Deanticoagulated Heparins Mediate Goblet Cell Differentiation to Restore Mucosal Barrier

for Ulcerative Colitis Therapy

Wei Hu[1, #], Zhen Kang Liu[1, #], Long Huang[1,2, #], Wen Zeng[2], Xiao Yi Ren[1], Yang Ji[3], Qin Xuan

Zhou[1], Bing Xu[1,4], Can Yang Zhang[1,2,5,6], Chong Zhang[2,6], Zhen Qing Zhang[7], Hong Chao

Zhang[8], Yun Sheng Yang[9], Ye Chen[10], Xuan Jiang[11, *], Yi Wang[2, *], Xin-Hui Xing[1,2,4,5, 6, *]

[1]Institute of Biopharmaceutical and Health Engineering, Shenzhen International Graduate

School, Tsinghua University, Shenzhen 518055, China

[2]Key Laboratory for Industrial Biocatalysis, Ministry of Education, Institute of Biochemical

Engineering, Department of Chemical Engineering, Tsinghua University, Beijing 100084, China

[3]School of Medicine, Southern University of Science and Technology, Shenzhen, Guangdong

Province 518112, China

[4]Institute of Biomedical Health Technology and Engineering, Shenzhen Bay Laboratory,

Shenzhen 518118, China

[5]Key Laboratory of Active Proteins and Peptides Green Biomanufacturing of Guangdong

Higher Education Institutes，Tsinghua Shenzhen International Graduate School, Shenzhen 518055,

China

[6]Center for Synthetic and Systems Biology, Tsinghua University, Beijing 100084, China

[7]Jiangsu Key Laboratory of Translational Research and Therapy for Neuro-Psycho-Diseases

and College of Pharmaceutical Sciences, Soochow University, Suzhou, Jiangsu 215021, China

[8]Department of Cardiovascular Surgery, Air Force Medical Center, Beijing 100142, China

[9]Department of Gastroenterology and Hepatology, Chinese PLA General Hospital, Beijing

100853, China

[10]Department of Gastroenterology, Southern Medical University Shenzhen Hospital,

Shenzhen 518101, China

[11]Department of Gastroenterology, Beijing Tsinghua Changgung Hospital, Beijing 102218,

China

Abstract

Impaired mucosal barrier function is a pathological hallmark of ulcerative colitis (UC), yet

current clinical therapeutic strategies primarily rely on anti-inflammatory agents or

surgery, lacking strategies to repair mucosal damage[1,2]. Here, through a systematic screen

of our established library of deanticoagulated heparins[3], we found that the

nonanticoagulant low-molecular-weight heparin NALHP (average Mw, 6400 Da; PDI=2.23)

and its separated representative fine fragment S6 (average Mw, 4200 Da; PDI=1.1)

significantly ameliorated dextran sulfate sodium (DSS)-induced UC in mice by restoring

intestinal integrity. Both compounds promoted crypt stem cell differentiation into goblet

cells, thereby repairing the colonic mucosal barrier. Notably, in human UC patient-derived

organoids, NALHP and S6 enhanced goblet cell differentiation, increased MUC2 secretion,

and modulated Wnt and Notch signaling to optimize epithelial composition. Our study is

the first to reveal the therapeutic mechanism of deanticoagulated heparin derivatives in UC

through the regulation of epithelial mucosal regeneration via the mediation of goblet cell

differentiation, providing crucial insights for the development of novel UC therapeutics

capable of targeting the mucosal barrier repair process.

Introduction

Ulcerative colitis (UC) is a chronic, idiopathic, and intractable disease that recurrently and

continuously triggers inflammation of the colonic epithelial mucosa[4-6] and is among the principal

inflammatory bowel diseases. Clinically, UC patients frequently exhibit symptoms such as

abdominal pain, loose stools, abscesses and bloody stools, low-grade fever, and malnutrition[5,7],

which can render them completely incapable of working and, further, potentially induce colon

cancer[8,9]. Although more than 160 years have passed since the first case of UC was reported in

the literature, there is still no clear and unified pathogenetic mechanism of UC. This lack is

attributed mainly to the complex pathogenesis and influencing factors of UC. It is generally

acknowledged that immunity, genes, the environment, and the gut microbiota are the four major

factors influencing the incidence of UC and that these four factors interact and jointly facilitate

the progression of UC. The complex and unknown pathogenesis of UC also poses difficulties and

challenges for drug development and clinical treatment. However, the main pathological feature

of UC at the endoscopic and molecular levels is substantial intestinal barrier damage, including

damage to the intestinal epithelial barrier and the mucous layer barrier, at the site of ulceration[2].

This feature is an important clinical hallmark indicating the efficacy of UC treatment[1]. However,

currently, the clinical treatment of UC mainly encompasses anti-inflammatory drug therapy

and/or surgical treatment[10]. Moreover, none of the existing treatments can completely cure UC.

More specifically, no treatment method can achieve complete tissue healing in the mucosal

layers of UC patients[2]. Given that there is currently no specific drug for UC treatment, drug

therapy regimens for UC generally consist of broad-spectrum anti-inflammatory drugs such as

nonsteroidal anti-inflammatory drugs, corticosteroids, immunosuppressants, and biologics[11].

