

[도1]

PMAS process

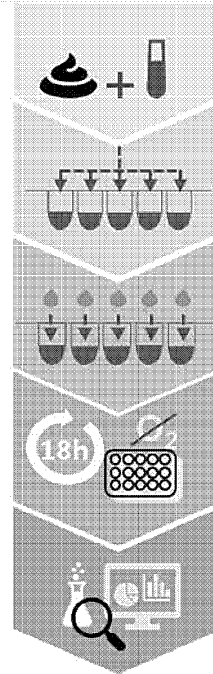
분변샘플을 PMAS배지와
혼합하여 균질화

시료를 동일 양으로 분주
(분변 내 장내 미생물 복제)

후보 물질을
분주된 시료에 처리

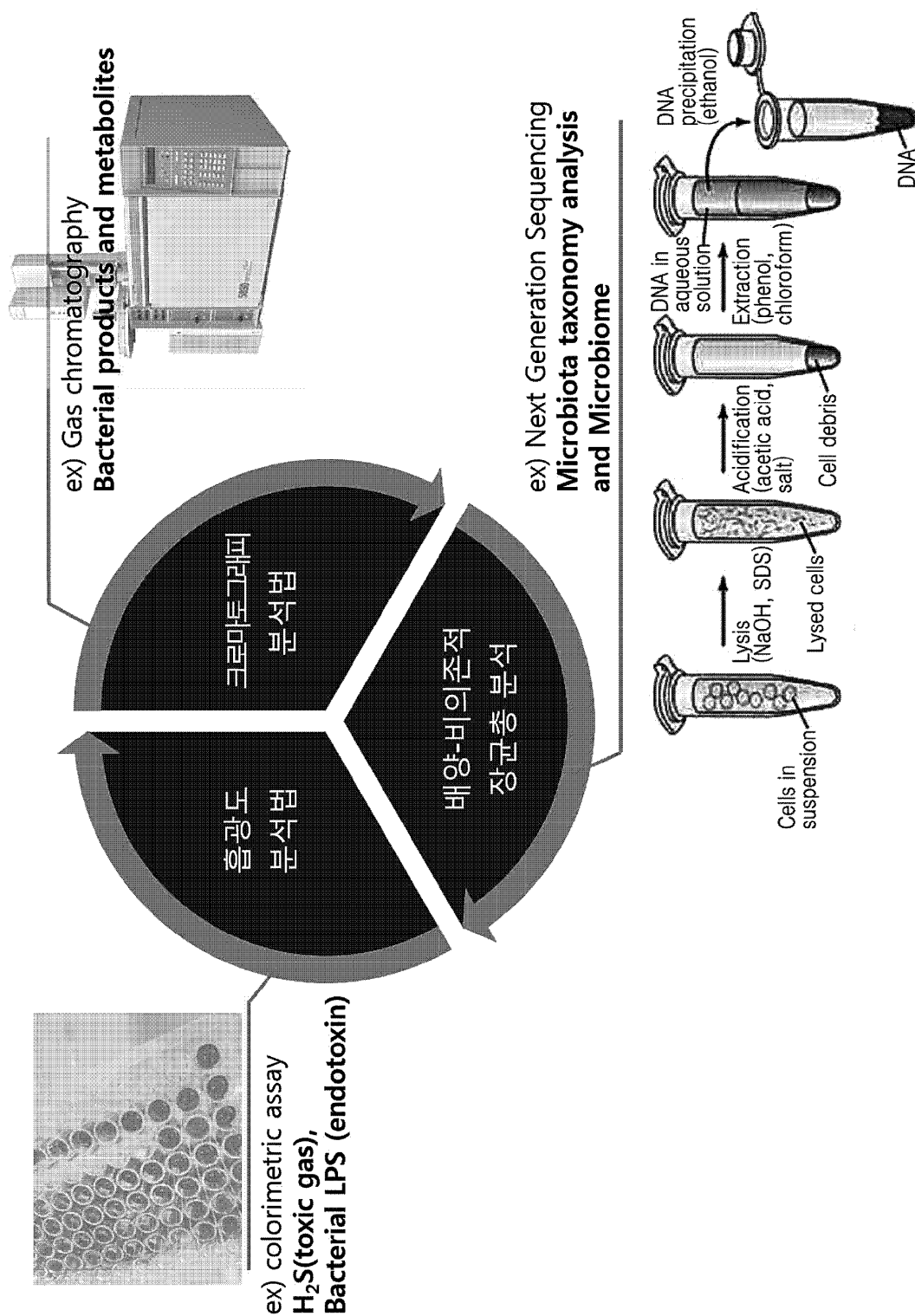
혐기 환경에서 일정 시간
배양

