T-cell specific GTPase	*Tgtp*	21822	-22.15	-9.32
96109_at	Kruppel-like factor 2 (lung)	*Klf2*	16598	-18.04	-6.15
93956_at	interferon-induced protein with tetratricopeptide repeats 3	*Ifit3*	15959	-15.19	-8.53
93321_at	interferon activated gene 203	*Ifi203*	15950	-14.18	-5.24
95546_g_at	insulin-like growth factor 1	*Igf1*	16000	-13.88	-2.89
92558_at	vascular cell adhesion molecule 1	*Vcam1*	22329	-12.54	-2.43
97844_at	regulator of G-protein signaling 2	*Rgs2*	19735	-11.98	-5.68
101793_at	Fc receptor, IgG, high affinity I	*Fcgr1*	14129	-11.93	-7.46
100946_at	heat shock protein 1B		15511	-11.47	-2.56
104750_at	interferon gamma inducible protein 47	*Ifi47*	15953	-11.2	-7.31
98562_at	complement component 1, q subcomponent, alpha polypeptide	*C1qa*	12259	-10.77	-3.86
104332_at	pentatricopeptide repeat domain 2	*1190005P08Rik*	68927	-10.77	-6.03
99500_at	solute carrier family 12, member 2	*Slc12a2*	20496	-10.66	-4.8

103736_at	SAM and SH3 domain containing 1	*2500002E12Rik*	70097	-10.66	-4.19
95151_at	RIKEN cDNA 2810052M02 gene	*2810052M02Rik*	67220	-10.21	-6.13
96020_at	complement component 1, q subcomponent, beta polypeptide	*C1qb*	12260	-9.61	-4.36
102065_at	ficolin A	*Fcna*	14133	-9.31	-2.11
95940_f_at	cDNA sequence BC052328		223433	-8.65	-3.9
102330_at	allograft inflammatory factor 1	*Aif1*	11629	-8.59	-4.39
96344_at	enolase 3, beta muscle	*Eno3*	13808	-8.22	-2.63
98579_at	early growth response 1	*Egr1*	13653	-7.76	-2.61
92223_at	complement component 1, q subcomponent, gamma polypeptide	*C1qg*	12262	-7.7	-2.65
101030_at	ras homolog gene family, member B	*Arhb*	11852	-7.69	-2.96
92913_at	ATP-binding cassette, sub-family D (ALD), member 2	*Abcd2*	26874	-6.76	-2.31
102204_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	*Mafb*	16658	-6.19	-4.17
94689_at	expressed sequence C79248	*C79248*	96982	-6.17	-2.37
95974_at	guanylate nucleotide binding protein 1	*Gbp1*	14468	-6.07	-2.43
93285_at	dual specificity phosphatase 6	*Dusp6*	67603	-6	-3.78
103689_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	*Abcc3*	76408	-5.92	-3.7
92830_s_at	zinc finger protein 36	*Zfp36*	22695	-5.53	-3.75
94192_at	ganglioside-induced differentiation-associated-protein 10	*Gdap10*	14546	-5.37	-2.51
101705_at	per-hexamer repeat gene 1	*Phxr1*	18686	-5.27	-3.41
100601_at	integrin beta 5	*Itgb5*	16419	-5.25	-2.91
93193_at	adrenergic receptor, beta 2	*Adrb2*	11555	-4.99	-2.37
160901_at	FBJ osteosarcoma oncogene	*Fos*	14281	-4.82	-3.53
98410_at	interferon inducible GTPase 2	*AI481100*	54396	-4.8	-2.73
102318_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	*Siat8d*	20452	-4.64	-2.95
100130_at	Jun oncogene	*Jun*	16476	-4.51	-2.22
162399_f_at	AV276058:AV276058 Mus musculus cDNA	*Sca2*		-4.39	-2.93
101487_f_at	lymphocyte antigen 6 complex, locus E	*Ly6e*	17069	-4.28	-2.97
103404_at	arginine glutamic acid dipeptide (RE) repeats	*Rere*	68703	-4.23	-2.93
104669_at	interferon regulatory factor 7	*Irf7*	54123	-4.17	-3.34
97949_at	fibrinogen-like protein 2	*Fgl2*	14190	-4.09	-2.6
102657_at	H2.0-like homeo box 1 (Drosophila)	*Hlx*	15284	-4.08	-2.71
95356_at	apolipoprotein E	*Apoe*	11816	-4.06	-2.32
93195_at	Malignant fibrous histiocytoma amplified sequence 1	*Mfhas1*	52065	-4.06	-2.02
96732_at	WD repeat domain 40A	*1500001L20Rik*	68970	-4.05	-2.51
160894_at	CCAAT/enhancer binding protein (C/EBP), delta	*Cebpd*	12609	-3.89	-2.34
103990_at	FBJ osteosarcoma oncogene B	*Fosb*	14282	-3.86	-2.52
103554_at	a disintegrin and metalloproteinase domain 19 (meltrin beta)	*Adam19*	11492	-3.82	-2.18
94774_at	interferon activated gene 202B	*Ifi202b*	26388	-3.7	-2.76
160101_at	heme oxygenase (decycling) 1	*Hmox1*	15368	-3.69	-2.24
94137_at	interleukin 8 receptor, beta	*Il8rb*	12765	-3.63	-2.63
100013_at	interferon-induced protein 35	*Ifi35*	70110	-3.63	-2.39
104305_at	arginyl-tRNA synthetase-like	*Rarsl*	109093	-3.6	-3.11
96331_at	sorting nexin 2	*Snx2*	67804	-3.55	-2.4
96594_at	Heat shock protein 4	*Hspa4*	15525	-3.45	-2.67
96060_at	serine (or cysteine) proteinase inhibitor, clade B, member 6a	*Serpinb6a*	20719	-3.43	-2.4
100944_at	AA958903:ua19f08.r1 Mus musculus cDNA	*AW112010*		-3.41	-2.45
93261_at	legumain	*Lgmn*	19141	-3.38	-2.89
93600_at	leptin receptor overlapping transcript	*Obrgrp*	230514	-3.35	-2.25
97963_at	signal-induced proliferation associated gene 1	*Sipa1*	20469	-3.23	-2.21
99622_at	Kruppel-like factor 4 (gut)	*Klf4*	16600	-3.18	-2.48
94224_s_at	interferon activated gene 203	*Ifi205*	15950	-3.16	-2.28
98002_at	interferon consensus sequence binding protein 1	*Icsbp1*	15900	-3.11	-2.26

94232_at	cyclin D1	*Ccnd1*	12443	-3.1	-2.15
94432_at	beta galactoside alpha 2,6 sialyltransferase 1	*St6gal1*	20440	-3.01	-2.52
160273_at	Brf2 gene, 3' UTR	*Zfp36l2*		-2.92	-2.47
104225_at	AI645050:vs46d05.y1 Mus musculus cDNA	*Snx5*		-2.91	-2.5
94228_at	exportin 1, CRM1 homolog (yeast)	*Xpo1*	103573	-2.83	-2.03
97758_at	peroxiredoxin 1	*Prdx1*	18477	-2.81	-2.26
98398_s_at	apolipoprotein B editing complex 1	*Apobec1*	11810	-2.78	-2.02
104155_f_at	activating transcription factor 3	*Atf3*	11910	-2.75	-2.03
97448_at	similar to phosphatidylserine decarboxylase	*2310047I15Rik*	236604	-2.57	-2.13
100323_at	S-adenosylmethionine decarboxylase 1	*Amd2*	11703	-2.57	-2.1
103620_s_at	survival motor neuron 1	*Smn*	20595	-2.35	-2.02

Table 3 - Differentially expressed transcripts in cultured CD11b+ from the spleen of tumor-bearing mice as compared to normal counterparts.