Among these drugs, 5-aminosalicylic acid (5-ASA) drugs (mesalamine and olsalazine) are the

most widely utilized first-line clinical drugs for the anti-inflammatory treatment of UC[12]; these

drugs can begin to have effects within 2 to 4 weeks and alleviate the condition in approximately

53% of patients[13]. UC patients treated with corticosteroids (prednisone and budesonide), the

second-line drugs for UC treatment, have a remission rate of approximately 50%[14]; these drugs

are typically employed as a fallback option when 5-ASA treatment is ineffective. Biologics

(infliximab and adalimumab) are utilized for the treatment of patients with moderate to severe

UC and can directly act on inflammatory signaling pathways such as the tumor necrosis factor

alpha (TNF-α) and Janus kinase (JAK) pathways[15]. However, biologics are relatively costly, and

fewer than 30% of UC patients respond to biologic therapy[16]. Additionally, most of the new UC

drugs under development are biologics that act mainly on JAK, Sphingosine-1-Phosphate

Receptor 1 (S1P1), α4β7 integrin and other mediators to regulate immunity and inflammation[17].

However, these new drugs are unable to overcome the limitation of the 20% to 30% remission

rate of UC patients treated with biologics[2].

Heparin (HP) is a high-molecular-weight linear polysaccharide[18] with a complex molecular

structure characterized by an intricate sugar chain framework comprising alternating

glucosamine (GlcN) and hexuronic acid (HexA)—namely, glucuronic acid (GlcA) or iduronic

acid (IdoA)—units linked through α(1→4) or β(1→4) glycosidic bonds with elaborate acetyl and

sulfonic acid group modifications[19]. Owing to its highly sulfonated nature along with its intricate

sugar chain architecture[20], HP exhibits binding affinity for numerous proteins, leading to diverse

biological activities encompassing anticoagulant and other activities that have led to its clinical

application for more than 80 years[21], such as anti-inflammatory[22], antitumor[23], and antiviral[24]

activities. While the anticoagulant function of HP arises from specific pentasaccharide sequences

(GlcNS6S/GlcNAc6S-GlcA-GlcNS6S3S-IdoA2S-GlcNS6S) within its sugar chains that interact

with antithrombin III (ATIII), these sequences account for only approximately 30% of its

content, leaving much unexplored territory awaiting further investigation[20], and elucidating the

nonanticoagulant functions of HP remains pivotal in current academic research and the

development of next-generation HP drugs. A profound challenge in glycoscience is posed by the

structural complexity resulting from the presence of diverse monosaccharides and their

modifications, which form repetitive disaccharide units and complicate both structural and

functional analyses.

Gaffney et al.[25] fortuitously discovered in 1995 that the combination of subcutaneous

anticoagulant HP drug injection and oral sulfasalazine administration in 10 patients with UC

refractory to traditional drug therapy alleviated the disease in 9 of the patients, thereby initiating

anticoagulant therapy with HP for UC[26]. However, studies on anticoagulant HP drug therapy for

UC often have limitations, such as inconsistent conclusions[27-29], a lack of clarity regarding the

effective molecular structure, unknown mechanisms of action and a high risk of massive

bleeding in UC lesions because of the anticoagulant activity[30], indicating that clinical HP drugs

with anticoagulant activity cannot be effective for the treatment of UC. However, the well-

known nonanticoagulant activity of low-molecular-weight HP, with its specific targeting of

integrin αM–mediated immune cells at inflammatory sites, has been successfully used to develop

oral bifunctional nanotherapeutics that treat UC by ameliorating oxidative stress and inhibiting

the activation of inflammation-associated signaling pathways[29]. To address the problems of the

instability of anticoagulant HP drugs and the bleeding risk associated with their use in the

treatment of UC, in this paper, the deanticoagulated HP derivative library constructed by our

group[3] was used for in vitro and in vivo screening of anti-UC activity, and NALHP, a

nonanticoagulant low-molecular-weight HP with significant and stable treatment efficacy for

UC, as determined by oral administration to mice with DSS-induced UC, was discovered.

Through discriminative analysis, we discovered that NALHP, with an average molecular weight

(Mw) of 6400 Da and a polydispersity index (PDI) of 2.23, and its representative fine fragment

S6 separated by gel chromatography, with an average Mw of 4200 Da and a polydispersity index

(PDI) of 1.1 and accounting for 15.3% (w/w) of the content of NALHP, which was the highest

among the fragments, can be effectively used to treat UC in mice. Notably, the effective

deanticoagulated HP derivatives significantly restored the colonic mucosal barrier in UC model

mice by restoring the proliferation and differentiation ability of colonic crypt stem cells.

Furthermore, using human UC patient-derived colon organoids, we elucidated the detailed

mechanism through which NALHP and S6 increase the proportion of functional cells, especially

goblet cells, in the organoids by simultaneously inhibiting the activity of the Wnt and Notch

signaling pathways to promote the differentiation of intestinal stem cells into goblet cells,

thereby profoundly restoring the mucosal barrier.

