Supporting Information 2

Transcriptome analysis illuminates a hub role of SREBP2 in cholesterol metabolism by α-mangostin

Hee-Sung Chae[†], Hyun Ji Kim[†], Hyun-Jeong Ko[‡], Chang Hoon Lee[†], Young Hee Choi[†], and Young-Won Chin[§,*]

[†]College of Pharmacy and Integrated Research Institute for Drug Development, Dongguk University_Seoul, 32 Dongguk-lo, Ilsandong-gu, Goyang-si, Gyeonggi-do 10326, Republic of Korea

[‡]Laboratory of Microbiology and Immunology, College of Pharmacy, Kangwon National University, 1 Gangwondaehakgil, Chuncheon-si, Gangwon-do 24341, Republic of Korea

[§] College of Pharmacy and Research Institute of Pharmaceutical Sciences, Seoul National University, 1 Gwanak-lo, Gwanak-gu, Seoul 08826, Republic of Korea

* Corresponding author. Tel.: +82 2 880 7859.

E-mail address: ywchin@snu.ac.kr

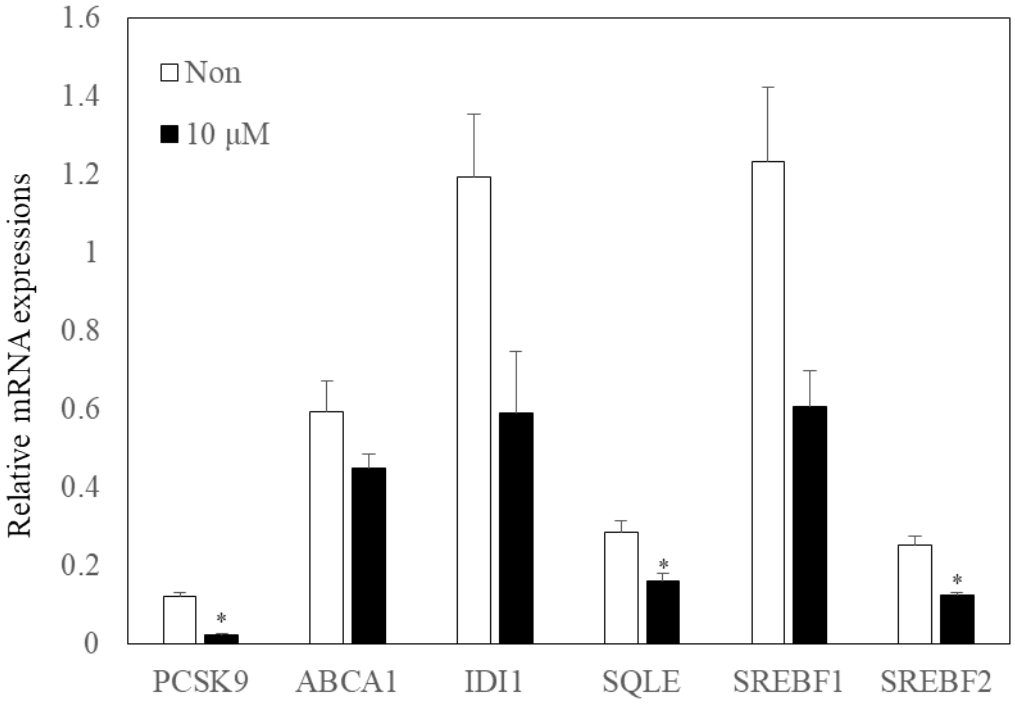

Figure S1. Validation of the metabolic gene expressions by qRT-PCR in Huh7 cells treated with α-mangostin (10 μM). Data represent the mean ± SD of triplicate samples. (*$p<0.05$)