Probe ID	Gene Name	Gene Symbol	Accession number	Fold Change	Lower Bound of FC
A. Over-expressed probe sets					
100773_at	interleukin 12a	*Il12a*	16159	139.2	70.51
93097_at	arginase 1, liver	*Arg1*	11846	32.75	14.33
103509_at	tumor necrosis factor receptor superfamily, member 9	*Tnfrsf9*	21942	24.75	7.15
98406_at	chemokine (C-C motif) ligand 5	*Ccl5*	20304	20.37	4.84
99329_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	*Abcc1*	17250	12.09	6.27
161817_f_at	RIKEN cDNA 4930422J18 gene	*4930422J18Rik*	74646	11.44	4.37
95338_s_at	matrix metalloproteinase 12	*Mmp12*	17381	10.51	4.44
98440_at	leukotriene B4 12-hydroxydehydrogenase	*Ltb4dh*	67103	9.47	4.47
93940_at	paraoxonase 3	*Pon3*	269823	9.15	5.25
98483_at	calcium channel, voltage-dependent, beta 3 subunit	*Cacnb3*	12297	8.3	2.07
104406_at	prostaglandin E synthase	*Ptges*	64292	8.28	3.95
161013_f_at	RIKEN cDNA 4930422J18 gene	*4930422J18Rik*	74646	7.86	3.28
99045_at	enolase 2, gamma neuronal	*Eno2*	13807	7.64	2.68
97198_at	ATP-binding cassette, sub-family A (ABC1), member 1	*Abca1*	11303	7.19	3.99
92368_at	receptor (calcitonin) activity modifying protein 3	*Ramp3*	56089	6.76	2.33
103094_at	small EDRK-rich factor 1	*Serf1*	20365	6.73	3.1
102780_at	neoplastic progression 3	*Npn3*	76650	6.62	2.73
95339_r_at	matrix metalloproteinase 12	*Mmp12*	17381	6.17	2.76
104443_at	chemokine (C-C motif) receptor 7	*Ccr7*	12775	6.1	3.65
97888_at	FGF receptor activating protein 1	*1810006G21Rik*	233575	5.91	2.33
92553_at	esterase D/formylglutathione hydrolase	*Es10*	13885	5.84	5.01
103977_at	coagulation factor X	*F10*	14058	5.7	2.79
96042_at	superoxide dismutase 2, mitochondrial	*Sod2*	20656	5.69	2.87
160335_at	glutamate-cysteine ligase , modifier subunit	*Gclm*	14630	5.56	2.12
99160_s_at	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	*Grina*	66168	5.52	2.88
97105_at	RIKEN cDNA C230027N18 gene	*C230027N18Rik*	330940	5.49	2.42
101963_at	cathepsin L	*Ctsl*	13039	5.4	2.34
100300_at	cytochrome b-245, beta polypeptide	*Cybb*	13058	4.94	2.83
97758_at	peroxiredoxin 1	*Prdx1*	18477	4.93	2.37
92858_at	secretory leukocyte protease inhibitor	*Slpi*	20568	4.9	2.93
160835_i_at	RIKEN cDNA 1110007C09 gene	*1110007C09Rik*	68480	4.87	2.52
102718_at	chemokine (C-C motif) receptor 5	*Ccr5*	12774	4.77	2.31
102921_s_at	Fas (TNF receptor superfamily member)	*Tnfrsf6*	14102	4.73	2.28

104420_at	nitric oxide synthase 2, inducible, macrophage	*Nos2*	18126	4.47	2.45
100584_at	annexin A4	*Anxa4*	11746	4.38	3.1
93779_at	AA261092:mz65g04.r1 Mus musculus cDNA	*5830484A20Rik*		4.24	3.63
100778_at	CD38 antigen	*Cd38*	12494	4.14	2.42
99864_at	adenosine A2b receptor	*Adora2b*	11541	3.94	2.56
92648_at	syntaxin binding protein 3	*Stxbp3*	20912	3.84	2.51
160106_at	capping protein (actin filament), gelsolin-like	*Capg*	12332	3.43	2.13
100332_s_at	peroxiredoxin 6	*Prdx6*	11758 /// 320769	3.35	2.63
98859_at	acid phosphatase 5, tartrate resistant	*Acp5*	11433	3.33	2.31
103773_at	RIKEN cDNA F830021D11 gene	*1110020K19Rik*	224648	3.27	2.02
103035_at	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	*Tap1*	21354	3.26	2.1
96956_at	peroxiredoxin 5	*0610038D11Rik*	54683	3.25	2.11
93318_at	ninjurin 1	*Ninj1*	18081	3.21	2.08
100154_at	AI836367:UI-M-AP0-abi-b-11-0-UI.s1 Mus musculus cDNA	*Tapbp*		3.2	2.33
93497_at	complement component 3	*C3*	12266	3.19	2.21
96191_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	*D130059B05Rik*	211673	3.15	2.63
92294_at	ADP-ribosylation factor-like 5	*2810410P22Rik*	75423	3.14	2.59
101933_at	RAB10, member RAS oncogene family	*Rab10*	19325	3.12	2.5
101902_at	recombining binding protein suppressor of hairless (Drosophila)	*Rbpsuh*	19664	2.96	2.31
100564_at	D-dopachrome tautomerase	*Ddt*	13202	2.9	2.21
92736_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	*Slc7a2*	11988	2.77	2.21
93500_at	aminolevulinic acid synthase 1	*Alas1*	11655	2.76	2.08
160637_at	molybdenum cofactor synthesis 2	*Mocs2*	17434	2.64	2.15
98007_at	ribosomal protein S6 kinase, polypeptide 2	*Rps6ka2*	20112	2.52	2.02
Under-expressed probe sets					
104590_at	myocyte enhancer factor 2C	*Mef2c*	17260	-38.88	-5.64
104592_i_at	myocyte enhancer factor 2C	*Mef2c*	17260	-33.57	-6.74
92558_at	vascular cell adhesion molecule 1	*Vcam1*	22329	-30.76	-6.17
96109_at	Kruppel-like factor 2 (lung)	*Klf2*	16598	-27.64	-10.37
102065_at	ficolin A	*Fcna*	14133	-26.25	-5.7
103226_at	mannose receptor, C type 1	*Mrc1*	17533	-25.56	-11.37
98976_at	ADAM-like, decysin 1	*Adamdec1*	58860	-22.19	-16.38
95356_at	apolipoprotein E	*Apoe*	11816	-20.69	-9.14
99500_at	solute carrier family 12, member 2	*Slc12a2*	20496	-18.13	-8.14
98562_at	complement component 1, q subcomponent, alpha polypeptide	*C1qa*	12259	-17.4	-5.8
93351_at	hydroxyprostaglandin dehydrogenase 15 (NAD)	*Hpgd*	15446	-16.64	-2.75
96020_at	complement component 1, q subcomponent, beta polypeptide	*C1qb*	12260	-15.06	-6.12
161062_r_at	DNA segment, Chr 5, Brigham & Women's Genetics 0860 expressed	*D5Bwg0860e*	52822	-14.86	-3.68
100888_at	sortilin-related receptor, LDLR class A repeats-containing	*Sorl1*	20660	-14.12	-3.77
103943_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	*Ppfia4*	68507	-14.09	-4.25
92223_at	complement component 1, q subcomponent, gamma polypeptide	*C1qg*	12262	-13.08	-4.39
104045_at	DNA segment, Chr 10, Brigham & Women's Genetics 0791 expressed	*2610102M01Rik*	72480	-12.82	-3.75
96122_at	RIKEN cDNA 2310016A09 gene	*2310016A09Rik*	69574	-12.22	-2.29
103990_at	FBJ osteosarcoma oncogene B	*Fosb*	14282	-11.6	-6.98
98579_at	early growth response 1	*Egr1*	13653	-10.47	-3.45
104014_at	hemochromatosis	*Hfe*	15216	-9.86	-3.18
100155_at	discoidin domain receptor family, member 1	*Ddr1*	12305	-9.16	-4.28

