

Chemopreventive Effect of Phytosomal Curcumin on Hepatitis B Virus-Related Hepatocellular Carcinoma in A Transgenic Mouse Model

Chiao-Fang Teng,^{1,2} Chun-Hui Yu,³ Hong-Yi Chang,³ Wen-Chuan Hsieh,⁴ Tzu-Hua Wu,² Jia-Hui Lin,¹ Han-Chieh Wu,⁴ Long-Bin Jeng,² Ih-Jen Su^{3,4,5}

¹Graduate Institute of Biomedical Sciences, China Medical University, Taichung, Taiwan

²Organ Transplantation Center, China Medical University Hospital, Taichung, Taiwan

³Department of Biotechnology, Southern Taiwan University of Science and Technology, Tainan, Taiwan

⁴National Institute of Infectious Diseases and Vaccinology, National Health Research Institutes, Tainan, Taiwan

⁵Department of Pathology, National Cheng Kung University Hospital, Tainan, Taiwan

Correspondence

Ih-Jen Su, M.D., Ph.D., Department of Biotechnology, Southern Taiwan University of Science and Technology, No. 1 Nantai Street, Yongkang District, Tainan City 710, Taiwan (R.O.C.). Tel: 886-6-700-0123; Fax: 886-6-208-3466; E-mail: suihjen0704@stust.edu.tw

Short Title

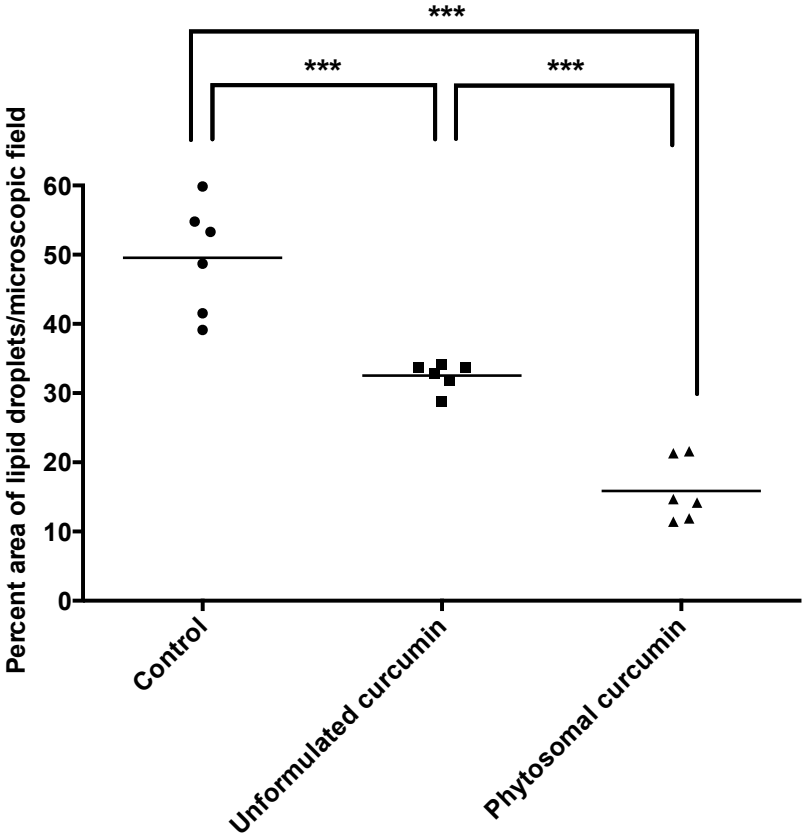
Chemoprevention of HBV-Related HCC by Phytosomal Curcumin

