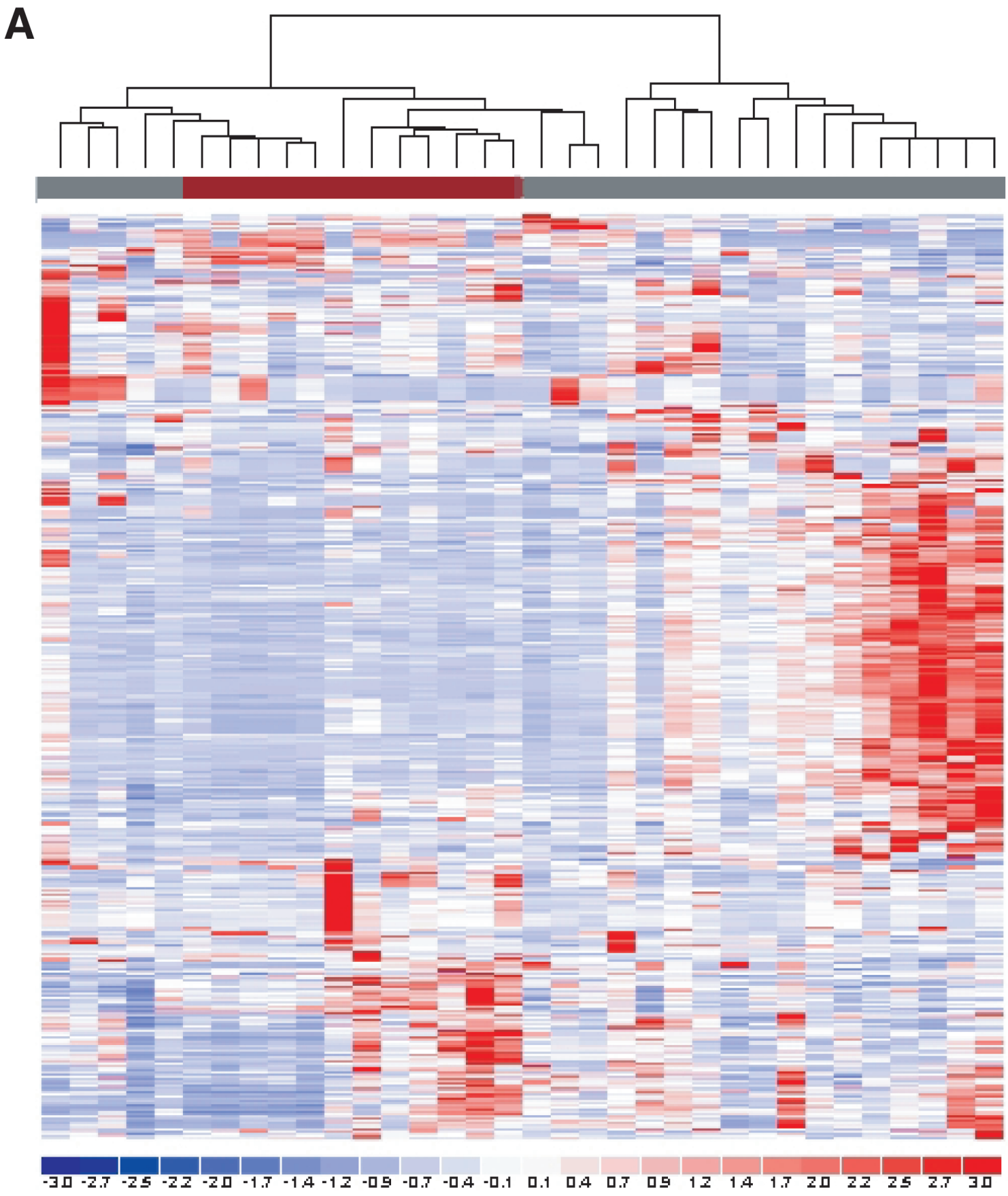
