Supplementary Information

Longitudinal Multiplexed Measurement of Quantitative Proteomic Signatures in Mouse Lymphoma Models Using Magneto-Nanosensors

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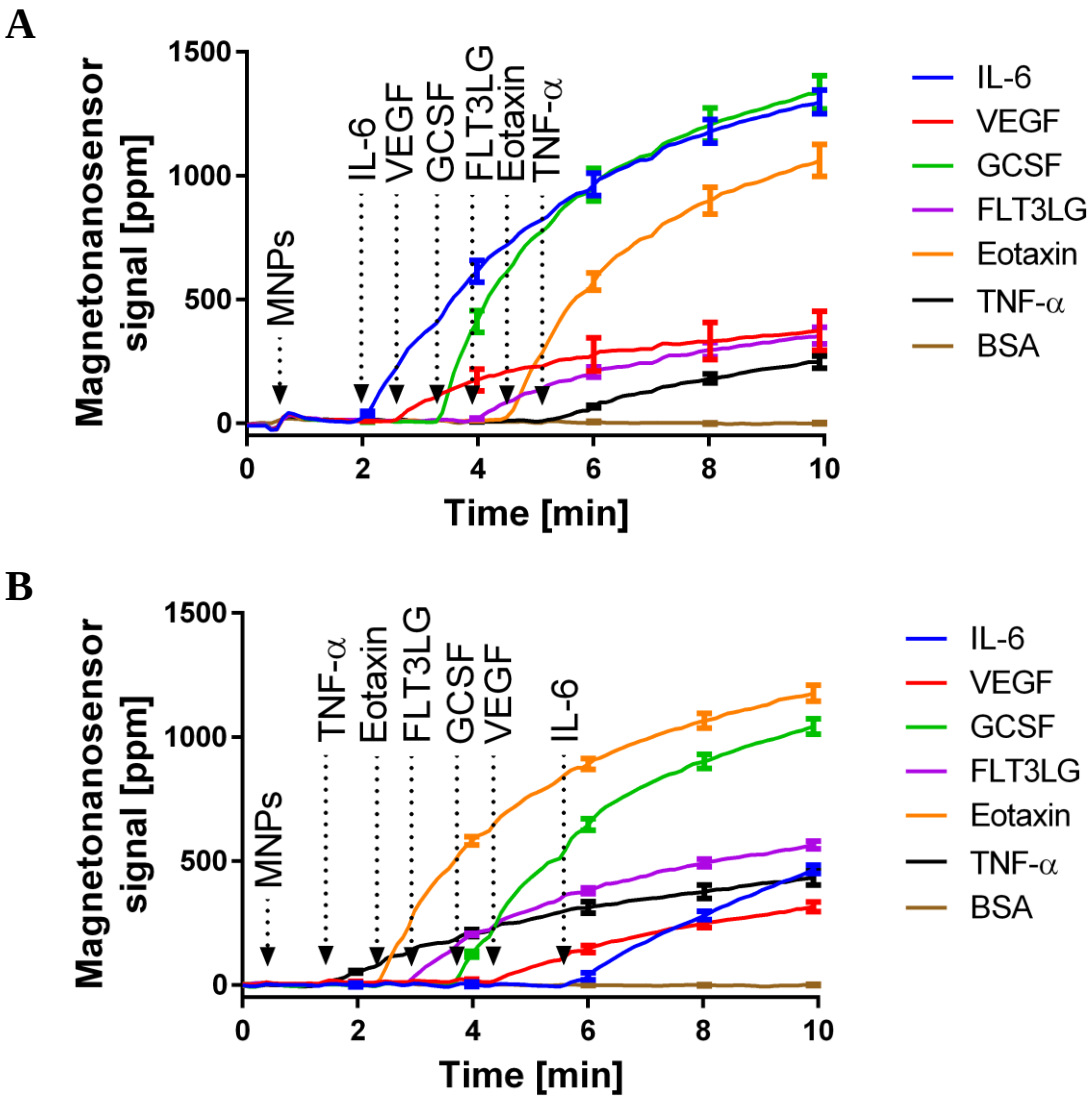

