We used iTRAQ approach to identify the proteins in **Sample A** and **Sample B**. In brief, both **Sample A** and **Sample B** were trypsin digested in solution. The peptides from **Sample A** and **Sample B** were labeled by iTRAQ 114 and 117, respectively. After labeling, peptides were combined and subjected to strong cation exchange and reversed phase 2D-LC separation. The eluted peptides were mixed with matrix-assisted laser desorption ionization (MALDI) matrix and spotted onto Opti-TOF MALDI target plates (ABI). Peptide analysis was performed on a 4800 Proteomics Analyzer tandem mass spectrometer (ABI) in a data-dependent fashion, where MS spectra (*m*/*z* 800–4000) were acquired in positive ion mode with internal mass calibration. Fifteen most intense MS ions (S/N ratio > 25) per spot were selected for subsequent MS/MS analysis in 1 keV mode. GPS Explorer software (v. 3.5, ABI) was used for protein identification. The proteins containing at least two peptides with C.I. value over 99% are considered to be identified. Six proteins were found in both **Sample A** and **Sample B**. Based on the criteria we used, we did not find the difference between two samples.

	Acc. No.	Protein Name	Coverage (50%)	A	B
1	RAGE_HUMAN	Advanced glycosylation end product-specific receptor precursor	71.04%	●	●
2	K2C1_HUMAN	Keratin, type II cytoskeletal 1	43.79%	●	●
3	K1C10_HUMAN	Keratin, type I cytoskeletal 10	33.05%	●	●
4	K1C9_HUMAN	Keratin, type I cytoskeletal 9	42.70%	●	●
5	K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	43.57%	●	●
6	K2C5_HUMAN	Keratin, type II cytoskeletal 5	11.36%	●	●