배양 후 각 well의 결과를 분석
- gut microbiota (NGS)
- short-chain fatty acids (GC)

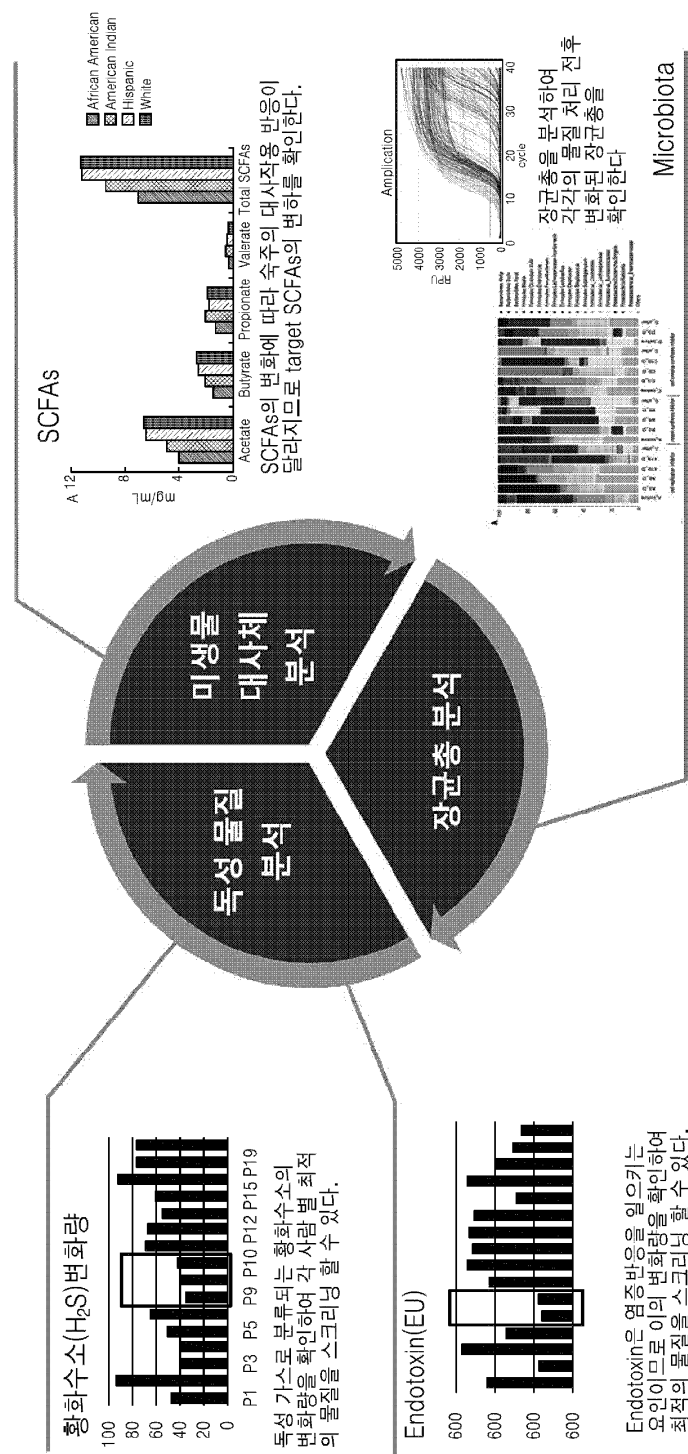


여러 후보 물질을 처리한 PMAS배양 과정 후의
장내 환경 지표 개선 여부 비교
→ 각 분변 내 장내 미생물 기반으로
장내 환경을 개선시키는 후보물질 스크리닝

