Table S1. The diet composition

Ingredients (g/kg)	NG Control diet (TP23402)	HG High fat diet (TP23400)	HG-L High fat diet (TP23400)	HG-H High fat diet (TP23400)
Dihydromyricetin	0	0	0.5	1
Casein	195	195	195	195
Maltodextrin	56	225	225	225
Sucrose	55	89	89	89
Corn starch	479	0	0	0
Soybean Oil	33	33	33	33
Lard	25	301	301	301
Cellulose	69	69	69	69
Mineral Mix (M1021)	68	68	68	68
Vitamin Mix (V1010)	14	14	14	14
L-Cystine	3	3	3	3
Choline Bitartrate	3	3	3	3
TBHQ	0.067	0.067	0.067	0.067
Energy, kcal/g	3.8	5.1	5.1	5.1
% kcal from Protein	14%	14%	14%	14%
% kcal from Carbohydrate	76%	26%	26%	26%
% kcal from Fat	10%	60%	60%	60%

Table S2. Whole blood analysis

group	NG	HG	HG-L	HG-H
WBC （10^3/μl）	4.90 ± 1.50	5.00 ± 1.87	5.73 ± 2.05	4.53 ±1.22
RBC （10^3/μl）	7.20 ± 0.34	7.51 ± 0.55	7.59 ± 0.33	7.29 ±0.36
HGB （g/dL）	104.17 ± 8.23	108.67 ± 9.24	112.67 ± 8.23	105.00 ± 4.77
HCT (%)	0.36 ± 0.03	0.38 ± 0.03	0.39 ± 0.02	0.37 ± 0.19
MCV (fL)	50.27 ± 0.96	51.00 ± 0.56	51.19 ± 1.12	50.71 ± 0.52
MCH (pg)	12.92 ± 3.36	14.47 ± 0.21	14.52 ± 0.59	14.39 ± 0.25
MCHC(g/dL)	256.50 ± 6.52	283.50 ± 1.97	283.67 ± 6.02	283.89 ± 3.48
PLT (10^3/μl)	736.50 ± 237.33	908.50 ± 139.05	870.67 ± 105.27	951.89 ± 127.28
LYM (%)	0.78 ± 0.14	0.79 ± 0.11	0.88 ± 0.04	0.80 ± 0.11
LYM (10^3/μl)	3.50 ± 2.36	4.10 ± 1.82	5.02 ± 1.87	3.60 ± 0.99
RDW-SD (fL)	27.72 ±0.59	27.72 ± 0.36	28.02 ± 0.55	28.09 ± 0.42
RDW-cv (%)	0.12 ± 0.01	0.12 ±0.01	0.12 ± 0.01	0.12 ± 0.01
PDW (fL)	6.95 ± 0.30	6.95 ± 0.64	6.67 ± 0.23	6.78 ± 0.20
MPV9(fL)	6.27 ± 0.15	6.23 ± 0.40	6.03 ± 0.18	6.16 ± 0.15

The data are expressed as the mean ± SD.(n=14); White blood cells (WBC), red blood cells (RBC), Hemoglobin (HGB), Hematocrit (HCT), mean corpuscular volume

(MCV), mean corpuscular hemoglobin (MCH), Platelet (PLT), Lymphocytes (LYM), red cell distribution width (RDW), platelet distribution width (PDW), and mean platelet volume (MPV).

Table S3. Detailed configurations and grid box parameters for molecular docking simulations.

Target Protein	Center Coordinates (x, y, z)	Grid Box Size (Å) (x, y, z)	Number of Poses	Best Binding Affinity (kcal/mol)
PAR-1	(-7.4, -8.8, 59.0)	29.0 × 20.0 × 21.0	15	-9.50
GPVI	(21.0, 17.3, 32.2)	19.0 × 20.0 × 21.0	15	-5.90
COX-1	(-21.6, -41.1, 3.2)	24.0 × 24.0 × 20.0	15	-7.30
NOX-2	(144.9, 141.8, 162.8)	24.0 × 24.0 × 44.0	15	-8.50
AR	(21.1, -4.6, 20.8)	24.0 × 26.0 × 39.0	15	-7.70