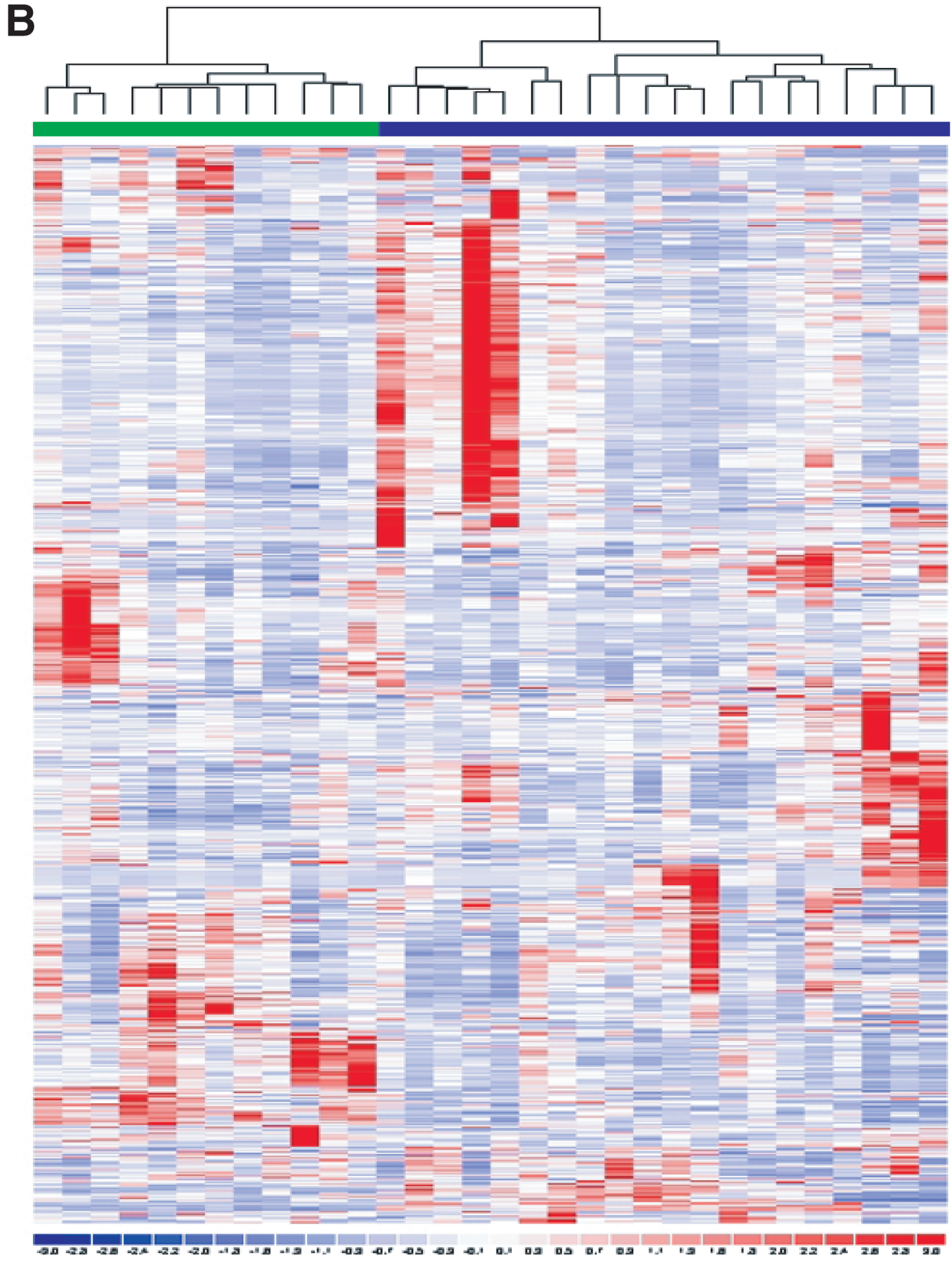
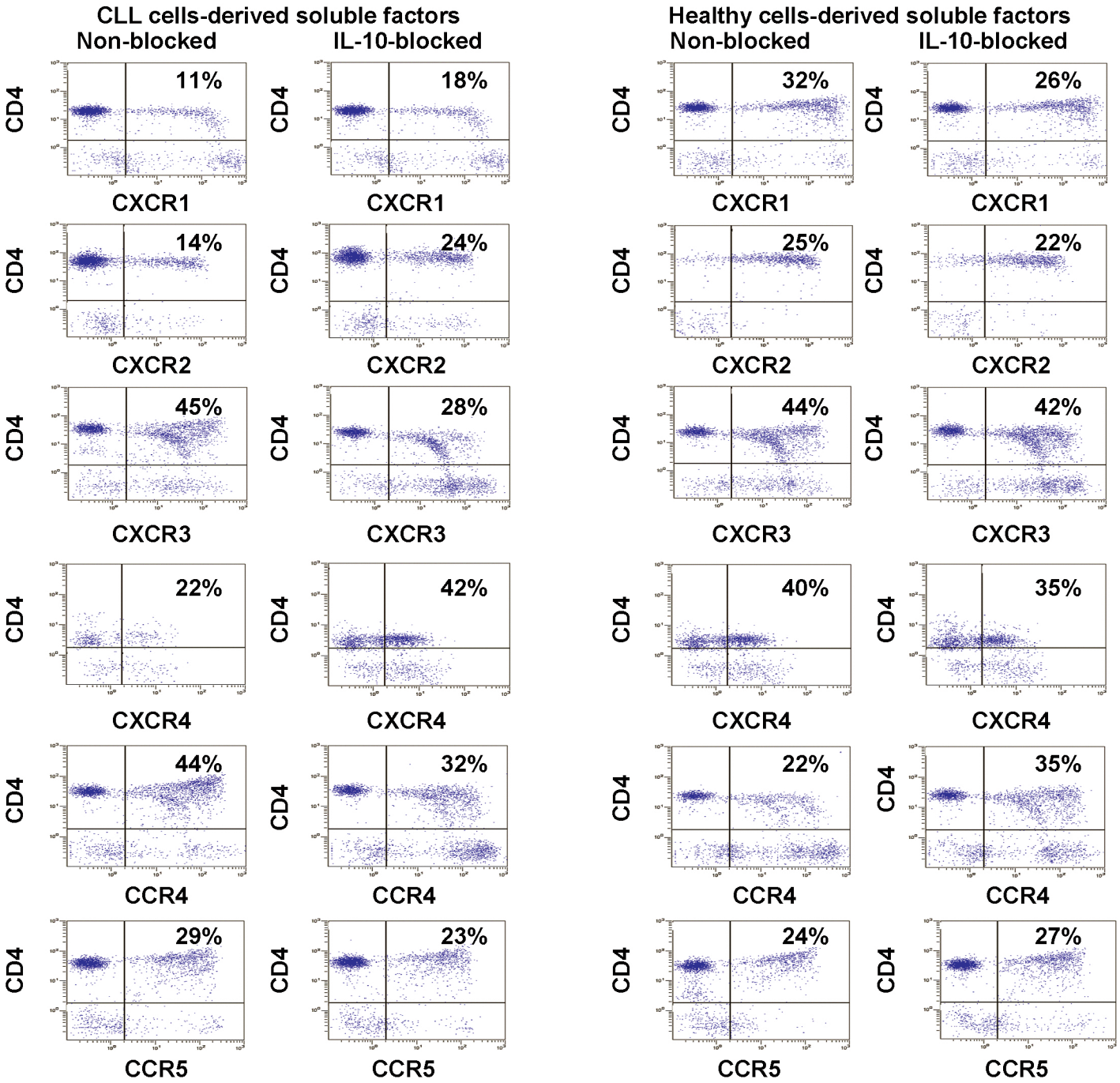