93193_at	adrenergic receptor, beta 2	*Adrb2*	11555	-9.06	-4.09
92593_at	periostin, osteoblast specific factor	*Postn*	50706	-9.02	-2.72
95120_at	transmembrane 4 superfamily member 13	*Tm4sf13*	66109	-8.4	-3.82
162023_f_at	thrombomodulin	*Thbd*	21824	-8.07	-4.21
103994_at	eukaryotic translation initiation factor 2C, 2	*Eif2c2*	239528	-8.07	-2.06
160927_at	angiotensin converting enzyme	*Ace*	11421	-8	-2.17
102371_at	nuclear receptor subfamily 4, group A, member 1	*Nr4a1*	15370	-7.49	-2.6
100554_at	PDZ and LIM domain 1 (elfin)	*Pdlim1*	54132	-7.25	-3.66
95940_f_at	cDNA sequence BC052328		223433	-7.17	-2.8
100130_at	Jun oncogene	*Jun*	16476	-7.14	-3.62
96344_at	enolase 3, beta muscle	*Eno3*	13808	-6.53	-2.06
96302_at	Splicing factor, arginine/serine-rich 7	*Sfrs7*	225027	-6.45	-3.61
92830_s_at	zinc finger protein 36	*Zfp36*	22695	-6.2	-3.77
94689_at	expressed sequence C79248	*C79248*	96982	-6.08	-3.23
103554_at	a disintegrin and metalloproteinase domain 19 (meltrin beta)	*Adam19*	11492	-5.91	-3.49
97844_at	regulator of G-protein signaling 2	*Rgs2*	19735	-5.7	-2.61
99622_at	Kruppel-like factor 4 (gut)	*Klf4*	16600	-5.55	-4.28
96168_at	kinesin family member 23	*Kif23*	71819	-5.43	-2.42
92406_at	CD7 antigen	*Cd7*	12516	-5.35	-2.5
99051_at	S100 calcium binding protein A4	*S100a4*	20198	-5.33	-3.29
94137_at	interleukin 8 receptor, beta	*Il8rb*	12765	-5.25	-3.14
102362_i_at	Jun-B oncogene	*Junb*	16477	-5.22	-3.18
103240_f_at	eosinophil-associated, ribonuclease A family, member 2	*Ear2*	13587	-5.19	-3.02
102224_at	hypothetical protein D930020L01	*Igf1r*	330557	-5.17	-3.57
103299_at	expressed sequence AI132321	*AI132321*	104759	-5.12	-2.1
94545_at	reticulon 1	*Rtn1*	104001	-5.11	-2.16
97949_at	fibrinogen-like protein 2	*Fgl2*	14190	-5.08	-2.79
97531_at	G0/G1 switch gene 2	*G0s2*	14373	-4.96	-2.42
102363_r_at	Jun-B oncogene	*Junb*	16477	-4.91	-3.08
103689_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	*Abcc3*	76408	-4.9	-3
104598_at	dual specificity phosphatase 1	*Dusp1*	19252	-4.78	-3.49
102397_at	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 homolog (human)	*Cbfa2t3h*	12398	-4.68	-2.56
97515_at	hydroxysteroid (17-beta) dehydrogenase 4	*Hsd17b4*	15488	-4.65	-2.31
95380_at	CD244 natural killer cell receptor 2B4	*Cd244*	18106	-4.64	-2.74
95886_g_at	CREB binding protein	*AW558298*	12914	-4.6	-2.78
98535_at	catechol-O-methyltransferase	*Comt*	12846	-4.52	-2.14
101972_at	napsin A aspartic peptidase	*Kdap*	16541	-4.27	-2.74
96060_at	serine (or cysteine) proteinase inhibitor, clade B, member 6a	*Serpinb6a*	20719	-4.26	-2.8
94232_at	cyclin D1	*Ccnd1*	12443	-4.11	-3.43
95029_at	ATPase type 13A1		170759	-4.04	-2.2
100032_at	trans-acting transcription factor 1	*Sp1*	20683	-4.04	-2.12
93100_at	actin, alpha 2, smooth muscle, aorta	*Acta2*	11475	-3.88	-2.32
160273_at	Brf2 gene, 3' UTR	*Zfp36l2*		-3.84	-3.25
94432_at	beta galactoside alpha 2,6 sialyltransferase 1	*St6gal1*	20440	-3.8	-3.09
99126_at	L04961:Inactive X specific transcripts	*Xist*		-3.76	-2.12
99956_at	kit oncogene	*Kit*	16590	-3.58	-2.17
104735_at	potassium channel tetramerisation domain containing 12	*Kctd12*	239217	-3.51	-2.18
160517_at	lamin B1	*Lmnb1*	16906	-3.5	-3.03
93198_at	colony stimulating factor 3 receptor (granulocyte)	*Csf3r*	12986	-3.48	-2.43
102204_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	*Mafb*	16658	-3.48	-2.64

92356_at	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	*Ptpn8*	19260	-3.47	-3.06
93285_at	dual specificity phosphatase 6	*Dusp6*	67603	-3.46	-2.16
95064_at	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	*Acaa2*	52538	-3.36	-2.23
93023_f_at	histone 2, H3c2	*Hist2h3c2*	97114	-3.31	-2.14
93261_at	legumain	*Lgmn*	19141	-3.19	-2.67
101542_f_at	fibroblast growth factor inducible 14	*Ddx3x*	14209	-3.1	-2.08
102414_i_at	DnaJ (Hsp40) homolog, subfamily C, member 3	*Dnajc3*	19107	-2.97	-2.27
104206_at	RIKEN cDNA 5730557B15 gene	*0610012A05Rik*	67434	-2.87	-2.22
99109_at	immediate early response 2	*Ier2*	15936	-2.86	-2.21
94257_at	Ras-related GTP binding A	*Rraga*	68441	-2.73	-2.16
160428_at	succinate-Coenzyme A ligase, GDP-forming, beta subunit	*Suclg2*	20917	-2.69	-2.21

between freshly isolated and cultured CD11b$^+$ splenocytes led to the identification of 220 differentially expressed probe sets (98 over-expressed and 122 under-expressed in cultured samples) with a median FDR of 2.3% over 100 permutations (Table 4).

Supplemental Table 4 – Over- and under-expressed transcripts in the comparison between cultured and freshly isolated CD11b$^+$ splenocytes.

Probe ID	Gene Name	Gene Symbol	Accession number	Fold Change	Lower Bound of FC
A. Over-expressed probe sets					
93097_at	arginase 1, liver	*Arg1*	11846	142.18	77.9
161817_f_at	RIKEN cDNA 4930422J18 gene	*4930422J18Rik*	74646	68.51	38.45
100773_at	interleukin 12a	*Il12a*	16159	29.65	13
103509_at	tumor necrosis factor receptor superfamily, member 9	*Tnfrsf9*	21942	29.06	9.37
96515_at	interleukin 4 induced 1	*Il4i1*	14204	26.24	2.19
95705_s_at	actin, beta, cytoplasmic	*Actb*	11461	17.19	2.25
95151_at	RIKEN cDNA 2810052M02 gene	*2810052M02Rik*	67220	15.32	8.18
97758_at	peroxiredoxin 1	*Prdx1*	18477	13.87	6.74
101465_at	signal transducer and activator of transcription 1	*Stat1*	20846	13.75	3.91
98483_at	calcium channel, voltage-dependent, beta 3 subunit	*Cacnb3*	12297	10.74	2.72
104332_at	pentatricopeptide repeat domain 2	*1190005P08Rik*	68927	10.63	5.03
102360_at	5,10-methylenetetrahydrofolate reductase	*Mthfr*	17769	10.37	4.31
97055_s_at	peroxiredoxin 1	*Prdx1*	18477	10.1	4.72
100944_at	AA958903:ua19f08.r1 Mus musculus cDNA	*AW112010*		9.9	2.15
98406_at	chemokine (C-C motif) ligand 5	*Ccl5*	20304	9.34	2.31
97888_at	FGF receptor activating protein 1	*1810006G21Rik*	233575	9.24	3.62
98018_at	protein C receptor, endothelial	*Procr*	19124	9.06	4.38
95338_s_at	matrix metalloproteinase 12	*Mmp12*	17381	9.01	4.52
98398_s_at	apolipoprotein B editing complex 1	*Apobec1*	11810	8.88	3.29
95339_r_at	matrix metalloproteinase 12	*Mmp12*	17381	7.46	3.64
104669_at	interferon regulatory factor 7	*Irf7*	54123	7.41	2.56
93940_at	paraoxonase 3	*Pon3*	269823	7.37	4.39
95611_at	lipoprotein lipase	*Lpl*	16956	6.81	4.03
98440_at	leukotriene B4 12-hydroxydehydrogenase	*Ltb4dh*	67103	6.5	3.52
94774_at	interferon activated gene 202B	*Ifi202b*	26388	6.3	2.6
102318_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	*Siat8d*	20452	6.28	2.58
99166_at	RIKEN cDNA 0610012G03 gene	*0610012G03Rik*	106264	6.06	3.23
160335_at	glutamate-cysteine ligase , modifier subunit	*Gclm*	14630	6.03	2.24