Number of figures and tables

8 figures and no tables

Figure S1

A



B

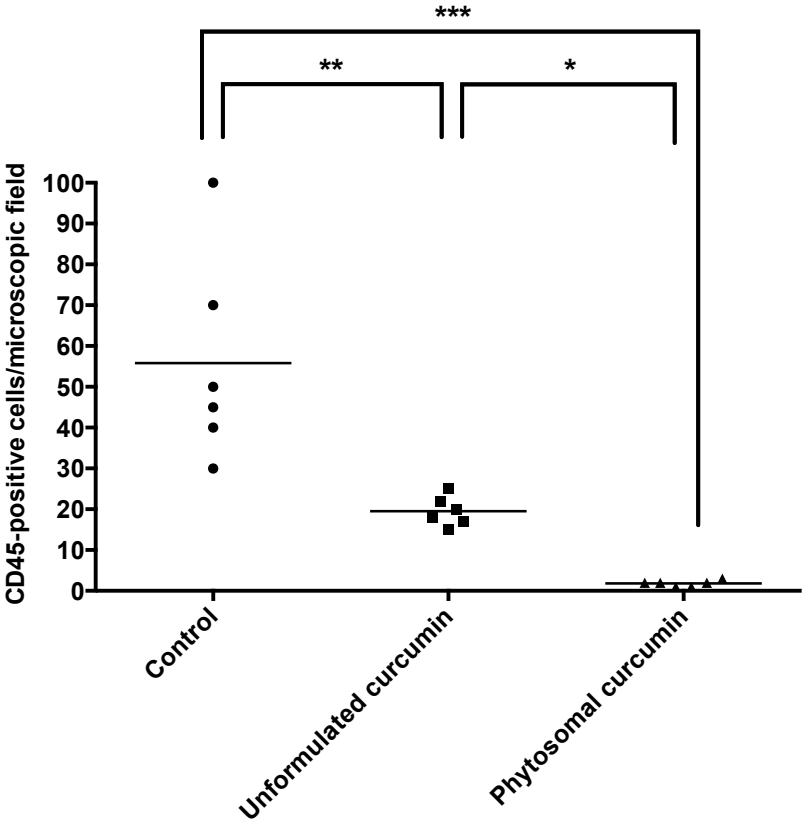