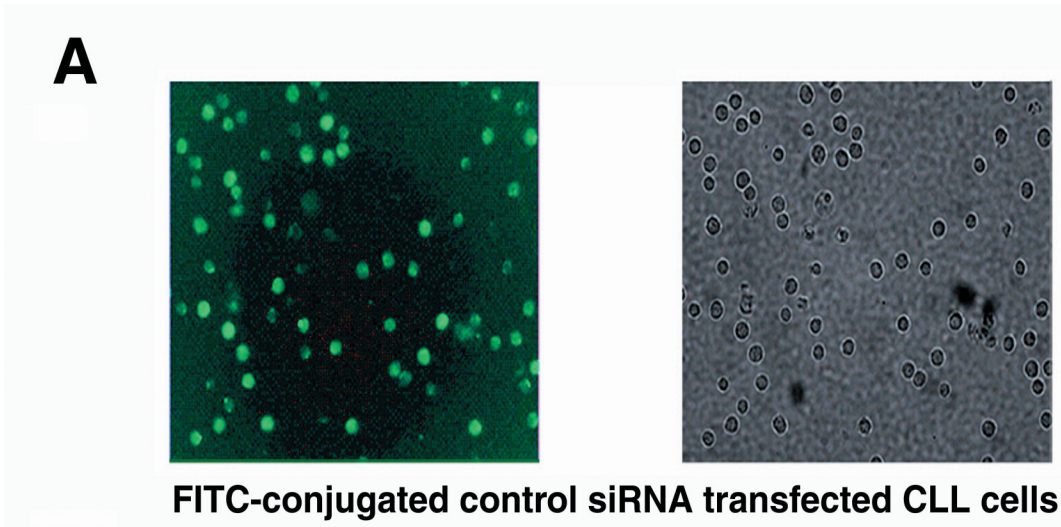