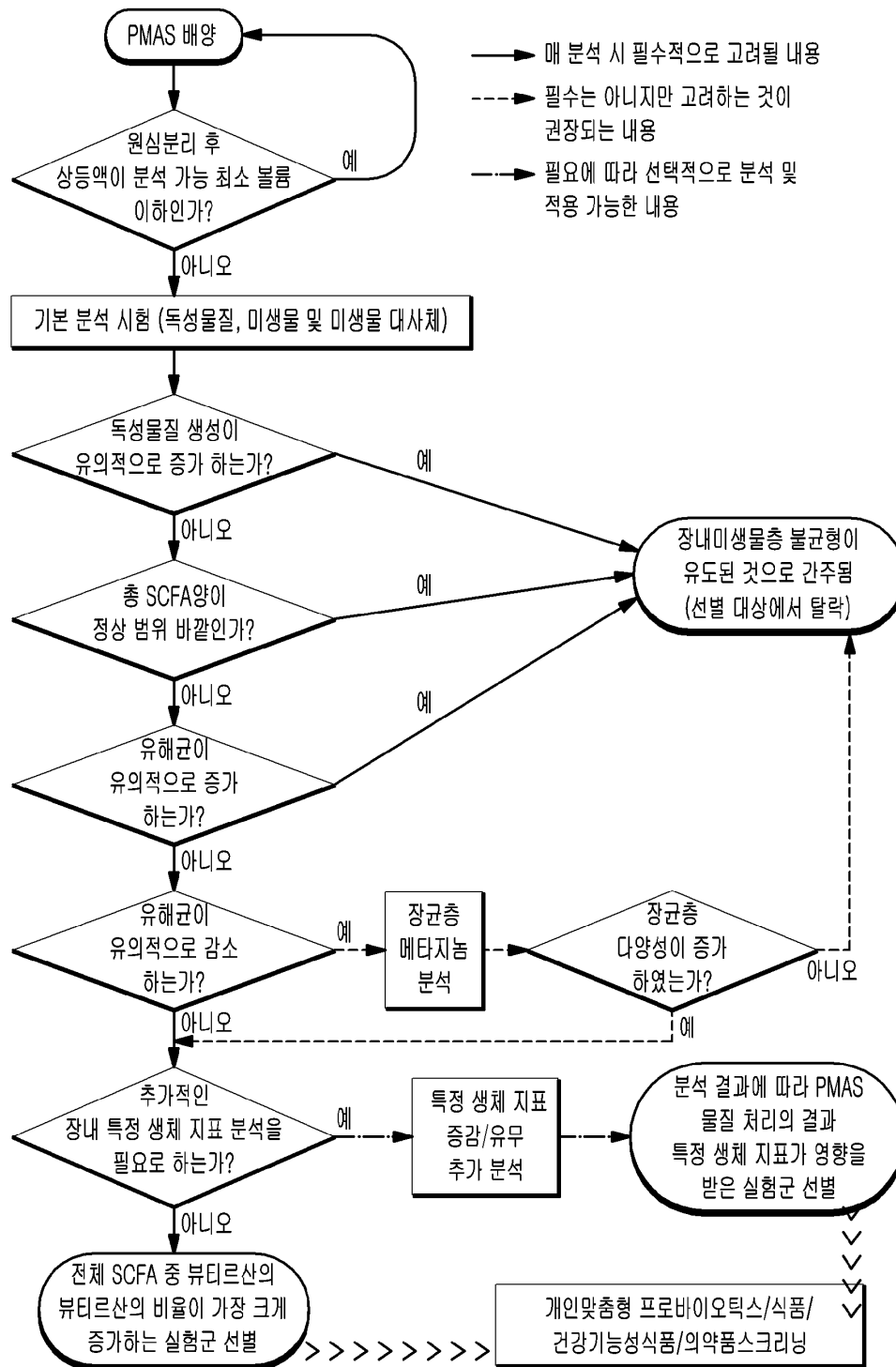
[도2]