Figure S3

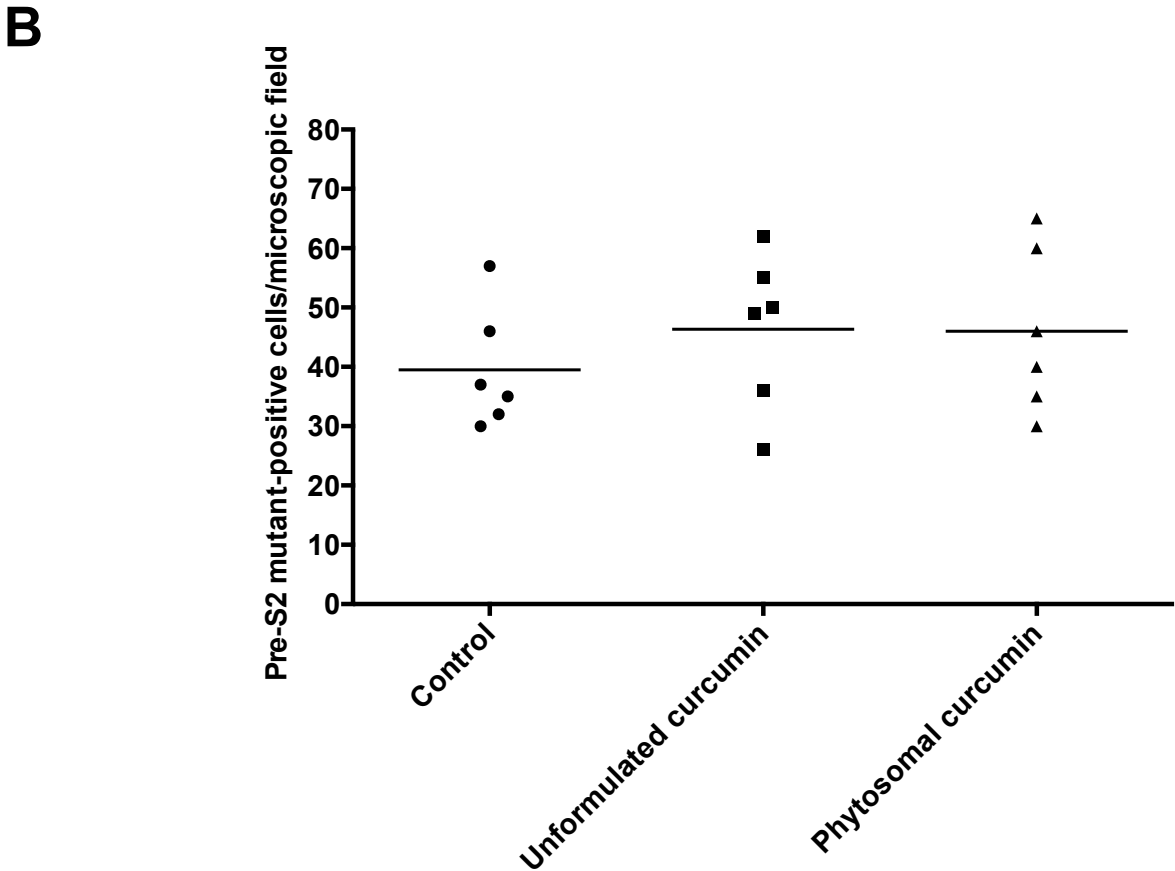
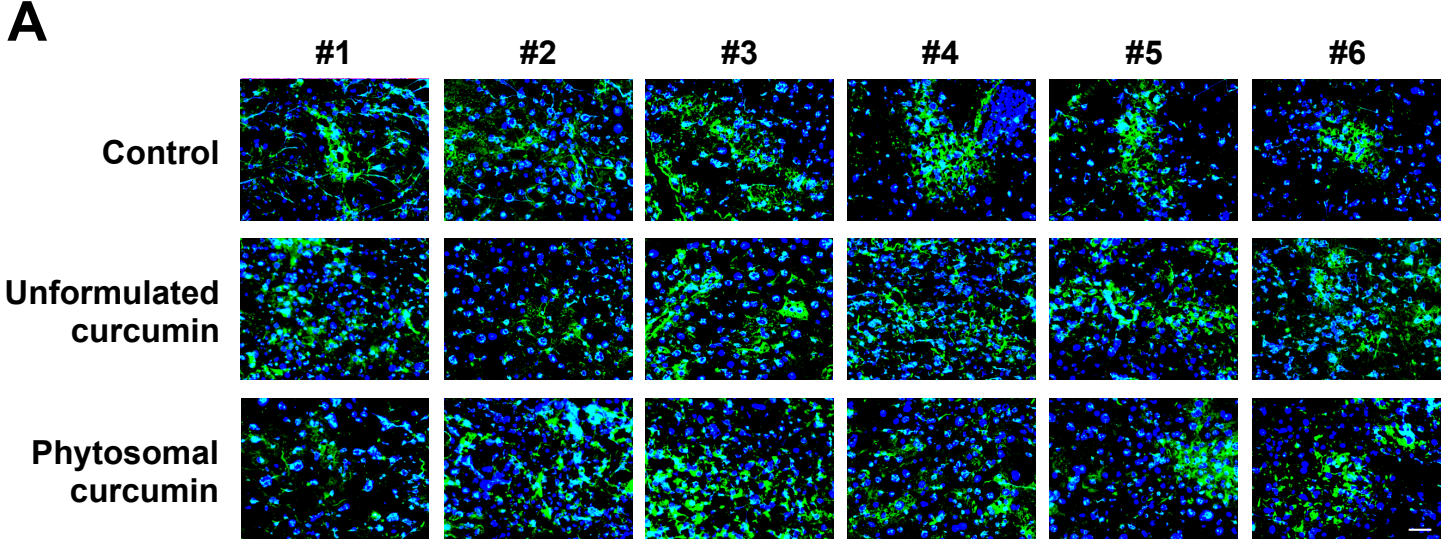