A
-3.0 -2.7 -2.5 -2.2 -2.0 -1.7 -1.4 -1.2 -0.9 -0.7 -0.4 -0.1 0.1 0.4 0.7 0.9 1.2 1.4 1.7 2.0 2.2 2.5 2.7 3.0
CD4 T cells from CLL
CD4 T cells from healthy donors


B
CD8 T cells from CLL
CD8 T cells from healthy donors


CLL cells-derived soluble factors
Non-blocked
IL-10-blocked
Healthy cells-derived soluble factors
Non-blocked
IL-10-blocked
CD4
CXCR1
11%
18%
32%
26%
CXCR2
14%
24%
25%
22%
CXCR3
45%
28%
44%
42%
CXCR4
22%
42%
40%
35%
CCR4
44%
32%
22%
35%
CCR5
29%
23%
24%
27%


A
FITC-conjugated control siRNA transfected CLL cells
B
Relative Vimentin mRNA expression (%)
120
100
80
60
40
20
0
Control siRNA
Vimentin siRNA
Relative IL-10 mRNA expression (%)
120
100
80
60
40
20
0
Control siRNA
IL-10 siRNA
C
Control siRNA
IL-10 siRNA
40kD
37kD
IL-10
GAPDH
Relative IL-10 protein expression
0.4
0.3
0.2
0.1
0
Control siRNA
IL-10 siRNA

Supplementary Table 1.