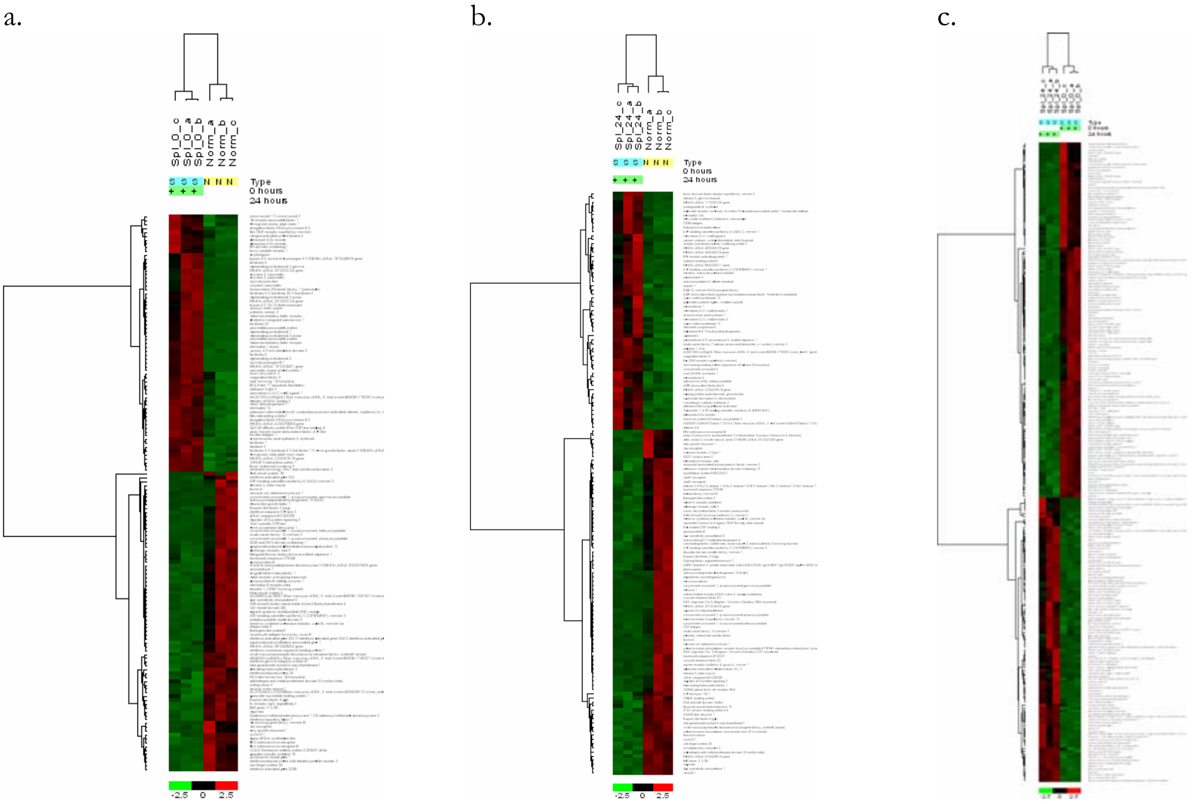
104102_at	protease, serine, 25	*Prss25*	64704	5.99	3.36
101876_s_at	histocompatibility 2, T region locus 10	*H2-T17*	15032	5.77	2.13
161013_f_at	RIKEN cDNA 4930422J18 gene	*4930422J18Rik*	74646	5.75	2.85
102401_at	interferon regulatory factor 1	*Irf1*	16362	5.74	3.95
160218_at	RIKEN cDNA 2310056P07 gene	*2310056P07Rik*	70186	5.67	2.54
160965_at	RAS p21 protein activator 4	*Rasa4*	54153	5.27	2.83
104406_at	prostaglandin E synthase	*Ptges*	64292	5.2	2.66
94394_at	Harvey rat sarcoma oncogene, subgroup R	*Rras*	20130	5.1	2.3
103035_at	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	*Tap1*	21354	5	3.34
93777_at	golgi phosphoprotein 3-like	*2010204I15Rik*	229593	4.94	3.26
95150_at	RIKEN cDNA 2810052M02 gene	*2810052M02Rik*	67220	4.86	2.25
99160_s_at	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	*Grina*	66168	4.83	2.62
101484_at	neighbor of Brca1 gene 1	*Nbr1*	17966	4.83	2.83
162399_f_at	AV276058:AV276058 Mus musculus cDNA	*Sca2*		4.57	2.85
160668_at	opioid growth factor receptor	*Ogfr*	72075	4.54	2.05
103094_at	small EDRK-rich factor 1	*Serf1*	20365	4.38	2.2
101963_at	cathepsin L	*Ctsl*	13039	4.38	3.44
97507_at	lectin, galactoside-binding, soluble, 3 binding protein	*Lgals3bp*	19039	4.29	2.74
99475_at	suppressor of cytokine signaling 2	*Socs2*	216233	4.27	3.1
160651_at	tumor-associated calcium signal transducer 2	*Tacstd2*	56753	4.2	2.28
101510_at	proteasome (prosome, macropain) 28 subunit, alpha	*Psme1*	19186	4.17	2.81
100444_at	cyclin-dependent kinase 5	*Cdk5*	12568	4.15	2.24
160344_at	Niemann Pick type C2	*Npc2*	67963	4.12	2.64
96732_at	WD repeat domain 40A	*1500001L20Rik*	68970	4.09	2.95
160637_at	molybdenum cofactor synthesis 2	*Mocs2*	17434	4.08	2.91
95152_g_at	RIKEN cDNA 2810052M02 gene	*2810052M02Rik*	67220	4.06	2
94744_at	killer cell lectin-like receptor subfamily B member 1B	*Klrb1b*	17058	3.98	2.17
101159_at	microphthalmia-associated transcription factor	*Mitf*	17342	3.94	3.43
99080_at	RIKEN cDNA 2810012H18 gene	*2810012H18Rik*	76551	3.91	2.53
104614_at	glypican 1	*Gpc1*	14733	3.85	2.23
104056_at	DNA segment, Chr 16, Brigham & Women's Genetics 1543 expressed	*D16Bwg1543e*	52910	3.84	2.14
101015_s_at	interferon (alpha and beta) receptor 2	*Ifnar2*	15976	3.78	2.01
96271_at	RIKEN cDNA 2310075C12 gene	*2310075C12Rik*	71929	3.75	2.1
104420_at	nitric oxide synthase 2, inducible, macrophage	*Nos2*	18126	3.67	2.41
92553_at	esterase D/formylglutathione hydrolase	*Es10*	13885	3.66	2.61
103671_at	HIV-1 tat interactive protein 2, homolog (human)	*Htatip2*	53415	3.63	2.03
95758_at	stearoyl-Coenzyme A desaturase 2	*Scd2*	20250	3.61	2.16
100450_r_at	activin A receptor, type II-like 1	*Acvrl1*	11482	3.59	2.12
94504_at	RIKEN cDNA 4930570C03 gene	*4930570C03Rik*	67739	3.56	2.2
97890_at	serum/glucocorticoid regulated kinase	*Sgk*	20393	3.55	2.51
160502_at	cellular repressor of E1A-stimulated genes 1	*Creg*	433375	3.55	2.44
100584_at	annexin A4	*Anxa4*	11746	3.43	2.26
93333_at	tubulin cofactor a	*Tbca*	21371	3.37	2.74
97198_at	ATP-binding cassette, sub-family A (ABC1), member 1	*Abca1*	11303	3.34	2.12
102896_at	docking protein 1	*Dok1*	13448	3.33	2.25
160101_at	heme oxygenase (decycling) 1	*Hmox1*	15368	3.3	2.83
100154_at	AI836367:UI-M-AP0-abi-b-11-0-UI.s1 Mus musculus cDNA	*Tapbp*		3.29	2.43
97963_at	signal-induced proliferation associated gene 1	*Sipa1*	20469	3.25	2.27
103216_f_at	inhibitor of kappaB kinase gamma	*Ikbkg*	16151	3.25	2.02
95675_at	mitogen-activated protein kinase kinase kinase	*Map4k3*	225028	3.18	2.37