Results

Deanticoagulated HPs: structural characterization

In clinical practice, the manufacturing process of anticoagulant HP drugs primarily aims to

preserve the structural integrity of the anticoagulant pentasaccharide sequence. However, the

enrichment of sequences with anticoagulant activity during production may disrupt or impair the

more abundant nonanticoagulant sequences of HP molecules, thereby reducing the stability and

reproducibility of their nonanticoagulant therapeutic efficacy in ulcerative colitis (UC). To more

effectively investigate the consistent nonanticoagulant biological activity of HP, we previously

established a library of different structurally modified deanticoagulated HP derivatives, including

NAHP, I-45, NAI45, III,II-2-Odes, Eno (enoxaparin) and NAEno (nonanticoagulant enoxaparin)[3]

(Fig. 1a). Using the well-established mouse model of 3% dextran sulfate sodium (DSS)-induced

UC (Extended Data Fig. 1a), we evaluated the therapeutic efficacy of various modified

deanticoagulated HP derivatives in this library. As shown in Extended Data Fig. 1,

deanticoagulated HP (NAHP; average Mw, 13444 Da; PDI=1.28), an HP derivative obtained

through periodate oxidation followed by sodium borohydride reduction of heparin (HP; average

Mw, 17928 Da; PDI=1.28), in which the glucuronic acid of the pentasaccharide unit was ring-

opened, resulting in the loss of anticoagulant activity (Fig. 1a), exhibited stable efficacy in

partially restoring the structure of the colon tissue (Extended Data Fig. 1b-g). However, the

anticoagulant HP and the other four deanticoagulated HP derivatives prepared differently did not

have this stable biological effect.

Fig. 1 Characterization of deanticoagulated HP derivatives. a, A library of deanticoagulated

HP derivatives was constructed: NAHP (deanticoagulated HP, prepared by opening the structure

of heparin with sodium periodate), I-45 (prepared by enzymatic hydrolysis with heparinase I

until the absorbance increased to 45), NAI45 (opening the structure of I-45 with sodium

periodate), III,II-2 (prepared by combined enzymatic hydrolysis with heparinase III and

heparinase II), Eno (enoxaparin) and NAEno (prepared by opening the structure of enoxaparin

with sodium periodate)[3]. **b,** Molecular weight HPLC chromatograms of S1-S11. **c,**

Physicochemical properties of HP and HP derivatives. **d,** Infrared spectra of HP and HP

derivatives. **e–g,** HSQC spectra of HP **(e)** and its derivatives NALHP **(f)** and S6 **(g)**.

Furthermore, compared with the first-line clinical drug 5-ASA, the respective nonanticoagulant

low-molecular-weight and ultra-low-molecular-weight HP derivatives of NAHP, i.e., NALHP

(average Mw, 6400 Da; PDI=2.33) and NAULHP (average Mw, 3800 Da; PDI=4.15), which

were obtained via controlled enzymatic hydrolysis of NAHP with heparinase I (Fig. 1a),

demonstrated even more pronounced therapeutic efficacy in UC model mice (Extended Data Fig.

2a-h). Both NALHP and NAULHP significantly ameliorated DSS-induced damage to the colonic

mucosal barrier and facilitated the restoration of intestinal crypt architecture (Extended Data Fig.

2a-h). They also effectively reduced the serum concentrations of inflammatory cytokines (IL-6

and TNF-α) by more than 50% (Extended Data Fig. 2g and h). Notably, compared with

NAULHP, NALHP, which can be prepared in a stable form by the established production process

(Extended Data Fig. 3a-d and Extended Data Tables 2-4), showed greater efficacy in decreasing

DSS-induced mortality (Extended Data Fig. 2i). Therefore, NALHP was selected for all

subsequent investigations. In addition, we found that the adsorption and desorption curves of

DSS and HP, NAHP, NALHP, and NAULHP were consistent with those of the water control

group by the biofilm layer interference technique, confirming that there was no interaction

between HP derivatives and DSS (Extended Data Fig. 2j and k).

Given the large difference in molecular weight between the enzymatic hydrolysis product

NALHP from NAHP (PDI=2.23 for NALHP vs. PDI=1.28 for NAHP), we performed fine

separation of NALHP using gel exclusion chromatography, collecting key fragments with an

average molecular weight difference of approximately 500 Da. A total of 11 distinct fractions

were obtained and designated S1 to S11 (Fig. 1a, b and Extended Data Table 1). Among these 11

separated fractions, S6, the intermediate-molecular-weight fraction of NALHP (Extended Data

Table 1, Extended Data Fig. 4c and d), with an average molecular weight of 4200 ± 150 Da

(PDI=1.1), exhibited bioactivity similar to that of NALHP (Fig. 1c and Extended Data Fig. 4). In

addition, S10 (average Mw, 1282Da; PDI=1.15) has no efficacy on mucosal remodeling. The

efficacy of NAULHP and S4 (average Mw, 6254Da; PDI=1.05) is inferior to that of NALHP and

S6. Structural characterization confirmed that S4 and S6 fully retained the characteristic

functional groups and sugar chain structure of the parent NALHP and NAULHP (Fig. 1d-g,

Extended Data Fig.9), but the main molecular structure of S10 is ΔHexA2S and the reducing end

is α-GlcNS6X, the Gal1, Gal2, Xyl and $GlcA_{LR}$ signal peaks in the LR region are missing

(Extended Data Fig.9). The above results together with the PCA of the UC treatment phenotypes

for HP, NAHP, NALHP, NAULHP, S4, S6 and S10 (Extended Data Fig.4j) indicate that in the

NALHP, the fragments with molecular weights ranging from 3000Da to 8000Da are the main

active components, and S6 is the representative fraction of NALHP with the similar biological

activity.

This consistent therapeutic efficacy is markedly distinct from that of native HP. Consequently,

we conducted a comparative structural analysis of UC-effective NALHP and S6 and UC-

ineffective native HP, NAI45 and other HP derivatives using Fourier transform infrared

spectroscopy (FTIR) and two-dimensional nuclear magnetic resonance spectroscopy (2D-NMR).

