Preprogrammed capillarity to passively control system-level sequential and parallel microfluidic flows

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Fig. S1. (a) Diagram showing $P_{\text{well } n}$ and node pressure ($P_{\text{node } m}$). The difference between $P_{\text{well } n}$ and $P_{\text{node } m}$ drives a flow. The node-to-well volume flow rate $Q_{\text{node} \rightarrow \text{well}} = C_i (P_{\text{node } m} - P_{\text{well } n})$ is equal to the increasing rate of the liquid drop volume $\frac{dV_n}{dt} = \frac{\pi (r_n^2 + h_n^2)}{2} \frac{dh_n}{dt}$, where $V_n$ is the volume of the convex drop in the well $n$, and $r_n$ and $h_n$ are the well radius and the drop height, respectively. Thus, $\frac{dh_n}{dt} = \frac{2C_i(P_{\text{node } m} - P_{\text{well } n})}{\pi (r_n^2 + h_n^2)}$. $P_{\text{well } n}$ is determined by the drop shape as $P_{\text{well } n} = \frac{4\sigma h_n}{h_n^2 + r_n^2}$, where $\sigma$ is the surface tension of the drop. (b) Diagram for $P_{\text{node } m}$. Analogous to Kirchhoff’s current law, the sum of the volume flow rates coming into node $m$ is 0. That is, $\sum_{i=1}^{j} C_i (P_{\text{node } m} - P_i) = 0$, where $P_i$ is either well or another node pressure. Thus, $P_{\text{node } m}$ is $\frac{\sum_{i=1}^{j} C_i P_i}{\sum_{i=1}^{j} C_i}$. The two types of equations for $\frac{dh_n}{dt}$ and $P_{\text{node } m}$ constitute simultaneous differential equations of the entire fluidic network, and they are solved numerically (MATLAB, Mathworks).
**Fig. S2.** Adjustment of contact angle for the device bottom layer. The contact angle was measured on surface-treated silicon for phosphate buffered saline (PBS) solution. The results show that the surface coated with the xylene-to-HMDS ratio of 400:1 was hydrophilically stable and maintained an appropriate contact angle value, which did not result in the edge wetting of a channel cross-section. Thus, we used the surface for the device.

**Figure S3.** Contact angles of various immunoassay solutions on a stable hydrophilic surface (xylene : HMDS = 400:1). Each solution was measured in triplicate. P11 and P12 were human plasmas from different donors. Ab1 and Ab2 are 6.7 µM C-reactive protein (CRP) antibody and 600 nM FITC-labeled CRP antibody (Bethyl Laboratory), respectively.
**Fig. S4.** Disturbance of sequential flows. (a) Schematic of 3-well system. (b) Photographs of sequential flows. Solutions 1, 2, and 3 were sequentially dispensed in wells 1, 2, and 3, respectively, and their initial well pressures ($P_1$, $P_2$, and $P_3$) were 7, 127 and 127 Pa, respectively. In step 3, solution 3 was dispensed in well 3 after $P_1$ and $P_2$ equilibrated. Note that solution 2 reflowed in step 3. (c) Fluidic circuit diagram of step 3 of (b). Each channel’s (ch $i$) fluidic conductance (unit: m$^5$ N$^{-1}$ s$^{-1}$) is shown in the diagram.

**Fig. S5.** Microfluidic circuit diagram showing entire fluidic network. The model includes well pressures ($P_i$) and fluidic channels (Ch $i$). Each channel’s fluidic conductance (unit: m$^5$ N$^{-1}$ s$^{-1}$), which is
the inverse of fluidic resistance, is noted in the diagram. In the $k$th step, a solution in an inlet well starts to flow upon turning on the corresponding switch ($SW_k$) by a timing channel.