	kinase 3				
96065_at	latexin	*Lxn*	17035	3.14	2.28
103404_at	arginine glutamic acid dipeptide (RE) repeats	*Rere*	68703	3.12	2.8
100622_at	peroxiredoxin 6	*Prdx6*	11758	3.07	2.24
94324_f_at	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	*Hmgcl*	15356	3.05	2.25
97541_f_at	histocompatibility 2, D region locus 1	*H2-D1*	14964	3.02	2.78
98859_at	acid phosphatase 5, tartrate resistant	*Acp5*	11433	2.95	2.13
100300_at	cytochrome b-245, beta polypeptide	*Cybb*	13058	2.94	2.1
100564_at	D-dopachrome tautomerase	*Ddt*	13202	2.93	2.02
160106_at	capping protein (actin filament), gelsolin-like	*Capg*	12332	2.87	2.16
94225_at	autophagy 5-like (S. cerevisiae)	*Apg5l*	11793	2.83	2.35
102854_s_at	ATPase, Cu++ transporting, alpha polypeptide	*Atp7a*	11977	2.81	2.31
98533_at	cytochrome b-5	*Cyb5*	109672	2.74	2.22
160769_at	Der1-like domain family, member 2	*BC005682*	116891	2.73	2.22
96191_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	*D130059B05Rik*	211673	2.7	2.42
101558_s_at	proteasome (prosome, macropain) subunit, beta type 5	*Psmb5*	19173	2.69	2.27
100332_s_at	peroxiredoxin 6 /// peroxiredoxin 6, related sequence 1	*Prdx6*	11758	2.69	2.09
100457_at	golgi apparatus protein 1	*Glg1*	20340	2.54	2.1
162486_f_at	Down syndrome critical region gene 3	*Dscr3*	13185	2.43	2.11
98120_at	mitochondrial ribosomal protein L27	*Mrpl27*	94064	2.37	2.03
96892_at	proteasome (prosome, macropain) subunit, alpha type 1	*Psma1*	26440	2.28	2.19
B. Under-expressed probe sets					
161642_f_at	regenerating islet-derived 3 alpha	*Reg3a*	19694	-147.7	-70.8
95786_at	regenerating islet-derived 2	*Reg2*	19693	-141.25	-59.04
101058_at	amylase 1, salivary	*Amy1*	11722	-124.54	-38.38
98041_at	ribonuclease, RNase A family, 1 (pancreatic)	*Rnase1*	19752	-100.93	-43.99
161890_f_at	pancreatitis-associated protein	*Pap*	18489	-73.81	-37.32
97523_i_at	amylase 2, pancreatic	*Amy2*	11723	-72.65	-22.21
96009_s_at	pancreatitis-associated protein	*Pap*	18489	-60.85	-33.13
160145_at	RIKEN cDNA 1810010M01 gene	*1810010M01Rik*	69036	-51.45	-32.04
97524_f_at	amylase 2, pancreatic	*Amy2*	11723	-51.43	-16.08
97413_at	RIKEN cDNA 1600029D21 gene	*1600029D21Rik*	76509	-48.63	-8.07
96064_at	regenerating islet-derived 3 gamma	*Reg3g*	19695	-47.64	-22.86
92601_at	pancreatic lipase related protein 1	*Pnliprp1*	18946	-40.48	-20.92
92873_f_at	protease, serine, 2	*Prss2*	22072	-39.62	-14.32
103954_at	regenerating islet-derived 3 alpha	*Reg3a*	19694	-33.54	-19.43
99915_at	amphiregulin	*Areg*	11839	-33.02	-18.22
101043_f_at	trypsin 4	*Try4*	22074	-23.74	-10.87
99479_at	deleted in malignant brain tumors 1	*Dmbt1*	12945	-21.91	-10.65
104495_f_at	kallikrein 5	*Klk5*	16622	-19.91	-11.12
100414_s_at	myeloperoxidase	*Mpo*	17523	-19.81	-3.65
98976_at	ADAM-like, decysin 1	*Adamdec1*	58860	-19.72	-11.09
160213_at	regenerating islet-derived 1	*Reg1*	19692	-19.71	-12.38
100437_g_at	orosomucoid 1	*Orm1*	18405	-18.62	-11.1
160421_r_at	chymotrypsinogen B1	*2200008D09Rik*	66473	-16.28	-10.71
160132_at	colipase, pancreatic	*Clps*	109791	-14.04	-6.51
101338_f_at	trypsin 4			-13.47	-6.87
99535_at	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	*Ccrn4l*	12457	-12.28	-8.11
161689_f_at	interleukin 1 receptor, type II	*Il1r2*	16178	-12.17	-8.91
100061_f_at	kallikrein 6	*Klk6*	16612	-12.13	-9.09
100436_at	orosomucoid 1	*Orm1*	18405	-11.77	-5.37
95348_at	chemokine (C-X-C motif) ligand 1	*Cxcl1*	14825	-11.29	-9.54

95349_g_at	chemokine (C-X-C motif) ligand 1	*Cxcl1*	14825	-11.27	-9.22
104658_at	leukemia inhibitory factor receptor	*Lifr*	16880	-11.24	-6.75
161637_f_at	kallikrein 6	*Klk5*	16612	-10.92	-4.47
102208_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	*Siat10*	54613	-10.18	-5.13
94036_at	CDC42 effector protein (Rho GTPase binding) 4	*Cdc42ep4*	56699	-9.96	-6.19
98988_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	*AA408868*	80859	-9.65	-6.75
102658_at	interleukin 1 receptor, type II	*Il1r2*	16178	-8.74	-4.49
104659_g_at	leukemia inhibitory factor receptor	*Lifr*	16880	-8.69	-5.82
92779_f_at	Z22552:M.musculus membrane glycoprotein gene			-8.53	-5.05
93573_at	metallothionein 1	*Mt1*	17748	-8.09	-3.16
100103_f_at	RIKEN cDNA 2210010C04 gene	*2210010C04Rik*	67373	-7.85	-3.65
103240_f_at	eosinophil-associated, ribonuclease A family, member 2	*Ear2*	13587	-7.84	-4.47
100104_r_at	RIKEN cDNA 2210010C04 gene	*2210010C04Rik*	67373	-7.38	-4.3
97531_at	G0/G1 switch gene 2	*G0s2*	14373	-7.32	-5.58
95509_at	syncollin	*Sycn*	68416	-7.3	-2.82
92398_at	cDNA sequence BC026744	*BC026744*	330192	-7.05	-3.86
100554_at	PDZ and LIM domain 1 (elfin)	*Pdlim1*	54132	-6.84	-3.05
104541_at	proteinase 3	*Prtn3*	19152	-6.7	-2.21
101561_at	metallothionein 2	*Mt2*	17750	-6.68	-4.5
103226_at	mannose receptor, C type 1	*Mrc1*	17533	-6.66	-4.1
100319_at	interleukin 10	*Il10*	16153	-6.66	-3.16
92780_f_at	M90535:Mouse endogenous proviral superantigen (Mtv-7 sag)			-6.31	-3.81
101289_f_at	kallikrein 22	*Klk22*	13646	-6.25	-4.52
100507_at	nephroblastoma overexpressed gene	*Nov*	18133	-6.25	-2.89
94716_f_at	kallikrein 9	*Klk9*	13648	-6.13	-4.76
95775_f_at	kallikrein 1	*Klk1*	16623	-6.1	-4.7
93444_at	basic leucine zipper transcription factor, ATF-like	*Batf*	53314	-6.1	-4.01
99939_at	carboxyl ester lipase	*Cel*	12613	-5.95	-3.73
103222_at	Epidermal growth factor receptor pathway substrate 8	*Eps8*	13860	-5.84	-3.67
94297_at	FK506 binding protein 5	*Fkbp5*	14229	-5.45	-2.43
93328_at	histidine decarboxylase	*Hdc*	15186	-5.26	-2.65
100311_f_at	eosinophil-associated, ribonuclease A family, member 1	*Ear1*	13586	-5.23	-2.53
93702_at	protein tyrosine phosphatase, non-receptor type 23	*AI462446*	104831	-5.14	-3.57
95356_at	apolipoprotein E	*Apoe*	11816	-5.1	-2.02
100755_at	neutrophil elastase	*NE*	50701	-5.04	-2.3
94755_at	interleukin 1 alpha	*Il1a*	16175	-5.01	-2.85
160517_at	lamin B1	*Lmnb1*	16906	-5	-3.91
101676_at	glutathione peroxidase 3	*Gpx3*	14778	-4.96	-3.26
92356_at	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	*Ptpn8*	19260	-4.74	-3.37
93454_at	complement component 1, q subcomponent, receptor 1	*C1qr1*	17064	-4.68	-2.65
93783_at	elastase 1, pancreatic	*Ela1*	109901	-4.62	-2.34
102371_at	nuclear receptor subfamily 4, group A, member 1	*Nr4a1*	15370	-4.61	-2.55
97740_at	dual specificity phosphatase 16	*Dusp16*	70686	-4.53	-2.98
103697_at	RIKEN cDNA A230075M04 gene	*A230075M04Rik*	319661	-4.5	-3.18
160084_at	ornithine decarboxylase, structural 1	*Odc*	18263	-4.43	-3.02
104761_at	anthrax toxin receptor 2	*Antxr2*	71914	-4.41	-2.09
92614_at	inhibitor of DNA binding 3	*Idb3*	15903	-4.34	-2.64
98596_s_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	*Siat9*	20454	-4.28	-2.02
101972_at	napsin A aspartic peptidase	*Kdap*	16541	-4.16	-3.66
92232_at	suppressor of cytokine signaling 3	*Socs3*	12702	-3.96	-2.36