The results indicated that (1) the chemical modifications did not significantly alter the

characteristic functional groups of the HP polysaccharide chain, such as the N-sulfate and O-

sulfate groups (Fig. 1d and Extended Data Fig. 6); and (2) enzymatic hydrolysis specifically

introduced novel structural units—ring-opened glucuronic acid (gsGlcA) and Δ4,5-unsaturated

glucuronic acid—without inducing extensive structural modifications to the monosaccharide

units (Fig. 1e, f, Extended Data Figs. 7-9, Extended Data Tables 5 and 6).

Deanticoagulated HPs relieve UC pathology via mucosal repair

The results obtained in the DSS-induced mouse model of colitis demonstrated that both NALHP

and S6 significantly improved the pathological phenotypes of DSS-induced UC in mice (Fig.

2a). Specifically, they effectively inhibited weight loss (Fig. 2b), restored the colon length to

92% of that in the normal group (Fig. 2c and e), and reduced the abnormal increase in the spleen

index by 40% (Fig. 2d and f). Furthermore, both NALHP and S6 significantly suppressed the

increase in the serum concentrations of IL-6 and TNF-α, decreasing the final concentrations by

62% and 90%, respectively (Fig. 2g and h). Histopathological analysis revealed that the colonic

crypt structure in the NALHP and S6 treatment groups was completely reconstructed (Fig. 2i4, i5

and j) and that the goblet cell density was restored to more than 85% of that observed in the

normal group (Fig. 2k4, k5 and l). These effects were significantly greater than those observed in

the HP treatment group (Fig. 2i3, k3 and j) and the positive control drug (5-ASA) group (p <

0.01) (Fig. 2i6 and k6). The combined results of glycoprotein staining with WGA, EdU

incorporation, and MUC2 immunohistochemical staining revealed marked restoration of the

colonic mucus layer in the NALHP and S6 groups (Fig. 2 m4 and m5), whereas no such

restoration was observed in the HP groups (Fig. 2m2 and m3). Slight restoration of the mucus

layer was observed in the 5-ASA group (Fig. 2m6), but the degree of restoration was much lower

than that observed in the NALHP and S6 groups. Additionally, the expression level of the mucin

MUC2 in the NALHP and S6 groups was significantly greater than that in the model group (p <

0.001) (Fig. 2l). EdU incorporation assay results further confirmed that the intestinal epithelial

cell proliferation index was significantly greater in the treatment groups than in the model group

(p < 0.001) (Fig. 2n), whereas traditional drugs such as anticoagulant HP and the anti-

inflammatory drug 5-ASA had no significant reparative effects. Collectively, these findings

indicate that treatment with either NALHP or S6 can effectively repair mucosal injury in mice

with DSS-induced colitis, restore colonic mucosal protein expression, and reconstruct the

mucosal barrier.

Fig. 2 Evaluation of the therapeutic efficacy of deanticoagulated HP derivatives. a, 3% DSS

was added to the drinking water for 7 days to induce acute colitis in mice (n=8). The mice in the

control group were given regular drinking water (n=8), and the mice in the drug treatment group

were given 30 mg/kg HP, NALHP, S6, or 5-ASA on the third day (n=8). **b,** Changes in weight.

c–f, Mice were sacrificed on day 7, and the colon (**c**) and spleen (**d**) were harvested. The colon

length (**e**) and the spleen index (**f**) were quantified. **g, h,** The serum concentrations of IL-6 (**g**)

and TNF-α (**h**) were determined by ELISA when the mice were sacrificed on day 7. **i1-i6.**

Representative images of colons stained with hematoxylin and eosin and their quantitative

histological scores (**j**). Scale bar, 100 μm. **k1-k6,** Representative images of colons stained with

hematoxylin and MUC2 and their quantitative immunohistochemical scores (**l**). Scale bar, 100

μm. **m1-m6,** Representative images of colons stained with EdU (red) and WGA (green) and their

quantitative immunohistochemical scores (**n**). Scale bar, 100 μm. Representative images or

quantitative analyses of n=6 biologically independent samples are shown (**b-h, j l, n**). The data

are presented as the mean ± SD values. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$

and ns (not significant) $p > 0.05$; the data were analyzed by ordinary one-way ANOVA (**b**) with

multiple comparison testing.

To further elucidate the mechanism underlying NALHP- and S6-mediated mucosal barrier

restoration, we employed multiomics approaches to analyze the whole-transcriptome and 16S

rRNA profiles of the colon and colon contents in DSS-treated mice. First, we investigated

whether the intestinal repair function of HP, as a carbohydrate, was attributable to short-chain

fatty acids generated through microbial metabolism in the gut. HP treatment did not alter the type

or composition of intestinal microbes in DSS-treated mice (Extended Data Fig. 10a-c). In

contrast, 5-ASA treatment led to the enrichment of genera such as *Porphyromonas*, *Neisseria*,

Thermicanus, and *Petrobacter* (Extended Data Fig. 10c), some of which have been associated

with exacerbated UC progression[31,32]. Notably, both NALHP and S6 improved the intestinal

microbial type and diversity in DSS-treated mice, increasing their similarity to the profiles

observed in wild-type (WT) mice (Extended Data Fig. 10a-c). Moreover, NALHP and S6

modulated the metabolite composition of the colonic contents, reducing the abundances of

inflammation-associated metabolites (Extended Data Fig. 10d). Integrated microbiome and

metabolome analyses revealed a significant positive correlation between gut microbial markers

in WT and DSS-treated mice (Extended Data Fig. 10e and f). The *genera Bacteroides* and

Parabacteroides, which were enriched in DSS-treated mice, were found to regulate the

metabolite profile. The abundances of *Prevotella* and *Sutterella* were significantly positively and

negatively correlated, respectively, with soluble colonic metabolites (Extended Data Fig. 10f).