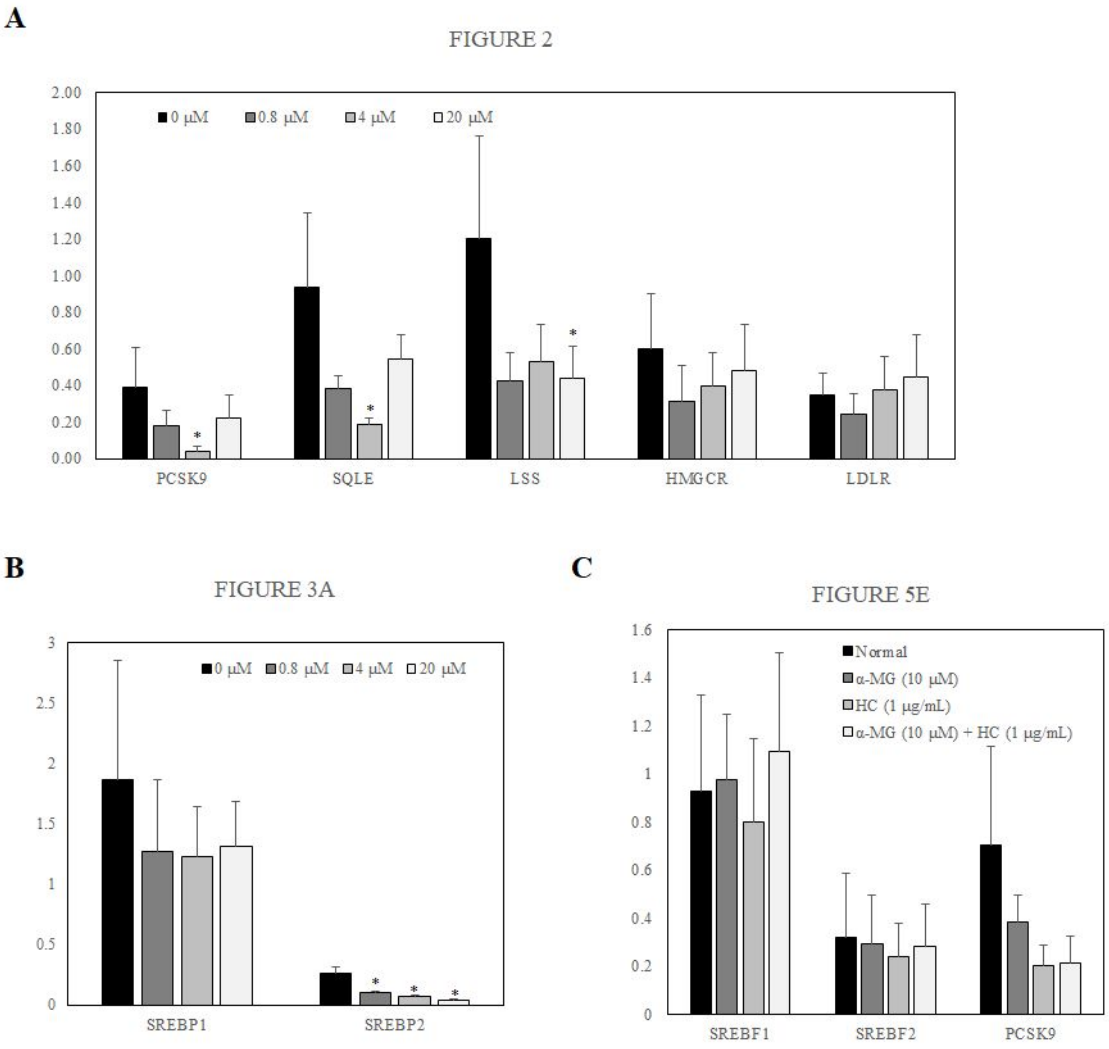

Figure S2. Quantitative analysis of Immunoblot analysis. (A) Densitometry analysis of immunoblot shows quantitation of PCSK9, SQLE, LSS, HMFCR and LDLR in figure 2. (B) Densitometry analysis of immunoblot shows quantitation of SREBP1 and 2 in figure 3A. (C) Densitometry analysis of Western blots shows quantitation of PCSK9, SREBP1 and 2 in figure 5E. *P < 0.05 versus non-treated group.