93975_at	RIKEN cDNA 1300002F13 gene	*1300002F13Rik*	74155	-3.86	-2.66
93315_at	mitogen activated protein kinase kinase 3	*Map2k3*	26397	-3.82	-2.23
101160_at	chemokine (C-X-C motif) ligand 2	*Cxcl2*	20310	-3.78	-2.74
160359_at	RIKEN cDNA 1190002H23 gene	*1190002H23Rik*	66214	-3.76	-2.14
103892_r_at	elongation factor RNA polymerase II 2	*Ell2*	192657	-3.73	-2.58
102218_at	interleukin 6	*Il6*	16193	-3.63	-2.29
93496_at	ELOVL family member 5, elongation of long chain fatty acids (yeast)	*Elovl5*	68801	-3.53	-2.86
94142_at	colony stimulating factor 3 (granulocyte)	*Csf3*	12985	-3.5	-2.24
96930_at	EH-domain containing 1	*Ehd1*	13660	-3.49	-2.13
102663_at	urokinase plasminogen activator receptor	*Plaur*	18793	-3.47	-2.44
93728_at	transforming growth factor beta 1 induced transcript 4	*Tgfb1i4*	21807	-3.37	-2.27
160184_at	RIKEN cDNA 1200007D18 gene	*1200007D18Rik*	67458	-3.33	-2.24
160320_at	sorbin and SH3 domain containing 1	*Sorbs1*	20411	-3.31	-2.75
95064_at	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	*Acaa2*	52538	-3.3	-2.67
99864_at	adenosine A2b receptor	*Adora2b*	11541	-3.26	-2.08
97426_at	epithelial membrane protein 1	*Emp1*	13730	-3.21	-2.01
162198_f_at	AV373027:AV373027 Mus musculus cDNA	*Ccl6*		-3.21	-2.13
160774_at	ectonucleoside triphosphate diphosphohydrolase 1	*Entpd1*	12495	-3.16	-2.1
102424_at	chemokine (C-C motif) ligand 3	*Ccl3*	20302	-3.15	-2.03
98059_s_at	lamin A	*Lmna*	16905	-3.08	-2.53
94085_at	proteoglycan 1, secretory granule	*Prg*	19073	-3.07	-2.25
97319_at	Ras-related associated with diabetes	*Rrad*	56437	-3.05	-2.24
103990_at	FBJ osteosarcoma oncogene B	*Fosb*	14282	-3	-2.25
161847_r_at	RIKEN cDNA 2210016L21 gene	*Tcf1*	72357	-2.98	-2.03
93041_at	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	*Mcm4*	17217	-2.97	-2.19
104014_at	hemochromatosis	*Hfe*	15216	-2.96	-2.28
103033_at	complement component 4 (within H-2S)	*C4*	12268	-2.96	-2.31
93974_at	RIKEN cDNA 1300002F13 gene	*1300002F13Rik*	74155	-2.92	-2.62
103891_i_at	elongation factor RNA polymerase II 2	*Ell2*	192657	-2.88	-2.5
104256_at	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	*Pscdbp*	227929	-2.85	-2.14
160961_at	signal-induced proliferation-associated 1 like 2	*Sipa1l2*	244668	-2.77	-2.48
99592_f_at	retinol dehydrogenase 11	*Rdh11*	17252	-2.74	-2.17
94489_at	protein tyrosine phosphatase 4a1	*Ptp4a1*	19243	-2.74	-2.28
94037_at	elastase 2	*Ela2*	13706	-2.73	-2.24
92778_i_at	Z22552:M.musculus membrane glycoprotein gene			-2.69	-2.15
94408_at	Ngfi-A binding protein 1	*Nab1*	17936	-2.64	-2
95695_at	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	*Slc25a20*	57279	-2.63	-2.14
104257_g_at	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	*Pscdbp*	227929	-2.63	-2.1
94769_at	matrix metalloproteinase 8	*Mmp8*	17394	-2.62	-2.26
100084_at	villin 2	*Vil2*	22350	-2.59	-2.02
102198_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	*Kcnn4*	16534	-2.48	-2.17
101554_at	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	*Nfkbia*	18035	-2.44	-2.09

To perform the hierarchical agglomerative clustering of the selected probe lists, Pearson's correlation coefficient and average-linkage were respectively used as distance and linkage methods in DNA-Chip Analyzer (dChip) software (Eisen et al., 1998; Li and Wong, 2001). Before clustering, the expression values for a gene across all samples have been standardized (linearly scaled) to have mean 0 and standard deviation 1, and these standardized values have been used to calculated correlations between genes and samples and served as the basis for merging nodes. In Figures 4a, 4b, and 4c are reported Eisen heat maps as determined by the differentially expressed genes identified in supervised comparisons of freshly isolated and cultured CD11b$^+$ splenocytes and normal samples.



Supplemental Figure 5 - Eisen heat maps as determined by the differentially expressed genes identified in supervised comparisons of: a. freshly isolated CD11b$^+$ splenocytes versus normal samples; b. CD11b$^+$ splenocytes cultured for 24 h versus normal samples; c.) freshly isolated versus cultured CD11b$^+$ splenocytes.

4. Functional annotation of relevant genes

Modulated probe sets have been functionally annotated using DAVID (Dennis et al., 2003). The Database for Annotation, Visualization and Integrated Discovery 2.0 (DAVID 2.0, http://david.niaid.nih.gov/david/version2/index.htm) is an expanded version of the original web-accessible program developed by the Laboratory of Immunopathogenesis and Bioinformatics at SAIC-Frederick, Inc. for the National Institute of Allergy and Infectious Diseases of the National Institutes of Health. DAVID 2.0 integrates functional genomic annotations with intuitive graphical summaries and provides a comprehensive set of tools for investigators to visually summarize annotation from large list of genes. Gene Ontology categories, PIR and SwissProt keywords, sequence feature information, protein-protein interaction data, protein domain information, and pathway maps are among the available annotation types. Functional annotations have been derived linking LocusLink accession numbers to gene accessioning systems like Genbank, Unigene, and

Affymetrix identifiers and to biological annotations including gene names and aliases, functional summaries, Gene Ontologies, protein domains, and biochemical and signal transduction pathways.
Functional categories have been ranked using the DAVID 2.0 co-occurrence procedure. Sorting can be based either the number of genes within each category or by the EASE-score, a method that identifies functional categories over-represented in a gene list relative to the representation within the proteome of a given species. The EASE-score is a modification of the Fisher Exact Test that allows ranking biological categories associated with sets of genes based on the co-occurrence/enrichment of the category with the gene list (Douglas et al., 2004).
Gene Ontology characterization in terms of Biological Process and Molecular Function for the list of over-expressed and under-expressed genes in freshly isolated CD11b+ splenocytes is reported in Tables 5 and 6, respectively. Similarly, Tables 7 and 8 enlists GO annotation for over- and under-expressed transcripts in cultured CD11b+ splenocytes. GO categories are sorted by p-value setting a maximum probability of 0.1 and a minimum count of 2 probes.

Supplemental Table 5 – Gene Ontology annotation of overexpressed transcripts in the comparison between freshly isolated CD11b$^+$ splenocytes and normal specimens.

GO Term	Gene Count	Gene Percentage	p_value
A. Biological Process			
DIGESTION	5	8.1	3.42E-07
MACROMOLECULE CATABOLISM	14	22.6	1.04E-06
INFLAMMATORY RESPONSE	7	11.3	3.12E-06
ACUTE-PHASE RESPONSE	5	8.1	3.40E-06
INNATE IMMUNE RESPONSE	7	11.3	4.73E-06
CATABOLISM	14	22.6	8.22E-06
ORGANISMAL PHYSIOLOGICAL PROCESS	17	27.4	1.80E-05
PROTEOLYSIS AND PEPTIDOLYSIS	11	17.7	6.84E-05
PROTEIN CATABOLISM	11	17.7	9.39E-05
RESPONSE TO PEST/PATHOGEN/PARASITE	9	14.5	3.77E-04
HETEROPHILIC CELL ADHESION	5	8.1	4.30E-04
RESPONSE TO WOUNDING	7	11.3	9.54E-04
IMMUNE RESPONSE	10	16.1	1.84E-03
RESPONSE TO STRESS	9	14.5	7.84E-03
DEFENSE RESPONSE	10	16.1	8.73E-03
CELL-CELL ADHESION	5	8.1	1.24E-02
RESPONSE TO BIOTIC STIMULUS	10	16.1	1.27E-02
LIPID CATABOLISM	3	4.8	1.76E-02
RESPONSE TO EXTERNAL STIMULUS	12	19.4	2.41E-02
MACROMOLECULE METABOLISM	17	27.4	3.28E-02
RESPONSE TO STIMULUS	12	19.4	5.29E-02
GAS TRANSPORT	2	3.2	5.93E-02
OXYGEN TRANSPORT	2	3.2	5.93E-02
PHYSIOLOGICAL PROCESS	41	66.1	6.67E-02
B. Molecular Function			
CHYMOTRYPSIN ACTIVITY	11	17.7	6.76E-12
TRYPSIN ACTIVITY	11	17.7	2.57E-11
SERINE-TYPE ENDOPEPTIDASE ACTIVITY	11	17.7	5.41E-10
SERINE-TYPE PEPTIDASE ACTIVITY	11	17.7	1.03E-09
ENDOPEPTIDASE ACTIVITY	11	17.7	1.67E-06

