中文題目：探索 SAA 變異體用於胃癌檢測
英文題目：Exploring the expression bar code of SAA variants for gastric cancer detection
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Background: We reported an integrated platform to explore serum protein variant pattern in cancer and its utility as a new class of biomarker panel for diagnosis.

Method and Material: On the model study of serum amyloid A (SAA), we employed nanoprobe-based affinity mass spectrometry for enrichment, identification and quantitation of SAA variants from serum of 105 gastric cancer patients in comparison with 54 gastritis patients, 54 controls, and 120 patients from other cancer.

Result: The result revealed surprisingly heterogeneous and most comprehensive SAA bar code to date, which comprises 24 SAA variants including SAA1- and SAA2-encoded products, polymorphic isoforms, N-terminal–truncated forms, and three novel SAA oxidized isotypes, in which the variant-specific peptide sequence were also confirmed by LC-MS/MS. A diagnostic model was developed for dimension reduction and computational classification of the 24 SAA-variant bar code, providing good discrimination (AUC = 0.85 ± 3.2E−3) for differentiating gastric cancer group from gastritis and normal groups (sensitivity, 0.76; specificity, 0.81) and was validated with external validation cohort (sensitivity, 0.71; specificity, 0.74).

Conclusion: Our platform not only shed light on the occurrence and modification extent of under-represented serum protein variants in cancer, but also suggested a new concept of diagnostic platform by serum protein variant profile.