Figure S4

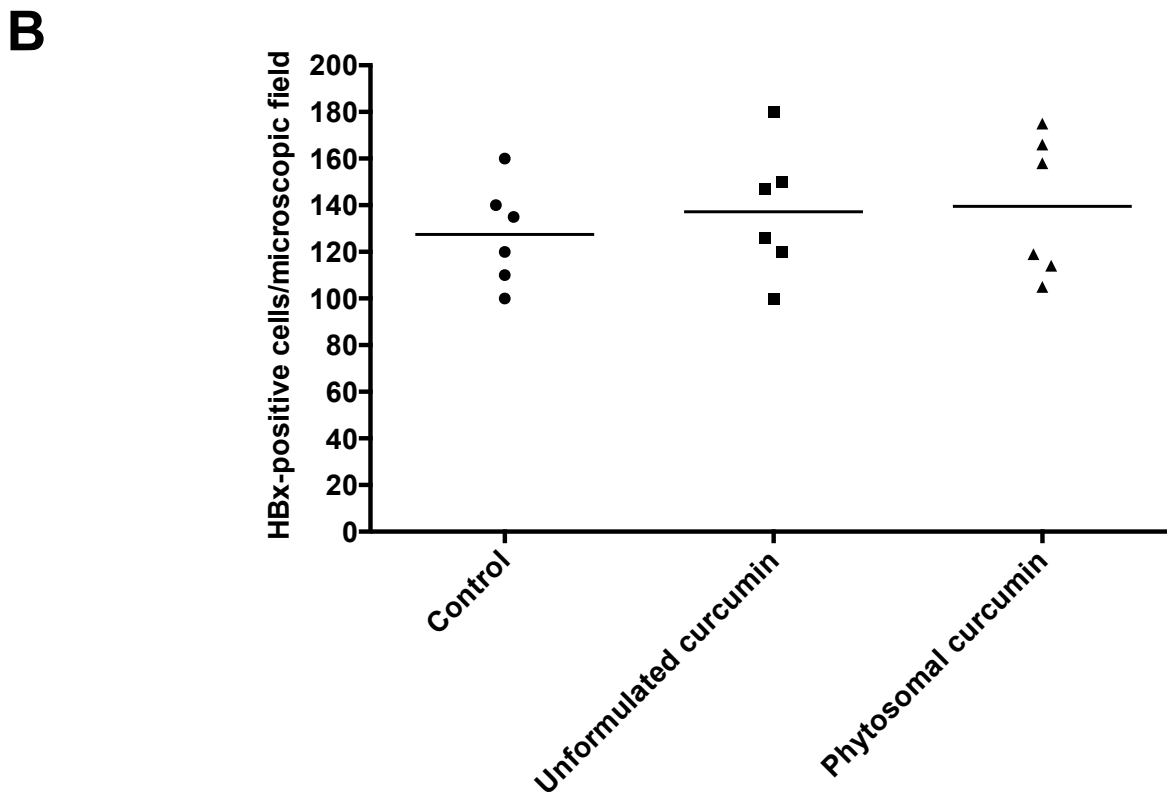