Figure S1. Cross-reactivity tests (A) A chip was incubated with all proteins (GCSF, TNF-α, Eotaxin, FLT3LG, IL-6, and VEGF) at 100 ng/mL. MNPs were added to the chip before adding detection antibodies. One kind of detection antibodies was sequentially added to the chip and mixed as indicated by arrows. The signals were monitored in real-time from the sensors coated with different antibodies (blue: IL-6, red: VEGF, green: GCSF, purple: FLT3LG, orange: Eotaxin, black: TNF-α, brown: BSA). (B) Another chip with the same proteins was probed with the same detection antibodies, but the opposite order of addition. Both cases did not display any significant cross-reactivity.

Table S1. Parameters of 4-PL regression

	IL-6	GCSF	Eotaxin	TNF-α	FLT3LG	VEGF
Max	2824	3640	2715	1933	2620	2829
Min	52.67	71.04	23.17	5.786	6.672	5.971
IC50	0.5449	0.6206	1.213	0.4883	1.2	2.438
Hill slope(α)	0.916	0.8377	1.134	0.9956	1.332	1.079

$$\text{Signal} = Max + \frac{Min - Max}{1 + \left(\frac{c}{IC50}\right)^{\alpha}}$$, where *c* is a concentration of each protein.

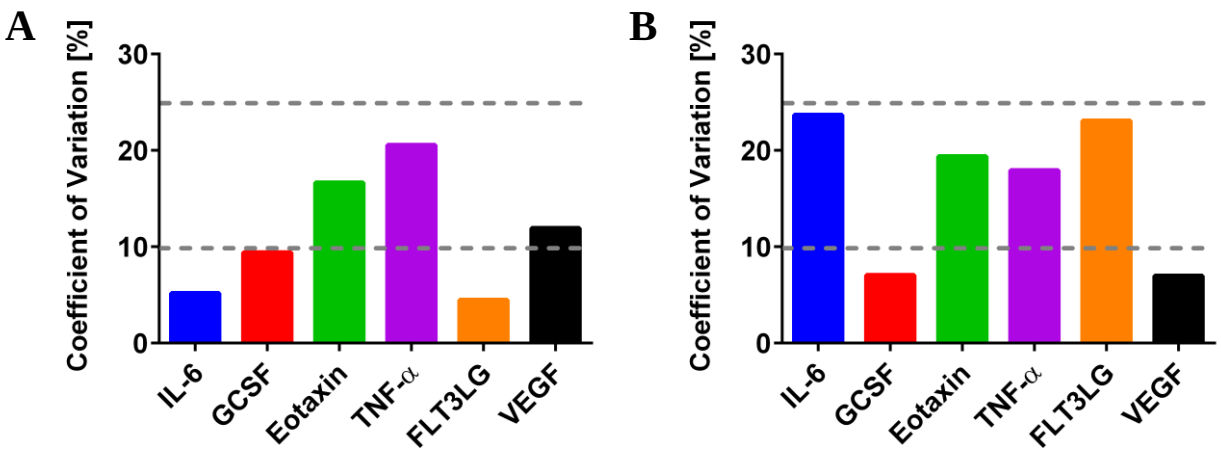

Figure S2. (A) A QC sample was aliquoted and frozen before the measurements, and each aliquot was used for each measurement day. The QC sample was measured with 3 different stations on 3 different days, and the CV for each assay was evaluated based on 9 data points. (B) The same QC sample was measured with a designated station on 12 different days, and the CVs of assays were calculated using 12 data points. 10% and 25% are marked with gray dashed lines.