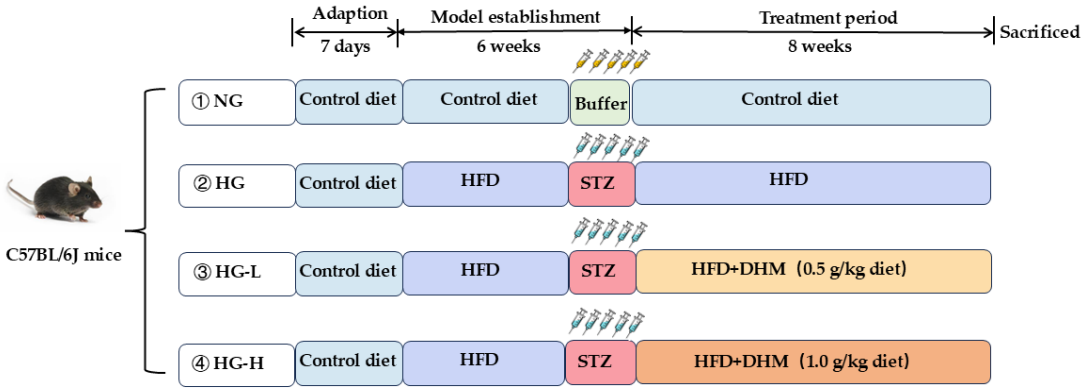

Figure S1. Flow chart of the animal experiment procedures.

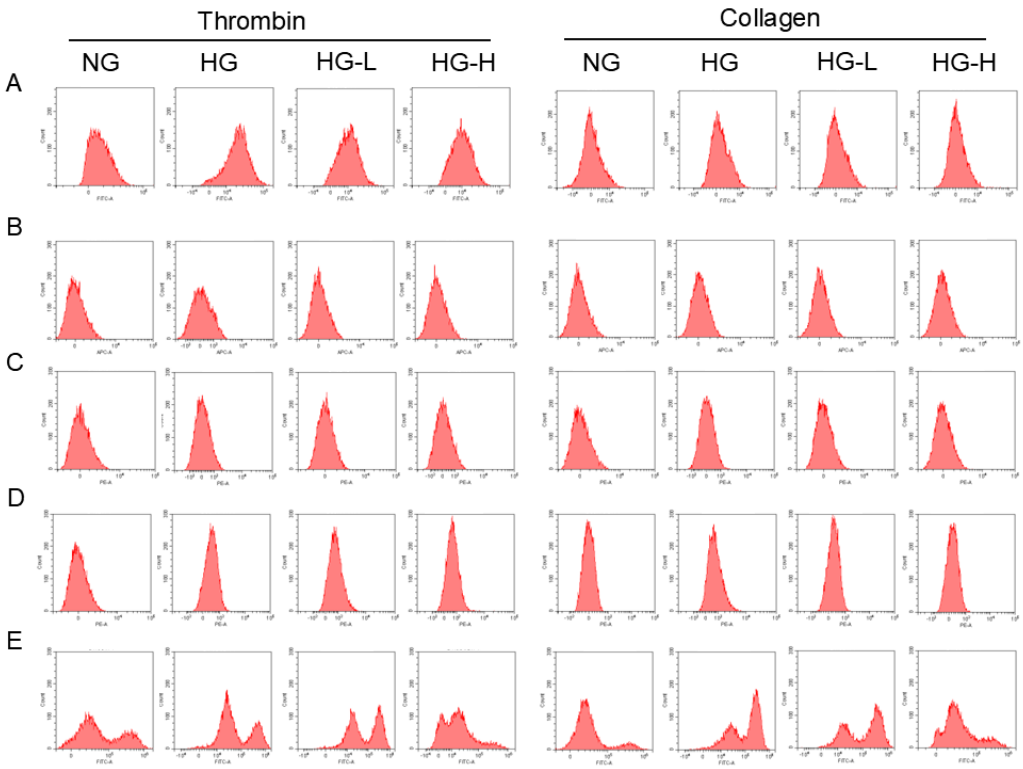

Figure S2. Representative flow cytometry histograms of platelet activation markers.

(A-C) Representative histograms showing the fluorescence intensity distributions of (A) CD62P, (B) CD63, and CD40L on the surface of platelets from different groups. (D-E) Representative histograms of JON/A binding (D) and ROS (E) generation in platelet stimulated with thrombin and collagen.