	Probe Set Number	Hugo Approved Gene Symbol	P value
Cell differentiation and proliferation/survival	215530_at	**FANCA** (Fanconi anemia, complementation group A)	0.049**
	202826_at	**SPINT1** (serine protease inhibitor Kunitz type 1)	0.001**
	201216_at	**C12ORF8** (chromosome 12 open reading frame 8)	0.002**
	205435_s_at	**AMPK1** (adaptor associated kinase 1)	0.025*
	205497_at	**ZNF175** (zinc finger protein 175)	0.018*
	205159_at	**CSF2RB** (granulocyte/macrophage colony stimulating factor 2 receptor-β)	0.018*
	215909_x_at	**MINK** (misshappen/NIK-related kinase)	0.091*
	213028_at	**NFRKB** (nuclear factor related to kappa B binding protein)	0.007*
	215483_at	**AKAP9** (A kinase (PRKA) anchor protein 9)	0.006*
	201864_at	**GDI1** (GDP dissociation inhibitor)	0.002*
	210743_s_at	**CDC14** (cell division cycle 14)	0.001*
Cytoskeleton formation-vesicle trafficking and cytokine secretion	218459_at	**ADIR** (ATP-dependent interferon responsive)	0.012**
	201954_at	**ARPC1B** (actin related protein 2/3 complex, subunit 1B, 41kDa (Arp 2/3))	< 0.001**
	205435_s_at	**AAK1** (adaptor-associated kinase 1)	0.025*
	203410_at	**AP3M2** (adaptor-related protein complex 3, mu2 subunit)	0.010*
	217620_s_at	**PIK3CB** (phosphoinositide-3-kinase catalytic beta polypeptide)	0.003*
	213914_s_at	**SPTBN1** (spectrin beta, non-erythrocytic 1)	0.001*

Supplementary Table 2.

	Probe Set Number	Hugo Approved Gene Symbol	P value
Vesicle trafficking-cytoskeleton formation and intracellular transportation	203315_at	**NCK2** (NCK adaptor protein 2)	0.044**
	218157_x_at	**SPEC1** (small protein effector 1 of CDC42)	0.031**
	206138_s_at	**PIK4CB** (phosphatidylinositol 4-kinase, catalytic, beta polypeptide (PI4K, beta))	0.020**
	201949_x_at	**CAPZB** (capping protein (actin filament) muscle Z-line beta)	0.012**
	221819_at	**RAB35** (RAB35 member of RAS oncogene family)	0.011**
	218320_s_at	**RAB22A**	0.010**
	208728_s_at	**CDC42** (cell division cycle 42 (GTP binding protein, 25kDa))	0.006**
	221754_s_at	**CORO1B** (coronin actin binding protein 1B)	0.005**
	202009_at	**PTK9L** (protein tyrosine kinase 9-like (A6-related protein))	0.004**
	200612_s_at	**AP2B1** (adaptor-related protein complex 2, beta (AP2, beta))	0.002**
	200859_x_at	**FLNA** (filamin A, alpha (actin binding protein 280))	<0.001**
	201954_at	**ARPC1B** (actin-related protein 2/3 complex (Arp 2/3))	<0.001**
	218950_at	**ARAP3** (ARF-GAP, RHO-GAP ankyrin repeat and plekstrin homology domains)	0.045*
	221393_at	**GPR57** (G protein-coupled receptor 57)	0.041*
	34478_at	**XAB2 or RAB11B** (RAB11B member RAS oncogene family, glycoprotein 2)	0.025*
	208416_s_at	**SPTB** (spectrin beta)	0.022*
	215493_at	**AKAP9** (A kinase (PRKA) anchor protein (yotiao) 9))	0.022*
	213022_s_at	**UTRN** (utrophin, homologous to dystrophin)	0.015*
	204789_at	**FMNL** (forming-like)	0.006*
	213729_at	**FNBP3** (formin binding protein 3)	0.003*
	201556_s_at	**VAMP2** (Vesicle-associated membrane protein 2 (synaptobrevin 2))	0.003*
	208452_x_at	**myosin IXB**	0.002*
Cotoxicity activity and Extra-cellular secretion	208315_x_at	**TRAF3** (TNF receptor- associated factor 3)	0.035**
	33304_at	**ISG20** (interferon stimulated gene 20kDa)	0.022**
	202257_s_at	**CD2 antigen** (cytoplasmic tail) binding protein 2	0.018**
	209050_s_at	**RALGDS or RALGEF** (ral guanine nucleotide dissociation stimulator)	0.006**
	208206_s_at	**RASGRP2** (RAS guanyl releasing protein 2 (calcium and Dag-regulated))	<0.001**
	1729_at	**TRADD** (TNFRSF1A-associated via death domain)	<0.001**
	215382_x_at	**TPSB1** (tryptase beta 1)	0.043*
	214325_at	**GP2** (zymogen granule 2)	0.038*
	202806_at	**DBN1** (drebrin 1)	0.032*
	218934_s_at	**Hsp27** (heath shock protein 27)	0.029*
	212425_at	**SCAMP1** (secretory carrier membrane protein 1)	0.017*
	216245_at	**IL-1RN** (interleukin 1 receptor antagonist)	0.010*
	214034_at	**ARTS-1** (type 1 tumor necrosis factor receptor shedding aminopeptidase regulator)	0.046*
	207298_at	**SLC17A1** (solute carrier family 17 member 3)	0.003*
	219229_at	**SLC21A11** (solute carrier family 21 member 11)	0.001*