TISSUE KALLIKREIN ACTIVITY	4	6.5	1.51E-05
PEPTIDASE ACTIVITY	11	17.7	3.09E-05
SUGAR BINDING	6	9.7	2.01E-04
CARBOHYDRATE BINDING	6	9.7	2.44E-04
HYDROLASE ACTIVITY	16	25.8	4.70E-04
GROWTH FACTOR ACTIVITY	4	6.5	1.17E-02
TRIACYLGLYCEROL LIPASE ACTIVITY	2	3.2	2.58E-02
CYTOKINE ACTIVITY	4	6.5	2.92E-02
OXYGEN TRANSPORTER ACTIVITY	2	3.2	4.81E-02
CATALYTIC ACTIVITY	20	32.3	8.97E-02

Supplemental Table 6 – Gene Ontology annotation of under-expressed transcripts in the comparison between freshly isolated CD11b$^+$ splenocytes and normal specimens.

GO Term	Gene Count	Gene Percentage	p-value
A. Biological Process			
RESPONSE TO BIOTIC STIMULUS	16	20	1.07E-04
PHYSIOLOGICAL PROCESS	58	72.5	5.54E-04
DEFENSE RESPONSE	14	17.5	7.39E-04
ANION TRANSPORT	6	7.5	9.34E-04
PHOSPHATE TRANSPORT	4	5	1.20E-03
INORGANIC ANION TRANSPORT	5	6.3	2.34E-03
RESPONSE TO EXTERNAL STIMULUS	17	21.3	2.65E-03
RESPONSE TO STIMULUS	18	22.5	3.67E-03
IMMUNE RESPONSE	11	13.8	3.96E-03
COMPLEMENT ACTIVATION, CLASSICAL PATHWAY	3	3.8	4.68E-03
ORGANISMAL PHYSIOLOGICAL PROCESS	14	17.5	1.37E-02
COMPLEMENT ACTIVATION	3	3.8	1.37E-02
REGULATION OF CELL CYCLE	6	7.5	1.51E-02
HUMORAL DEFENSE MECHANISM (SENSU VERTEBRATA)	3	3.8	1.72E-02
REGULATION OF BIOLOGICAL PROCESS	18	22.5	4.80E-02
RESPIRATORY GASEOUS EXCHANGE	2	2.5	4.81E-02
DEVELOPMENT	13	16.3	4.99E-02
POSITIVE REGULATION OF TRANSCRIPTION	3	3.8	5.08E-02
POSITIVE REGULATION OF NUCLEOBASE, NUCLEOSIDE, NUCLEOTIDE AND NUCLEIC ACID METABOLISM	3	3.8	5.20E-02
CELL DIFFERENTIATION	5	6.3	5.77E-02
CELL CYCLE	7	8.8	6.31E-02
NEGATIVE REGULATION OF GROWTH	2	2.5	8.16E-02
POSITIVE REGULATION OF METABOLISM	3	3.8	8.81E-02
CELL DEATH	5	6.3	9.51E-02
DEATH	5	6.3	1.00E-01
B. Molecular Function			
DNA BINDING	14	17.5	1.32E-02
TRANSCRIPTION FACTOR ACTIVITY	9	11.3	1.37E-02
TRANSCRIPTION REGULATOR ACTIVITY	10	12.5	1.47E-02
PROTEIN BINDING	15	18.8	2.18E-02
BINDING	41	51.3	5.67E-02
NUCLEIC ACID BINDING	17	21.3	7.53E-02

GTPASE ACTIVITY	3	3.8	7.54E-02
HYDROLASE ACTIVITY, ACTING ON ACID ANHYDRIDES, IN PHOSPHORUS-CONTAINING ANHYDRIDES	5	6.3	7.87E-02
HYDROLASE ACTIVITY, ACTING ON ACID ANHYDRIDES	5	6.3	7.91E-02
SIALYLTRANSFERASE ACTIVITY	2	2.5	8.04E-02
GTP BINDING	4	5	9.50E-02

Supplemental Table 7 – Gene Ontology annotation of over-expressed transcripts in the comparison between cultured CD11b$^+$ splenocytes and normal specimens.

GO Term	Gene Count	Gene Percentage	p-value
A. Biological Process			
RESPONSE TO BIOTIC STIMULUS	13	21	3.10E-05
RESPONSE TO EXTERNAL STIMULUS	14	22.6	3.74E-04
DEFENSE RESPONSE	11	17.7	4.52E-04
OXYGEN AND REACTIVE OXYGEN SPECIES METABOLISM	4	6.5	5.27E-04
RESPONSE TO STIMULUS	14	22.6	1.23E-03
PHYSIOLOGICAL PROCESS	36	58.1	6.70E-03
IMMUNE RESPONSE	8	12.9	7.24E-03
CHEMOTAXIS	3	4.8	2.62E-02
TAXIS	3	4.8	2.62E-02
COENZYME AND PROSTHETIC GROUP BIOSYNTHESIS	3	4.8	2.78E-02
PIGMENT BIOSYNTHESIS	2	3.2	4.03E-02
INFLAMMATORY RESPONSE	3	4.8	4.33E-02
DEFENSE RESPONSE TO BACTERIA	2	3.2	4.56E-02
ORGANISMAL PHYSIOLOGICAL PROCESS	9	14.5	4.67E-02
INNATE IMMUNE RESPONSE	3	4.8	4.92E-02
SUPEROXIDE METABOLISM	2	3.2	5.08E-02
PIGMENT METABOLISM	2	3.2	5.60E-02
RESPONSE TO WOUNDING	4	6.5	6.56E-02
COENZYME AND PROSTHETIC GROUP METABOLISM	3	4.8	6.56E-02
BIOSYNTHESIS	7	11.3	6.59E-02
PIGMENTATION	2	3.2	7.15E-02
NITROGEN METABOLISM	2	3.2	7.40E-02
RESPONSE TO BACTERIA	2	3.2	7.40E-02
TRANSPORT	10	16.1	8.39E-02
RESPONSE TO STRESS	6	9.7	8.46E-02
RESPONSE TO OXIDATIVE STRESS	2	3.2	9.41E-02
B. Molecular Function			
CATALYTIC ACTIVITY	25	40.3	7.81E-04
HYDROLASE ACTIVITY	14	22.6	2.47E-03
ANTIOXIDANT ACTIVITY	3	4.8	8.15E-03
TRANSPORTER ACTIVITY	11	17.7	1.11E-02
C-C CHEMOKINE BINDING	2	3.2	4.26E-02
C-C CHEMOKINE RECEPTOR ACTIVITY	2	3.2	4.26E-02
OXIDOREDUCTASE ACTIVITY	6	9.7	4.82E-02
CHEMOKINE BINDING	2	3.2	6.07E-02
CHEMOKINE RECEPTOR ACTIVITY	2	3.2	6.07E-02
ATPASE ACTIVITY, COUPLED TO TRANSMEMBRANE MOVEMENT OF SUBSTANCES	3	4.8	7.48E-02
HYDROLASE ACTIVITY, ACTING ON ACID ANHYDRIDES, CATALYZING TRANSMEMBRANE MOVEMENT OF SUBSTANCES	3	4.8	7.55E-02
P-P-BOND-HYDROLYSIS-DRIVEN TRANSPORTER ACTIVITY	3	4.8	8.75E-02
PEROXIDASE ACTIVITY	2	3.2	9.83E-02

Supplemental Table 8 – Gene Ontology annotation of under-expressed transcripts in the comparison between cultured CD11b$^+$ splenocytes and normal specimens.