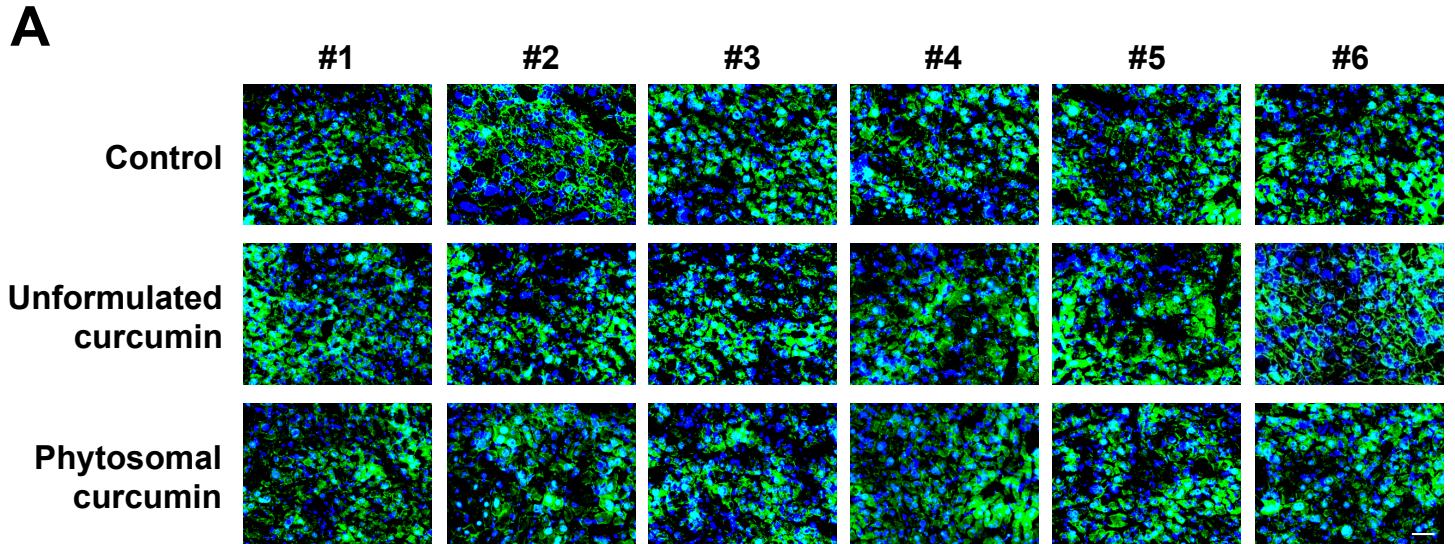
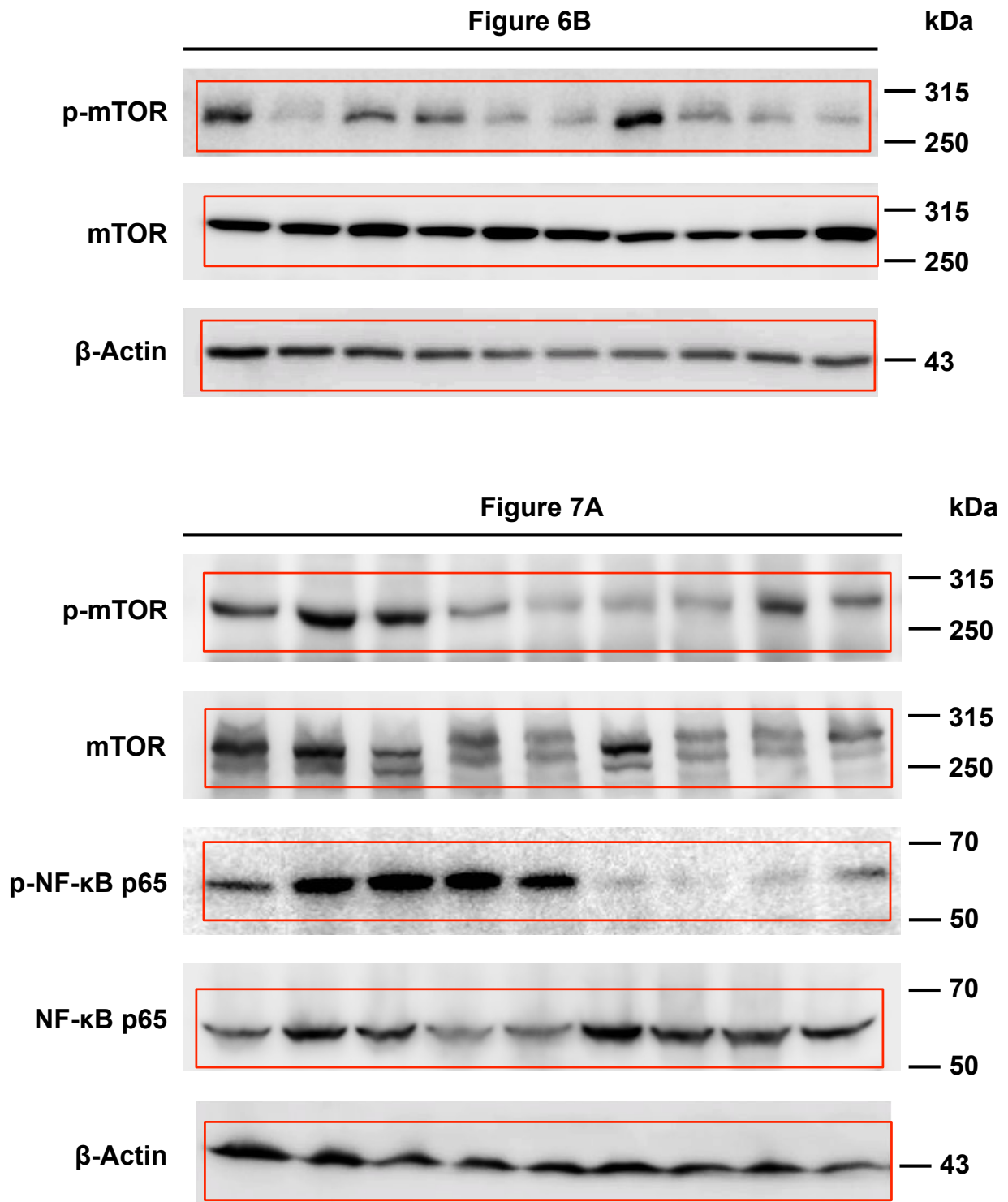


