

Supplementary materials

Table S1. Identified significantly changed metabolites between the RA cold pattern and the RA heat pattern.

| Metabolite | Fold change ^a (heat/cold) | <i>p</i> ^b | Data origin |
|---|---|-----------------------|-------------|
| Glycochenodeoxycholic acid ^c | 2.0 | 0.025 | LC/MS |
| PC 1-acyl 32:1 ^c | 1.4 | 0.03 | LC/MS |
| PC 1-acyl 32:0 ^c | 1.2 | 0.009 | LC/MS |
| PC 1-acyl 34:1 ^c | 1.1 | 0.004 | LC/MS |
| PC 1-acyl 38:5 ^c | 0.8 | 0.049 | LC/MS |
| Urea ^c | 0.8 | 0.016 | GC/MS |
| Proline | 1.4 | 0.049 | GC/MS |
| FFA C18:0 | 0.9 | 0.045 | GC/MS |

^a Fold change was calculated from the mean values of each group. ^b *p* values were calculated from the Student's *t*-test. ^c Potential biomarkers were selected based on the threshold of VIP>1.0 and *p*<0.05.

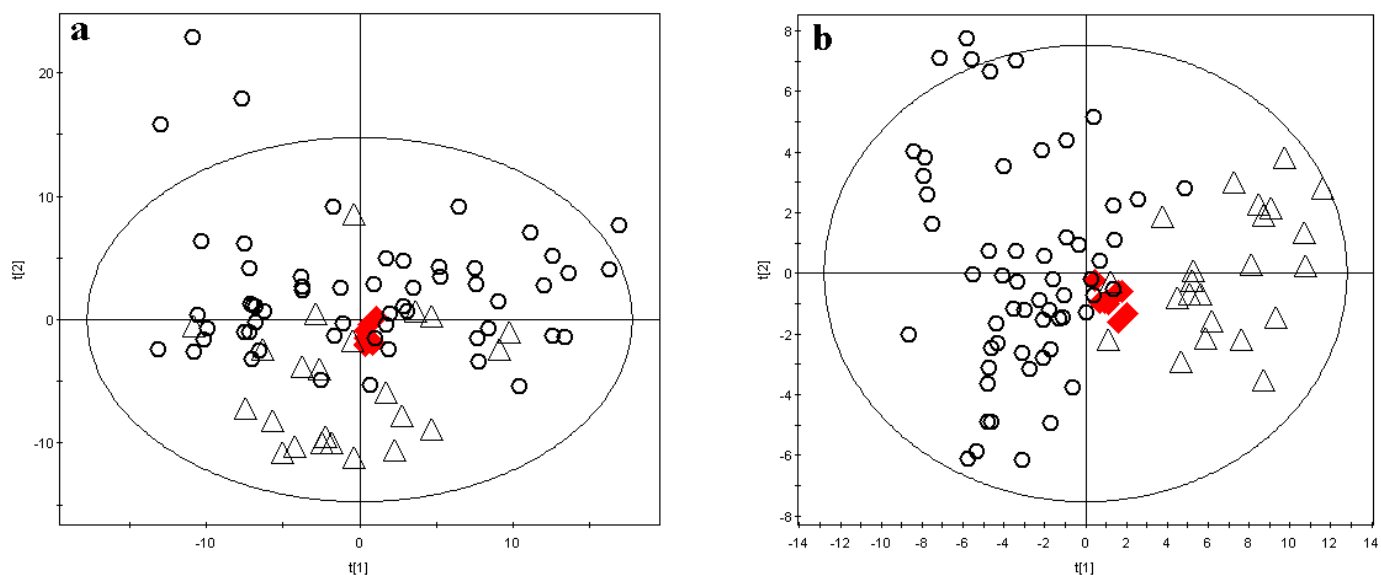


Figure S1 PCA score plots based on the data from all samples. (a) PCA model generated from LC/MS (8 components, $R^2X=0.60$), (b) PCA model generated from GC/MS (6 components, $R^2X=0.61$). (◆): QCs, (Δ): healthy controls, (○): RA patients.