NALHP and S6 treatment also affected the intestinal epithelial transcriptome in DSS mice,

altering the transcription of thousands of genes (Extended Data Fig. 11a). Enrichment analysis of

the genes associated with mucosal repair, including those involved in inflammation, metabolism,

and cell differentiation, revealed substantial changes in gene expression following treatment with

NALHP and S6 (Extended Data Fig. 11b). Further Gene Ontology (GO) analysis indicated that

mucosal barrier repair was a manifestation of the wound healing process, which was mediated

primarily through pathways such as the Notch and Wnt pathways, which regulate intestinal

epithelial cell development and regeneration in UC mice (Extended Data Fig. 11c). On the basis

of the results of the multiomics analysis, we concluded that the primary effects of NALHP and

S6 on DSS-induced colitis in mice were centered on the regulation of intestinal epithelial cell

development. During the active phase of UC, changes in epithelial cell proliferation occur at the

sites of colonic ulceration. Therefore, we selected PCNA as a marker of cell proliferation and

TCF1 as a downstream effector of the Wnt signaling pathway. Immunohistochemical staining

revealed that NALHP and S6 treatment normalized PCNA expression following ulceration and

restored TCF1 expression downstream of the Wnt pathway, but these effects were not observed

in mice treated with HP or 5-ASA (Extended Data Figs. 12 and 13).

NALHP & S6 promote goblet cell differentiation in UC organoids

Intestinal organoids derived from human patients with inflammatory bowel disease (IBD) can

effectively recapitulate the absence of goblet cells clinically observed in vivo (Extended Data

Fig. 14 a and b). Therefore, we established a UC organoid model based on intestinal epithelial

cells isolated from the mucosal layer of Chinese patients diagnosed with ulcerative colitis

(Extended Data Fig. 15a). During the organoid culture process, NALHP, S6, and 5-ASA were

added to further investigate the potential mechanism by which deanticoagulated HP contributes

to the restoration of the mucosal barrier in UC mice, as observed above (Fig. 2). Morphological

analysis demonstrated that NALHP and S6 significantly altered the three-dimensional structural

features of the organoids during culture (Fig. 3a1-a3, Extended Data Video 1): compared with

those in the control group, the organoids in the NALHP/S6 groups exhibited decreased sphericity

(Fig. 3b) and an increased surface density and smoothness. In contrast, no morphological

alterations were observed following culture with 5-ASA (Fig. 3a4). To characterize the cellular

heterogeneity among the groups of organoids, single-cell transcriptome profiling was conducted.

The results revealed that the percentage of LGR5+ stem cells and PCNA+ transient amplifying

(TA) cells in the UC organoid control group was greater than 90% (Fig. 3c, d and Extended Data

Fig. 15b-e), confirming the robust proliferative and differentiation capabilities—which are

predominantly stem cell-driven—of these UC patient-derived organoids, as reported

previously[33]. Culture with NALHP or S6 induced substantial remodeling of the cellular

composition in the UC organoids: the percentage of stem/TA cells decreased to less than 10%,

whereas the percentage of goblet progenitor cells and their mature subtypes was greater than

80%. Additionally, approximately 5% of the intestinal epithelial cells exhibited markers of

differentiation, indicating that the culture of UC organoids with NALHP or S6 induced the

development of a functionally differentiated phenotype (Extended Data Fig. 15d and e), but no

functionally differentiated phenotype was detected in UC organoids cultured with 5-ASA (Fig.

3c and d).

Fig. 3 NALHP and S6 promote the directed differentiation of goblet cells in organoids. a1–

a4, Brightfield images of organoids. UC (a1), NALHP (a2), S6 (a3), and 5-ASA (a4) groups. **b,**

Changes in the sphericity of the organoids. **c,** The percentages of cells in UC organoids in the

different groups. **d,** UMAP dimensionality reduction plot of UC organoids in the different

groups. **e,** Pseudotime analysis of UC organoids in the different groups and of cell types by

Monocle 2.**f1-f4.** Representative images of colons with hematoxylin and MUC2 staining and

quantitative immunohistochemical scores **(g)**. Scale bar, 50 μm. **h1-h4,** Representative images of

colons with hematoxylin and PCNA staining and quantitative immunohistochemical scores **(i)**.

Scale bar, 50 μm. **j–m,** Relative mRNA expression levels of LYZ **(j)**, CHGA **(k)**, LGR5 **(l)**, and

MUC2 **(m).**

Representative images or quantitative analysis results from n=3 biologically independent

samples are shown **(b, g, i, j-m)**. The data are presented as the mean ± SD values. * $p < 0.05$, **

$p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ and ns (not significant) $p > 0.05$; the data were

analyzed by ordinary one-way ANOVA.

