Figure S1. Summary of study samples
A total of 24 treatment naïve patients were included, in 12 patients cells from all 3 anatomic compartments were available, in 10 patients these were obtained on the same day, in 2 patient the BM and LN samples were collected on different days, each paired with a PB sample.

Figure S2. Unsupervised hierarchical clustering of all 62 arrays
Probesets with no expression signal in any of the samples were removed. Patients are numbered as in table 1, compartmental origin: BM, red; LN, blue; PB, green.

Figure S3. Expression of CXCR4 on CLL cells in PB and BM
Comparative analysis of PB, BM aspirate (BMA), and BM biopsy (BMB) samples. Cells from BM biopsy were eluted in vitro by crushing and flushing of the core. The % CXCR4 expression above isotype control for $CD19^+$ gated cells is shown. Samples from the same patient are connected by lines.

Figure S4. UM-CLL cells have a higher E2F score than M-CLL cells
The E2F was computed individually as the average of the mRNA expression level of the leading edge genes for each LN sample. Comparison between M-CLL (n=5) and U-CLL cells is by Student’s t-test.

Figure S1

PB	BM	LN	Patients
14	12	12	**12**
7	7		**7**
5		5	**5**
26	**19**	**17**	**24**

Figure S2

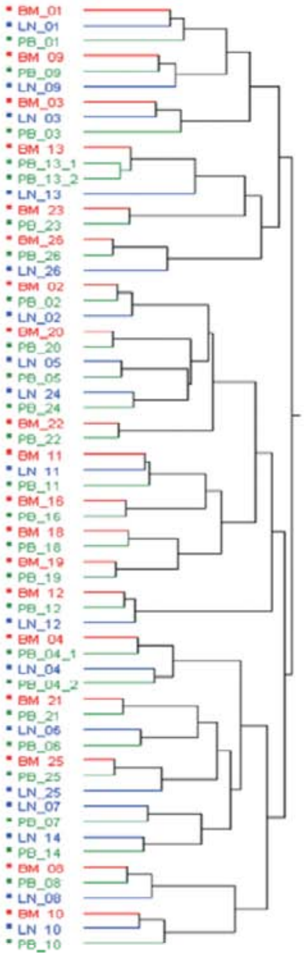

Figure S3

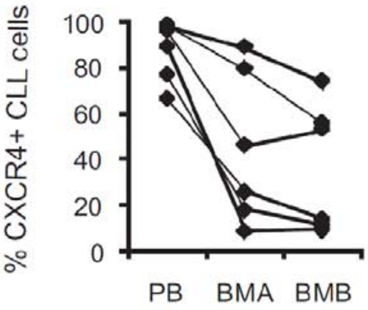

Figure S4