Figure S5



Supplementary Figure Legends

Figure S1. Quantitative evaluation of decreased lipid accumulation and leukocyte infiltration in liver of transgenic mice expressing both HBx and pre-S2

mutant. Graphs showing the percent area of lipid droplets (A) and the number of CD45-positive cells (B) per microscopic field (original magnification, $\times 40$) in liver tissues of normal diets, unformulated curcumin diets, and phytosomal curcumin diets treatment groups of mice ($n=6$). The horizontal lines represented the mean values.

The significance of the difference of the percent area of lipid droplets and the number of CD45-positive cells per field between different treatment groups of mice was analyzed. $*P < 0.05$, $**P < 0.01$, $***P < 0.001$.

Figure S2. Quantitative evaluation of PPAR γ activation in liver of transgenic

mice expressing both HBx and pre-S2 mutant. Graph showing the number of nuclear PPAR γ -positive cells per microscopic field (original magnification, $\times 40$) in liver tissues of normal diets, unformulated curcumin diets, and phytosomal curcumin diets treatment groups of mice ($n=6$). The horizontal lines represented the mean values. The significance of the difference of the number of nuclear PPAR γ -positive

cells per field between different treatment groups of mice was analyzed. *** $P < 0.001$.

Figure S3. Pre-S2 mutant was consistently expressed in liver of transgenic mice

expressing both HBx and pre-S2 mutant. (A) Expression of pre-S2 mutant (green

in color) in liver tissues of normal diets, unformulated curcumin diets, and

phytosomal curcumin diets treatment groups of mice was detected by fluorescent IHC

staining. Nuclei were stained with DAPI (blue in color). Shown were representative

results of each mouse. Original magnification, $\times 40$. Scale bar, 50 μm . (B) Graph

showing the number of pre-S2 mutant-positive cells per microscopic field in liver

tissues of each treatment group of mice ($n=6$). The horizontal lines represented the

mean values. No significant difference in the number of pre-S2 mutant-positive cells

per field between different treatment groups of mice was observed.

Figure S4. HBx was consistently expressed in liver of transgenic mice expressing

both HBx and pre-S2 mutant. (A) Expression of HBx (green in color) in liver

tissues of normal diets, unformulated curcumin diets, and phytosomal curcumin diets

treatment groups of mice was detected by fluorescent IHC staining. Nuclei were stained with DAPI (blue in color). Shown were representative results of each mouse. Original magnification, $\times 40$. Scale bar, 50 μm . (B) Graph showing the number of HBx-positive cells per microscopic field in liver tissues of each treatment group of mice (n=6). The horizontal lines represented the mean values. No significant difference in the number of HBx-positive cells per field between different treatment groups of mice was observed.

Figure S5. Full immunoblots with indicated areas of selection.