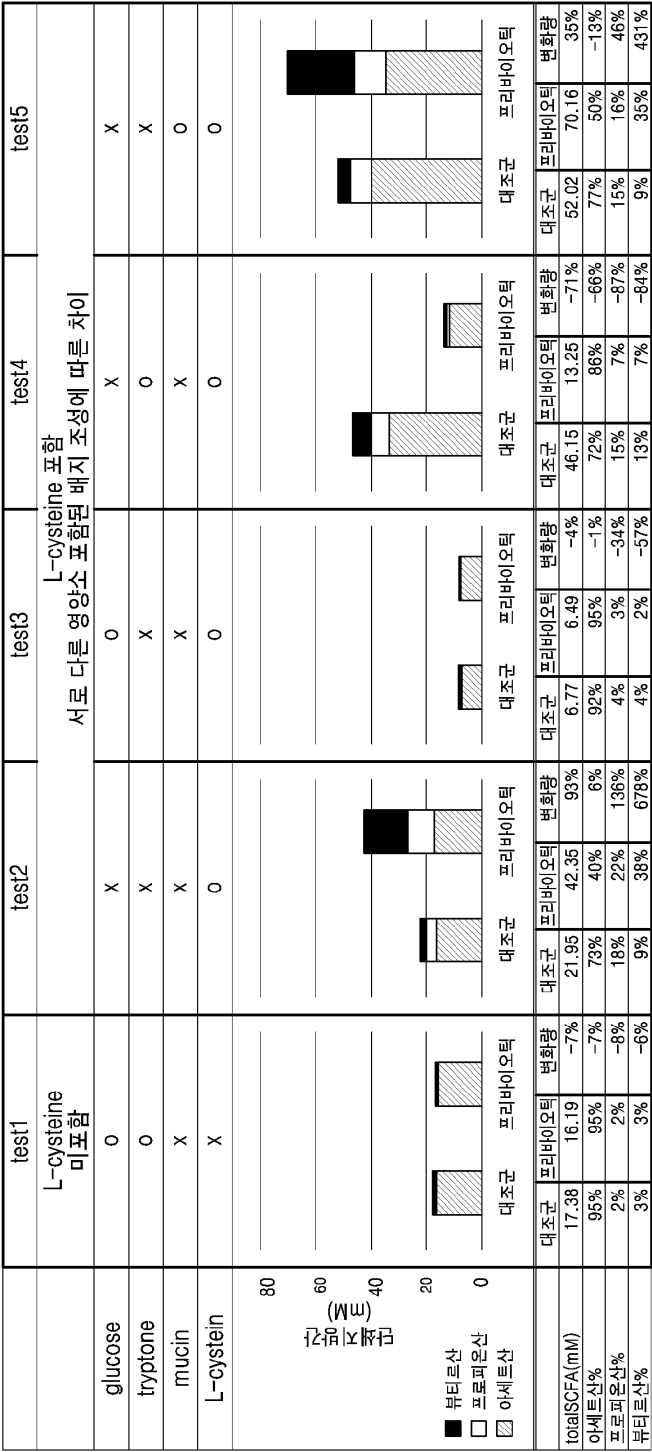
[도3]