Furthermore, through the sequencing of temporal genes in the individual cells of UC organoids,

it was observed that organoids cultured with NALHP or S6 were composed of cells in the highly

differentiated stage, whereas the cells in the untreated group and in the group cultured with 5-

ASA remained in the early stage of differentiation (Extended Data Fig. 16a); moreover, the

highly differentiated cells originated from the intestinal stem cell–TA cell hierarchy in the

organoids (Fig. 3e), leading to a marked increase in the abundance of mucus-secreting goblet

cells (Extended Data Fig. 16b). Considering this differentiation pattern, we examined the

transcription of secretory cell markers and detected no significant differences in the mRNA

expression levels of lysozyme (LYZ) and chromogranin A (CHGA) among the groups (Fig. 3j

and k). However, the mRNA expression level of MUC2 significantly increased, whereas the

mRNA expression level of LGR5 significantly decreased when the organoids were cultured with

NALHP or S6 (Fig. 3l and m). On the basis of these findings, we hypothesized that the primary

function of NALHP and S6 is to mediate the directed differentiation of intestinal stem cells

toward the goblet cell lineage. Immunohistochemical analysis further confirmed that the

fluorescence intensity of the MUC2 protein was more than tenfold greater in the NALHP/S6-

treated groups than in the control UC and 5-ASA-treated groups (Fig. 3f1-f4), while the PCNA

signal was correspondingly reduced (Fig. 3h1-h4). These findings were highly consistent with

the results of the single-cell transcriptomic analysis (Fig. 3c). Moreover, the above results were

verified in organoids derived from three patients (Extended Data Figs. 15e and 17). Taken

together, these findings suggest that NALHP and S6 specifically promote the generation of

goblet cell lineages by activating the directed differentiation of intestinal stem cells in UC

organoids, thereby increasing the expression level of the mucin protein, similar to the effects

observed in mice with DSS-induced UC (Fig. 2k4, k5, and Extended Data Fig. 13).

Interestingly, during the process of dissociating organoids into single cells by treatment with

pancreatic enzymes, we found that the organoids in the NALHP/S6 culture groups were more

resistant to dissociation into single cells, suggesting stronger connections between the cells in the

UC organoids cultured with NALHP or S6 than between those in the control UC organoids.

Next, we stimulated NCM460 cells, a kind of normal human colonic epithelial cell, with IL-6 to

reduce the strength of the connections between cells mediated by the ZO-1 junction protein cells

and found that treatment with NALHP or S6 reversed the IL-6-induced damage to this tight

junction protein connecting NCM460 cells (Extended Data Fig. 18). These findings also suggest

that NALHP and S6 may restore the tight junction proteins connecting stimulated colonic

epithelial cells.

NALHP & S6 drive stem cell differentiation to goblet cells in UC organoids via separate

Wnt/Notch inhibition

UC organoids from the groups cultured with various drugs (NALHP, S6 and 5-ASA) and the

control group were collected and subjected to transcriptome analysis. KEGG and GO enrichment

analyses of the differentially expressed genes in the organoids cultured with NALHP and S6

revealed significant enrichment of these genes in the Wnt, Hippo, and Notch signaling pathways

(Extended Data Fig. 19a), which are key regulators of intestinal stem cell proliferation and

differentiation[33]. Notably, NALHP and S6 significantly inhibited the Wnt and Notch signaling

pathways through transcriptional regulation. Given that Wnt and Notch are critically involved in

the differentiation of intestinal stem cells[34], modulating their activity enables precise control over

the induction and differentiation of various intestinal epithelial cell types, including goblet cells.

Both NALHP and S6 promoted the differentiation of intestinal stem cells into goblet cells (Fig.

3j and m). Furthermore, when the UC organoids were cultured with the combination of the Wnt

pathway inhibitor IWP-2 and the Notch pathway inhibitor DAPT, the percentage of goblet cells

within the organoids increased to more than 60% (Extended Data Fig. 19b-e), which is consistent

with the mediation effects observed upon culture with NALHP or S6. To validate the central role

of Wnt and Notch pathway inhibition in NALHP/S6-mediated differentiation, functional rescue

experiments were conducted using CHIR99021 (C), a Wnt pathway agonist, and sodium

valproate (VPA, V), a Notch pathway agonist. In the presence of these agonists, the ability of

NALHP and S6 to promote the differentiation of intestinal stem cells (marked by LGR5) into

goblet cells (marked by MUC2) was partially abolished: UC organoid budding morphology was

restored (Extended Data Fig. 20), and the expression levels of Wnt- and Notch-related proteins,

whose expression was previously suppressed by NALHP/S6 treatment, were restored. Coculture

with the agonists significantly restored LGR5 expression and reduced MUC2 mRNA expression

(p < 0.001) in UC organoids (Fig. 4a and b). Additionally, the transcription and translation of

TCF1, a downstream effector of the Wnt pathway, were markedly inhibited in the agonist-treated

UC organoids (Fig. 4c and f). These findings clearly indicate that dual inhibition of the Wnt and

Notch pathways in UC organoids constitutes the primary mechanism underlying the biological

activity of NALHP/S6 in mediating the differentiation of goblet cells to increase the secretion of

mucosal layer components.

Fig. 4 Changes in UC organoids upon treatment with different inhibitors. a–d, The relative

mRNA expression levels of LGR5 (**a**), MUC2 (**b**), TCF1 (**c**), and HES1 (**d**) in UC organoids

after treatment with CHIR99021 (C), VPA (V) and NALHP/S6. **e-h,** The relative mRNA

expression levels of LGR5 (**e**), MUC2 (**f**), TCF1 (**g**), and HES1 (**h**) in UC organoids after

treatment with CHIR99021 (C) and NALHP or S6. **i–l,** The relative mRNA expression levels of

LGR5 (**i**), MUC2 (**j**), TCF1 (**k**), and HES1 (**l**) in UC organoids after treatment with VPA (V) and

NALHP or S6.