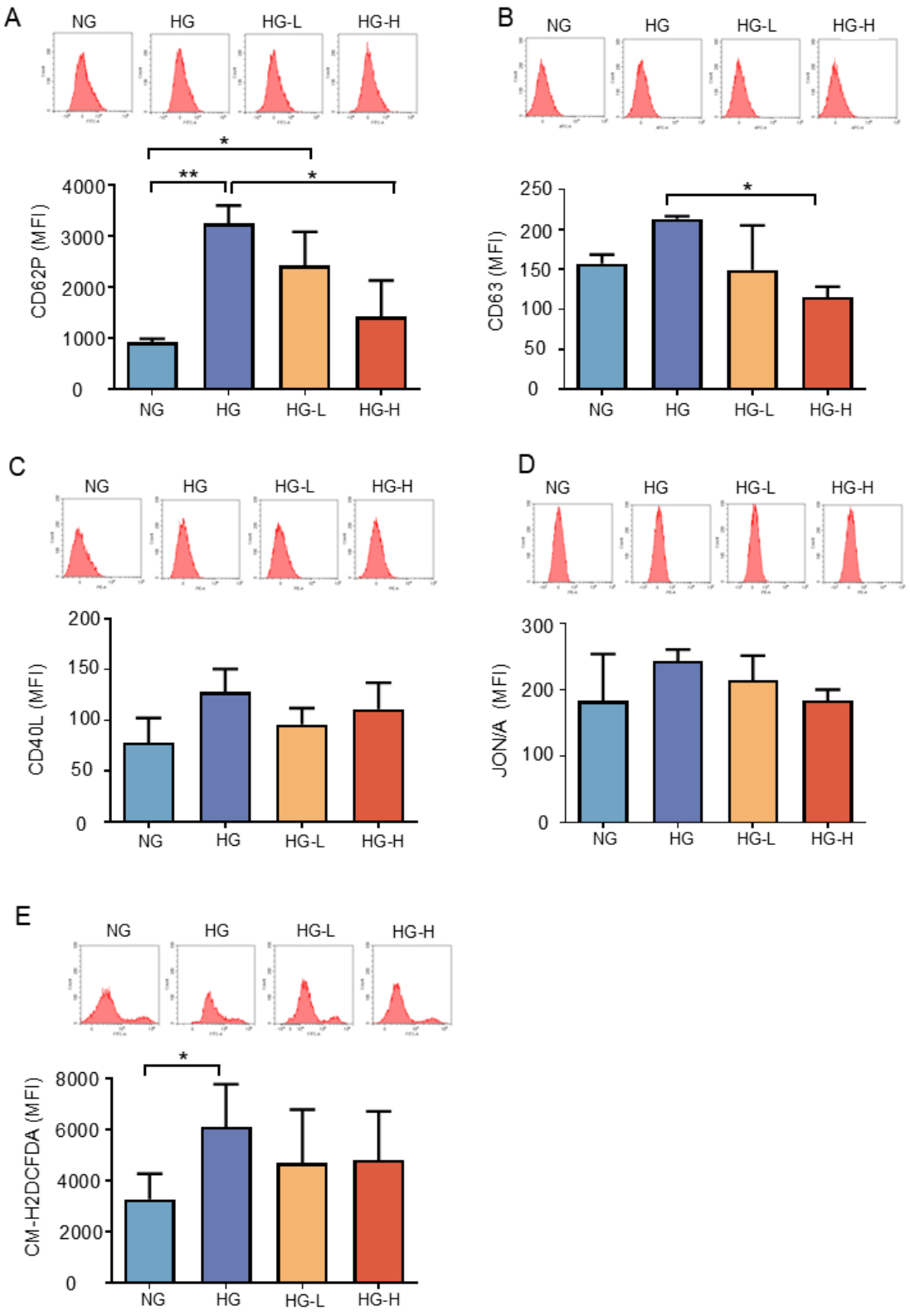

Figure S3. Effects of DHM on the expression of platelet activation markers and ROS formation in resting platelets.

Gel-filtered platelets were isolated from T2DM mice and incubated with FITC-conjugated anti-mouse CD62P antibody, FITC-conjugated anti-mouse CD63 antibody, PE-conjugated anti-mouse CD40L antibody or PE-conjugated JON/A antibody. Flow

cytometric analysis was performed to assess the expression of CD62P (A), CD63 (B), CD40L (C), integrin αIIbβ3 activation (D), and intraplatelet ROS formation (E) in resting platelets. Data are presented as the mean ± SD (n = 7). * $p < 0.05$, ** $p < 0.01$.