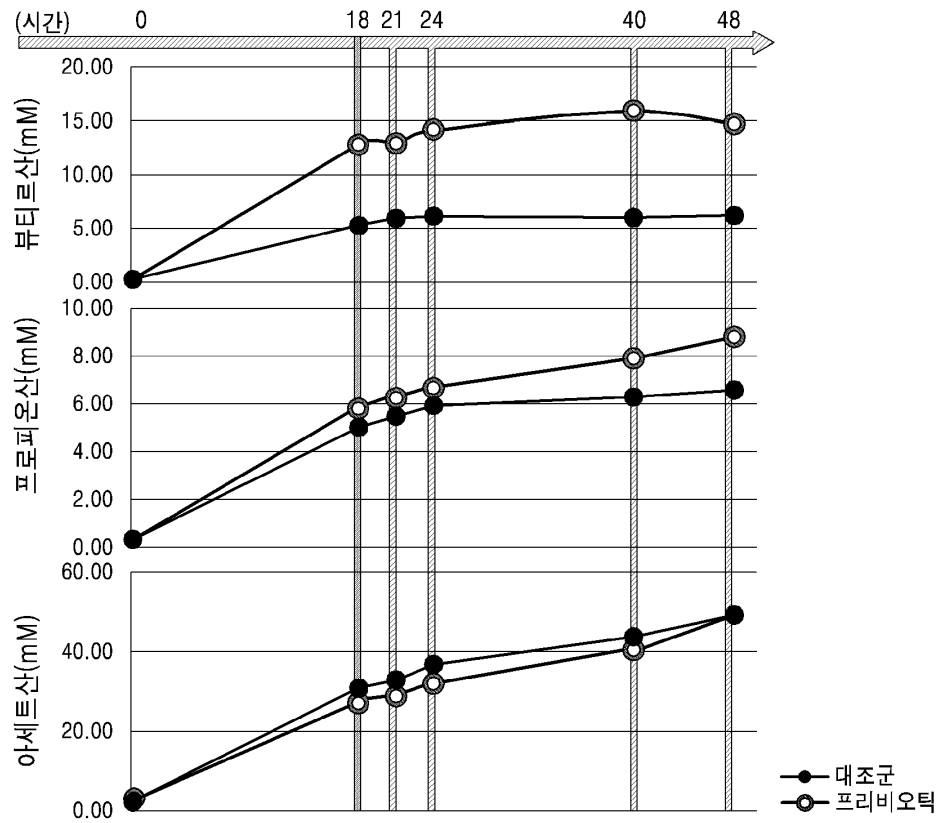
[도4]



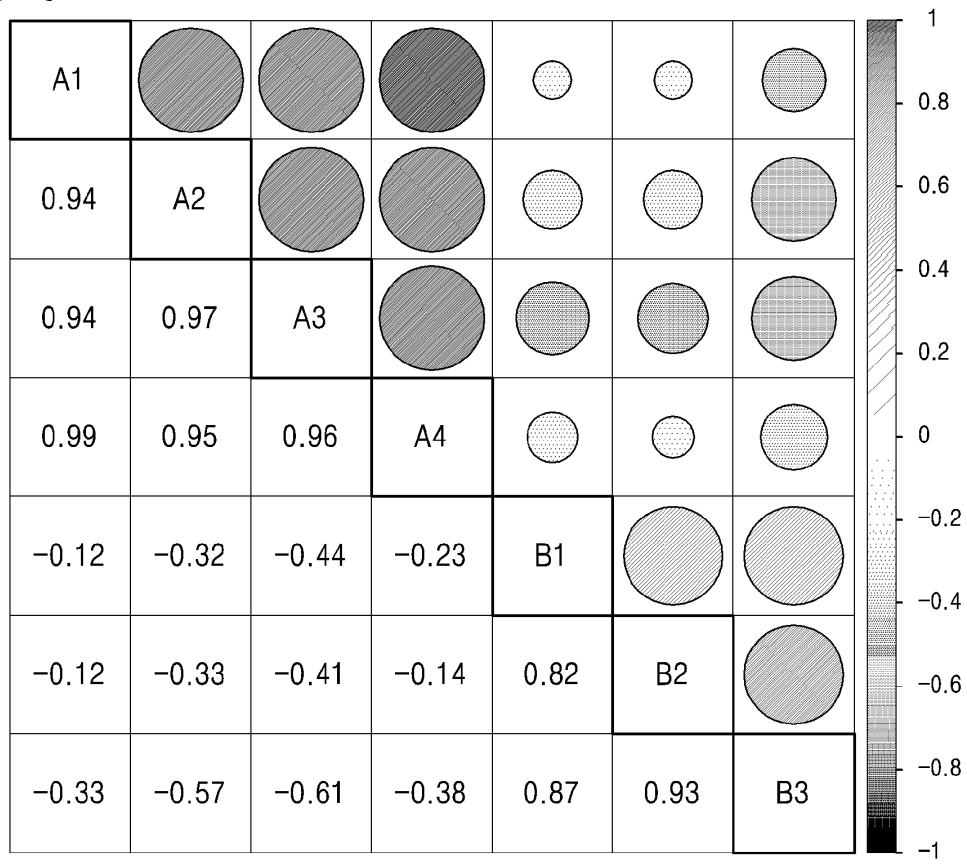
[도5]