Representative results of the quantitative analysis of n=3 biologically independent samples are

shown (**a–l**). The data are presented as the mean ± SD values. * $p < 0.05$, ** $p < 0.01$, *** $p <$

0.001, **** $p < 0.0001$ and ns (not significant) $p > 0.05$; the data were analyzed by ordinary one-

way ANOVA.

During the development of the intestinal tract, Wnt and Notch signaling can determine the fate of

intestinal stem cells. We selected the downstream effectors TCF1 and HES1, which are related to

the Wnt and Notch signaling pathways, to further determine the influence of these pathways. The

expression level of HES1 during the development of goblet cells is highly important. High

expression levels of HES1 inhibit the process of differentiation toward goblet cells. Culture with

NALHP or S6 led to significant inhibition of Hes1 and TCF1 mRNA expression (Fig. 4c and d),

and agonist treatment partially reversed this effect, with a consistent effect at the translational

level (Extended Data Fig. 21). To determine the individual contributions of each pathway,

CHIR99021 and VPA were applied separately in combination with NALHP or S6. Gene

expression analysis revealed that CHIR99021 restored LGR5 mRNA expression (indicative of

stemness) (Fig. 4e) and activated the Wnt signaling pathway (Fig. 4g and Extended Data Fig. 22)

but did not inhibit the upregulation of MUC2 (Fig. 4f) or regulate the Notch signaling pathway

(Fig. 4h). Conversely, VPA suppressed the induction of MUC2 expression by activating the

Notch signaling pathway (Fig. 4j, m and Extended Data Fig. 23), but it did not regulate the Wnt

signaling pathway (Fig. 4k) to restore the expression of LGR5 (Fig. 4i). Collectively, these

results demonstrate that NALHP and S6 exert their effects by coordinately modulating both the

Wnt and Notch pathways to drive the directed differentiation of intestinal stem cells into goblet

cells.

Discussion

The absence of a mucus layer and the impairment of the intestinal epithelial barrier—

pathological features whose complexity imposes stringent demands on existing therapeutic

agents—are the central challenges in UC treatment[35]. In the development of anti-UC

medications, HP, a classic anticoagulant drug, has demonstrated potential in alleviating intestinal

inflammation. However, the data from nearly three decades of trial-and-error studies reveal

substantial variability and even contradictory outcomes regarding its efficacy; these limitations

are compounded by the inherent hemorrhagic risks of these drugs, preventing the in-depth and

broad exploration of their nonanticoagulant activity. In this study, we innovatively propose the

critical hypothesis that the anticoagulant activity of HP enriched during drug production may

interfere with its anti-UC effects. By employing the strong oxidation performance of sodium

periodate to open the ring of glucuronic acid, one of the anticoagulant pentasaccharides[3], the

ability of sodium borohydride reduction to stabilize the open ring structure, and subsequent

depolymerization by heparinase I[3], we obtained a novel deanticoagulated HP derivative, NALHP,

which has no anticoagulant activity but does exhibit stable and effective anti-UC activity (Fig.

1a, Extended Data Figs. 2 and 3).

The interference of anticoagulant activity enriched during heparin drug manufacturing is one of

the reasons that the nonanticoagulant activity of conventional heparin drugs is difficult to

explore. We have adopted various methods to prepare heparin derivatives without anticoagulant

activity. The derivative III,II-2-Odes, which does not contain sulfonate groups, did not exhibit

significant therapeutic activity against UC. The derivative NAHP, obtained by opening the ring

with potassium periodate, exhibited obvious therapeutic activity against UC, indicating that

sulfonation is one of the key factors for the ability of heparin to treat UC. Molecular weight is

another key factor for the release of heparin activity. Chemical degradation of Eno and NAEno

did not result in a therapeutic effect on UC, indicating that chemical degradation destroys the

active anti-UC fragments. Therefore, we used our previously established heparinase expression

system and expressed heparinases I, II, and III. Using the recombinant heparinases, we

controlled the reduction in the molecular weight of NAHP to obtain NALHP, NAULHP and 11

fine separation fragments from the NALHP (Extended Data Fig. 3, Extended Data Table.1).

The reduction in molecular weight increased the therapeutic activity against UC, but NALHP

treatment resulted in a higher survival rate in UC model mice. In addition, among the 11

separated fragments, the efficacy of S6 is consistent with that of NALHP, the efficacy of S4 is

like that of NAULHP, and S10 shows no significant efficacy, indicating that an appropriate

molecular weight (3000Da-8000Da) is another key factor for the ability of deanticoagulated

heparin to treat UC (Extended Data Fig. 4j, Extended Data Table.1). The unique structural

modification of the anticoagulant pentasaccharide domain[3] in NALHP not only eliminated the

anticoagulant properties of HP but also resulted in anti-UC activity. The formation of gsGlcA

results from redox reaction-induced ring opening of glucuronic acid residues, whereas $\Delta 4,5$-

unsaturated glucuronic acid is a characteristic product generated during the heparinase I-

mediated cleavage of glycosidic bonds (Fig. 1e-g and Extended Data Fig. 9).

