Electronic Supplementary Information (ESI)

Label-free breast cancer detection using fiber probe-based Raman spectrochemical biomarker-dominated profiles extracted from a mixture analytic algorithm

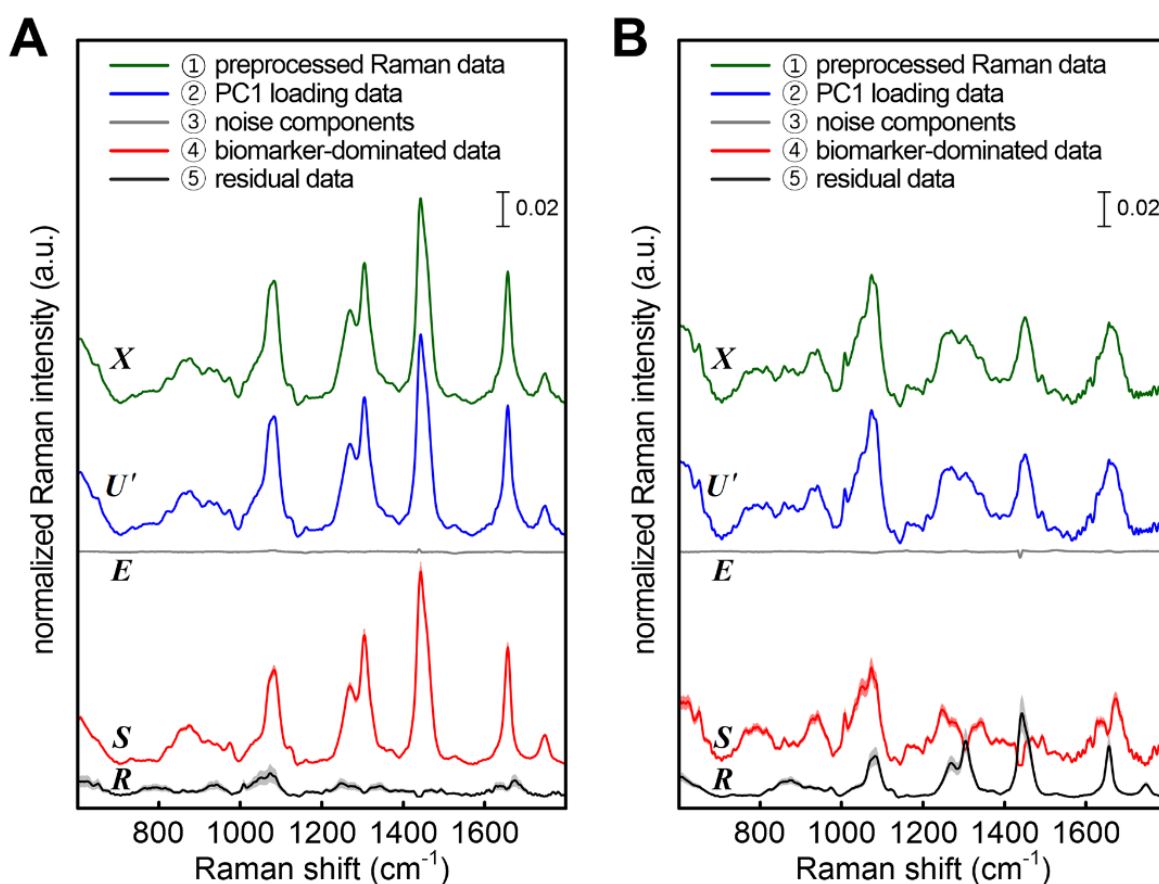■ **Procedure of the PCMA mixture analytic algorithm**

Fig. S1　The procedure of the PCMA mixture analytic algorithm to find the biomarker-predominated data for (A) normal and (B) cancer groups. Each waveform indicates the representative Raman spectrochemical spectrum in each step where ① X denotes $m \times n$ preprocessed Raman spectrochemical data sets, ② U' denotes the PC loading matrix, ③ E denotes the noise components ($X - U'$), ④ S denotes the biomarker-dominated PCMA Raman spectrochemical data, and ⑤ R denotes the residual matrix ($U' - S$).

■ Signal-to-noise ratio (SNR) of the Raman peaks
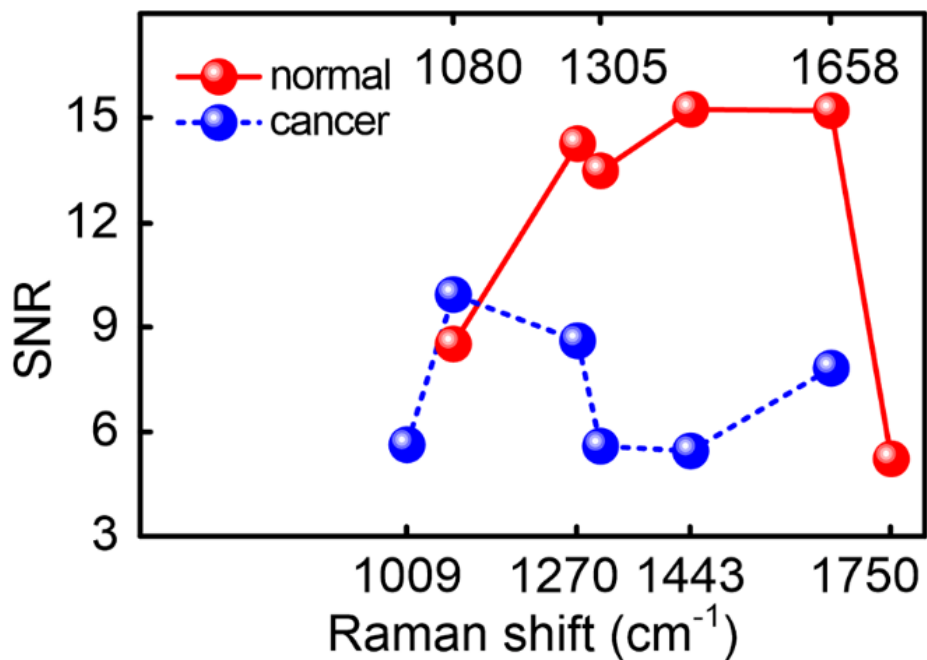

Fig. S2   The SNR of unique Raman peaks associated with candidate biomarkers for screening the presence of tumors in breast tissues, such as 1009, 1080, 1270, 1305, 1443, 1658, and 1750 cm^{-1}.