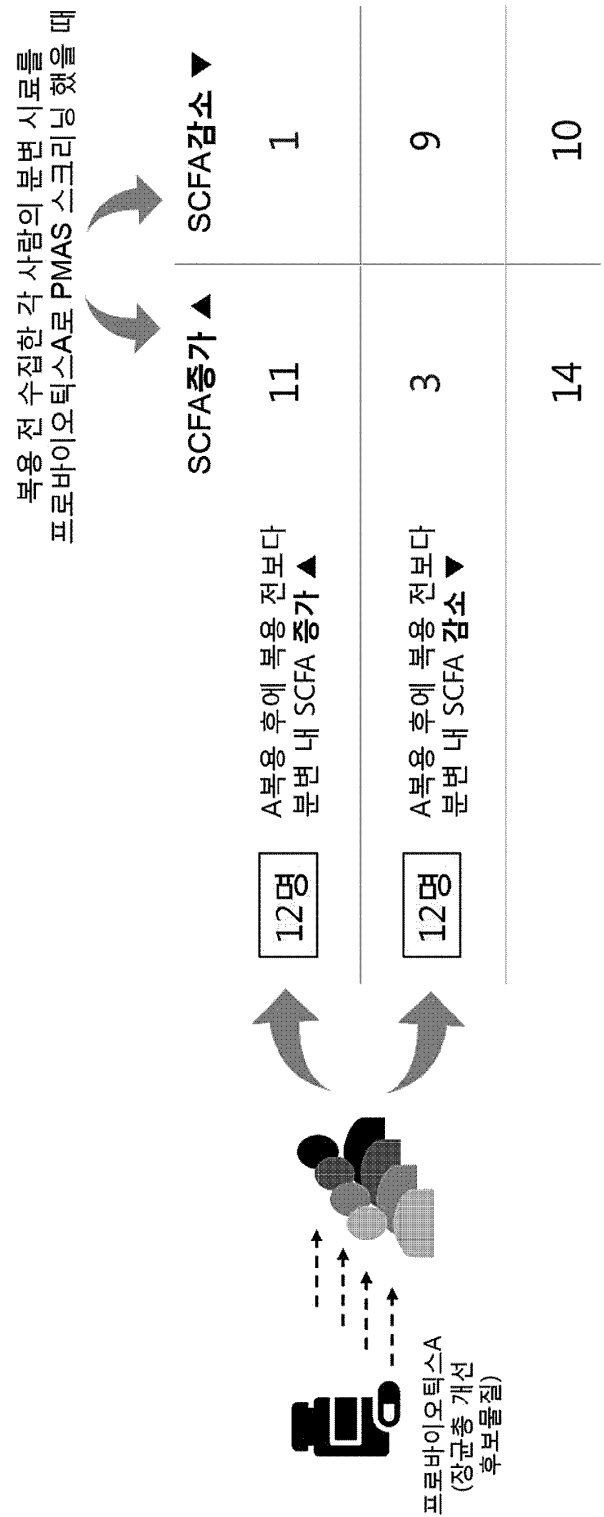
[도6]



[도7]