Supplementary Figure 1. Hierarchical clustering of T cells from patients with CLL and healthy donors by unsupervised statistical analysis. A. Hierarchical clusters of CD4 T cells from patients with CLL and healthy donors. Using dChip analyzer, 620 differentially expressed genes were detected. The filtering criteria required that a gene's coefficient of variation across all samples be between 0.4 and 10 and a gene be called "present" in more than 20% of the arrays. **B**. Hierarchical clusters of non-malignant CD8 T cells from patients with CLL and healthy donors. Using dChip analyzer 839 differentially expressed genes were detected . The filtering criteria required that a gene's coefficient of variation across all samples be between 0.4 and 10 and a gene be called "present" in more than 20% of the arrays.

Supplementary Figure 2. Impact of CLL cell derived soluble factors on chemokine receptor expression in healthy T cells. Analysis of chemokine receptor expression on T cells cultured in presence of sera from CLL or healthy donors with or without IL-10 blocking shown in healthy CD4 cells. The figure represents three experiments ($p<0.05$).

Supplementary Figure 3. Inhibition of IL-10 using RNAi. Non-specific control siRNA, vimentin siRNA or IL-10 siRNA was transfected into CLL cells by electroporation and transfection and inhibition efficiency was determined after 24 hours. **A.** The transfection efficiency was determined by FITC-conjugated siRNA transfection into CLL cells. The fluorescein microscopy picture shows intracytoplasmic FITC-siRNA in CLL cells after electroporation. **B.** The silencing efficiency was detected by quantitative PCR. CLL cells were transfected with non-specific control siRNA, vimentin siRNA or IL-10 siRNA and mRNA expression was normalized by 18S mRNA level. **C.** Inhibition of IL-10 protein expression was analyzed by western immunoblot. The figure shows relative expression

of IL-10 protein in non-specific control siRNA or IL-10 siRNA transfected CLL cells. The figure is representative of three different experiments ($p<0.05$).

Supplementary Table 1. Classification of significantly differentially expressed genes in CD4 T cells by their involvement in specific signaling pathways. Ras-dependent JNK, p38 MAPK cell differentiation, proliferation and survival pathways and cytoskeleton formation, vesicle trafficking and cytokine secretion pathways were represented by selected genes that were identified by gene expression profiling in CD4 T cells from CLL compared to healthy donors. Comparison of expression level between CLL and healthy CD4 cells were detected using a supervised analysis ($p<0.05$). (**) increased gene expression and (*) decreased gene expression in CD4 cells from CLL compared to healthy donors.

Supplementary Table 2. Classification of significantly differentially expressed genes in CD8 T cells by their involvement in specific signaling pathways. Cytoskeleton formation, vesicle trafficking and intracellular transport and cytotoxic activity, and extra-cellular secretion pathways were represented by selected genes identified as differentially expressed by gene expression profiling in CD8 T cells from CLL compared to healthy donors. Comparison of expression level between CLL and healthy CD4 cells were detected using a supervised analysis ($p<0.05$). (**) Increased gene expression and (*) decreased gene expression in CD8 cells from CLL compared to healthy donors.