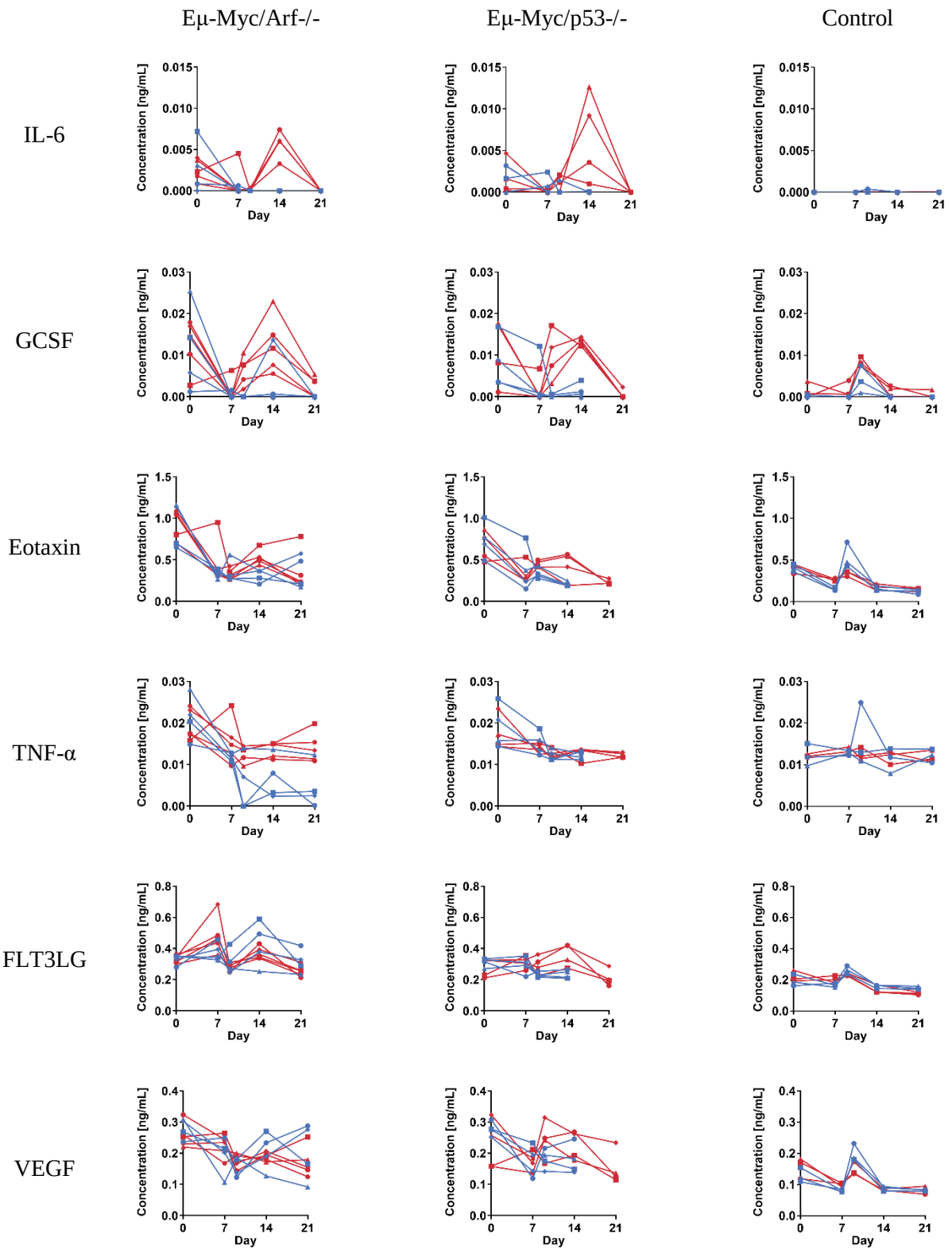

Figure S3. Protein profiles converted into the concentrations. The protein profiles shown in Figure 3 (magnetonanosensor signals) are converted into the concentrations using the titration curves shown in Figure 1D.