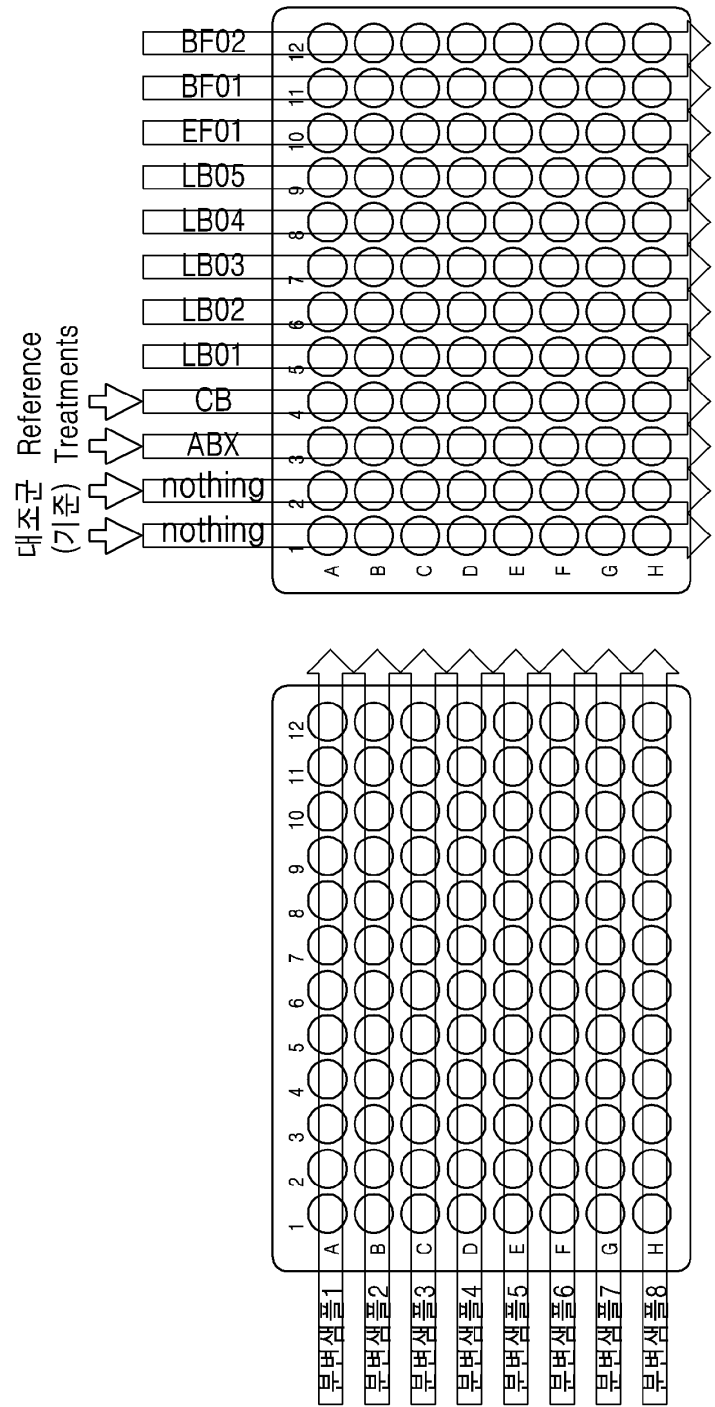


[도8]