GO Term	Gene Count	Gene Percentage	p-value
A. Biological Process			
PHYSIOLOGICAL PROCESS	59	69.4	4.47E-04
ANION TRANSPORT	6	7.1	1.01E-03
PHOSPHATE TRANSPORT	4	4.7	1.26E-03
INORGANIC ANION TRANSPORT	5	5.9	2.48E-03
COMPLEMENT ACTIVATION, CLASSICAL PATHWAY	3	3.5	4.83E-03
CHEMOTAXIS	4	4.7	8.41E-03
TAXIS	4	4.7	8.41E-03
COMPLEMENT ACTIVATION	3	3.5	1.42E-02
HUMORAL DEFENSE MECHANISM (SENSU VERTEBRATA)	3	3.5	1.77E-02
CELLULAR PHYSIOLOGICAL PROCESS	28	32.9	2.16E-02
METABOLISM	39	45.9	2.61E-02
DEVELOPMENT	14	16.5	2.65E-02
REGULATION OF BIOLOGICAL PROCESS	19	22.4	2.91E-02
ION TRANSPORT	8	9.4	3.05E-02
ORGANISMAL PHYSIOLOGICAL PROCESS	13	15.3	3.52E-02
CELL GROWTH AND/OR MAINTENANCE	24	28.2	3.64E-02
RESPIRATORY GASEOUS EXCHANGE	2	2.4	4.89E-02
POSITIVE REGULATION OF TRANSCRIPTION	3	3.5	5.23E-02
POSITIVE REGULATION OF NUCLEOBASE, NUCLEOSIDE, NUCLEOTIDE AND NUCLEIC ACID METABOLISM	3	3.5	5.35E-02
ALCOHOL METABOLISM	4	4.7	5.67E-02
CATABOLISM	9	10.6	5.79E-02
CELL CYCLE	7	8.2	6.72E-02
CELL PROLIFERATION	8	9.4	7.26E-02
PROTEIN METABOLISM	17	20	8.98E-02
POSITIVE REGULATION OF METABOLISM	3	3.5	9.05E-02
FATTY ACID METABOLISM	3	3.5	9.33E-02
B. Molecular Function			
TRANSCRIPTION REGULATOR ACTIVITY	11	12.9	1.21E-02
DNA BINDING	15	17.6	1.64E-02
TRANSCRIPTION COACTIVATOR ACTIVITY	3	3.5	1.67E-02
TRANSCRIPTION FACTOR ACTIVITY	9	10.6	2.76E-02
PRENYLATED PROTEIN TYROSINE PHOSPHATASE ACTIVITY	3	3.5	3.47E-02
MAP KINASE PHOSPHATASE ACTIVITY	2	2.4	3.89E-02
PROTEIN TYROSINE PHOSPHATASE ACTIVITY	3	3.5	5.45E-02
TRANSCRIPTION COFACTOR ACTIVITY	3	3.5	5.55E-02
HYDROLASE ACTIVITY	14	16.5	5.64E-02
PROTEIN BINDING	15	17.6	5.84E-02
TRANSCRIPTION FACTOR BINDING	3	3.5	7.84E-02
CATALYTIC ACTIVITY	26	30.6	8.70E-02

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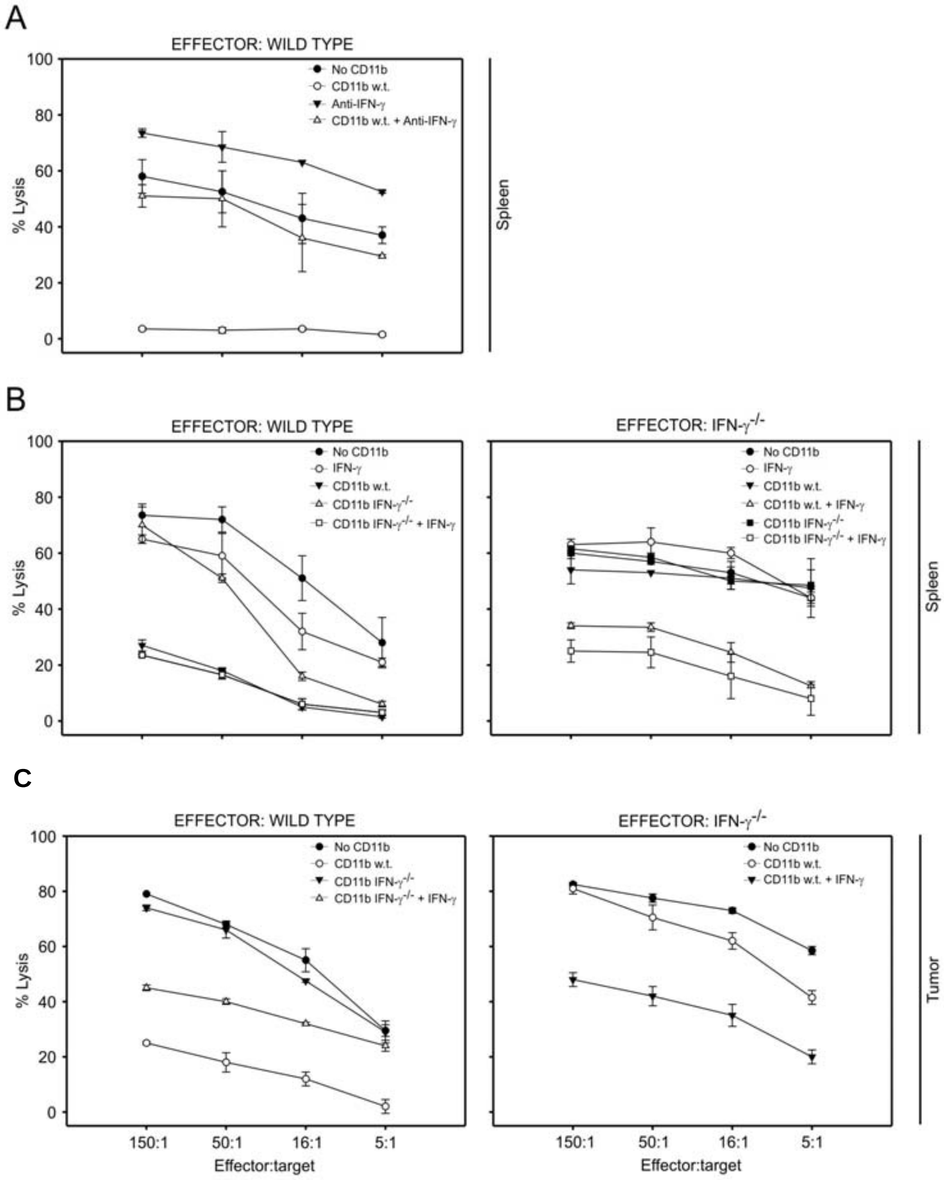

Supplemental Figure 6. Evaluation of IFN-γ requirement for the inhibition of CTL stimulation by spleen and tumor-infiltrating CD11b$^+$ cells. CD11b$^+$ cells sorted from the spleen or tumor of tumor-bearing wild type (w.t.) or IFN-γ$^{-/-}$ knockout mice were added at a final concentration of 3% to an MLC set up with BALB/c effectors, either w.t. or IFN-γ$^{-/-}$, stimulated with an equal number of γ-irradiated C57BL/6 splenocytes, in the presence of anti-IFN-γ mAbs (50 μg/ml, **A**) or IFN-γ (25 ng/ml, **B,C**) added at the beginning and at third day of culture (for a total of 50 ng/ml). Initial E:T ratio was 150:1 and then 1:3 dilutions of the effectors were set up.

Supplemental Table 9. RNA transcripts up-regulated in both CD11b$^+$ sorted from the spleen of tumor-bearing mice cultured for 24 hours and in MSC cell line 2 (MSC2) treated with IL-4 for 24 hours

Gene Name	Gene symbol	Accession number[a]	MSC-2[b]	MSC-2 + IL4	CD11b$^+$ 0 h	CD11b$^+$ 24h
Amylase 1, salivary	*Amy1*	11722	23.44±8.6	7043.82±198.36	42.86±22.35	6094.8±298.99
Matrix metalloproteinase 12	*Mmp12*	17381	123.62±58.06	6284.92±112.06	597.2±109.36	5378.2±258.47
Interferon activated gene 202B	*Ifi202b*	26388	235.12±53.67	1033.44±214.38	129.76±23.57	817.46±203.78
Serum/glucocorticoid regulated kinase	*Sgk*	20393	99.02±35.89	1539±258.21	1457.76±212.65	5174.83±103.89
Annexin A4	*Anxa4*	11746	1977.90±127.58	5037.30±178.95	542.33±47.89	1857.53±99.71
Lectin,galactose binding, soluble 1	*Lgals1*	16852	3195.92±356.12	8022.24±187.56	790.06±203.45	1865.21±173.85

[a] Locuslink accession number

[b] Values are given intensity signal values ± SD from 3 (CD11b cells) or 6 (MSC2 cells) different biological replicates. Signal values assign a relative measure of abundance to the transcript.