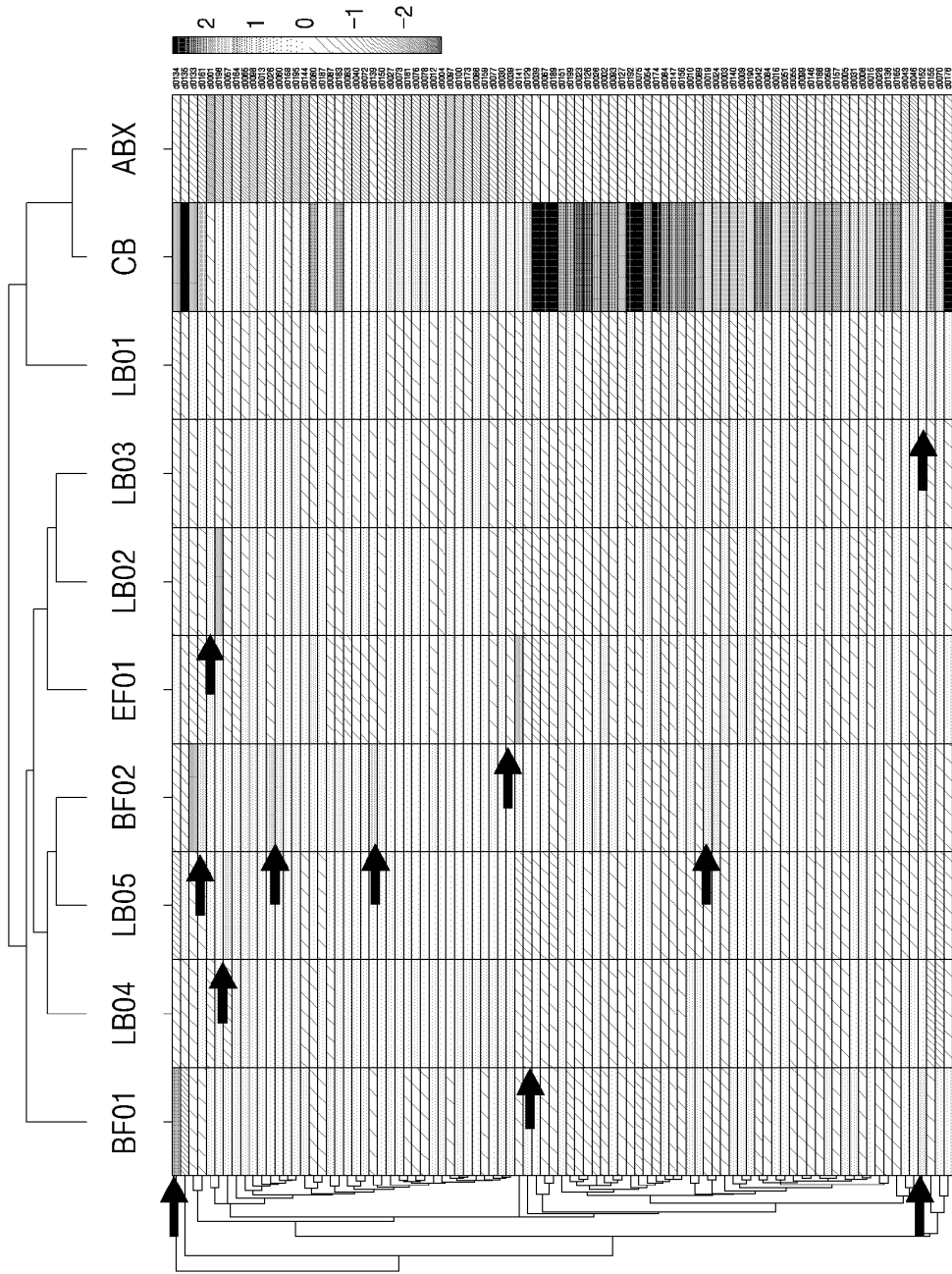
1. PMAS에서 SCFA증가했을 때 실제로도 SCFA증가인 경우 $11/14 = 0.79$
2. PMAS에서 SCFA감소했을 때 실제로도 SCFA감소인 경우 $9/10 = 0.9$

[도9]



ABX 항생제 혼합; CB *Clostridium butyricum* MIYAIRI 588; LB *Lactobacillus* strains;
EF *Enterococcus faecium* strain BF *Bifidobacterium* strains

[도 10]



Heatmap showing the correlation of fecal samples (feces1 to feces7) with bacterial taxa (LB03, BF02, LB01, CB, LB04, EF01, ABX, LB05, LB02, BF01). The color scale ranges from -2 (dark gray) to 2 (white). The taxa are grouped into two main clusters: one containing LB03, BF02, LB01, and CB; the other containing LB04, EF01, ABX, LB05, LB02, and BF01. The fecal samples are grouped into two main clusters: one containing feces7, feces6, feces2, feces1, feces3, feces4, and feces5. The heatmap shows that feces7 and feces6 are highly correlated with the first cluster of taxa, while feces1 and feces2 are highly correlated with the second cluster of taxa.

[도12]