The primary structural differences between HP and NALHP are the presence and absence,

respectively, of the active anticoagulant pentasaccharide sequence and variations in the

molecular weight distribution. Thus, this unique preparation process enabled the discovery of the

unique therapeutic mechanism of deanticoagulated HP derivatives in UC. NALHP has a broad

molecular weight distribution (PDI=2.23). After separation by gel chromatography, fragment S6,

with a molecular weight within the range of 3000Da to 5000Da and a PDI of 1.1 and accounting

for 15.3% of the structure of NALHP (Extended Data Table 1 and Extended Data Fig. 3), had the

same or an even greater therapeutic effect on UC relative to NALHP (Fig. 2). We also attempted

to change the order of preparation of the nonanticoagulant by sodium borohydride reduction and

enzymatic depolymerization of HP and found that NAI45, a product generated by an initial

enzymatic reaction resulting in a low molecular weight followed by a reaction resulting in the

nonanticoagulant property[3], did not exhibit therapeutic activity against UC (Extended Data Fig.

4), indicating that the unique preparation route is also one of the reasons that the different

structure of NALHP allows it to exert therapeutic effects on UC (Extended Data Figs. 2 and 4).

In addition, we cultured organoids with fondaparinux sodium and nonanticoagulant fondaparinux

sodium but found that it did not have the same effect as NALHP did (Extended Data Fig. 24).

These results indicate that the intestinal stem cell differentiation-promoting activity and

anticoagulant activity are independent in HP molecules. We also further explored the effects of

the S6 administration method. Intravenous injection, intraperitoneal injection, and subcutaneous

injection failed to achieve the effects of oral S6 in repairing the intestinal mucosal barrier of mice

with DSS-induced colon damage (Extended Data Fig. 5). Oral administration is the best route for

NALHP/S6 to exert their effects.

To elucidate how NALHP/S6 alleviate UC, comprehensive in vitro and in vivo experiments

using DSS-treated mice were conducted. Initial observations indicated that oral NALHP

administration reduced inflammatory cell infiltration in colonic crypts, decreased serum

inflammatory cytokine concentrations, and restored the orderly proliferation of damaged crypt

structures in DSS-treated mice, effects that collectively ameliorated UC pathology (Fig. 2).

Subsequent multiomics analysis revealed that the mechanism underlying the effects of NALHP

in UC model mice is dependent on intestinal epithelial wound healing and stem cell

proliferation/differentiation (Extended Data Figs. 10 and 11). Further validation using a human

patient-derived UC organoid model revealed that NALHP/S6 restored the differentiation

trajectory of LGR5+ stem cells, in turn increasing the proportion of mucus-secreting goblet cells

in UC organoids from <10% to ≥80% (Fig. 3c), which was consistent with the findings in the

mouse model (Extended Data Figs. 11-13). This unique differentiation-promoting mechanism

effectively repaired colonic crypt structural units, reestablishing the dual protection offered by

the intestinal mechanical and chemical barriers. Transcriptome analysis revealed significant

alterations in UC organoids after NALHP treatment (Extended Data Fig. 19), particularly

inhibition of the Wnt and Notch pathways, which are associated with crypt stem cell

proliferation/differentiation. The results of mechanistic rescue experiments confirmed that

NALHP primarily suppressed these pathways to drive stem cell differentiation (Fig. 4, Extended

Data Fig. 20 and Extended Data Videos 1-6). These findings indicate that NALHP/S6 not only

alleviates UC by inhibiting inflammatory responses, as do 5-ASA[36] and infliximab, but also

promotes the repair of the mucosal layer barrier at a deeper level to cure UC.

As all intestinal crypt cells originate from LGR5+ stem cells at the crypt base, crypt destruction

contributes to the refractory nature of UC[37-39]. Endoscopic mucosal healing is considered the

gold standard for the success of clinical UC therapy. Using UC mouse model and human patient-

derived UC organoid model, we proved that NALHP/S6 promoted goblet cell differentiation in

the mucus layer, reduced the abnormal proliferation of intestinal stem cells and reinforced the

crypt self-renewal capacity by regulating the Wnt and Notch signaling pathways (Fig. 4 and

Extended Data Fig. 19), thereby repairing the intestinal mucosal barrier and disrupting the

malignant pathological cycle of UC. This study demonstrates for the first time that the

deanticoagulated HP derivatives NALHP and S6 exert mucosal barrier repair effects by

regulating crypt stem cell fate, offering an innovative strategy to overcome the limitations of

current drugs in UC therapy. The successful development of NALHP provides a promising

strategy for identifying the pleiotropic mechanisms of glycosaminoglycan-based drugs, which

has substantial translational value.

References

1. Villablanca, E. J., Selin, K. & Hedin, C. R. H. Mechanisms of mucosal healing: treating inflammatory bowel disease without immunosuppression? *Nat. Rev. Gastroenterol. Hepatol.* **19**, 493–507 (2022).

2. Alsoud, D., Verstockt, B., Fiocchi, C. & Vermeire, S. Breaking the therapeutic ceiling in drug development in ulcerative colitis. *Lancet Gastroenterol. Hepatol.* **6**, 589–595 (2021).

3. Ji, Y. et al. A heparin derivatives library constructed by chemical modification and enzymatic depolymerization for exploitation of non-anticoagulant functions. *Carbohydr. Polym.* **249**, 116284 (2020).

4. Feuerstein, J. D. et al. AGA clinical practice guidelines on the management of moderate to severe ulcerative colitis. *Gastroenterology* **158**, 1450–1463 (2020).

5. Ulcerative colitis. *Journal* **6**, 73 (2020). doi: 10.1038/s41572-020-00215-4

6. Alatab, S. et al. The global, regional, and national burden of inflammatory bowel disease in 195 countries and territories, 1990-2017: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet Gastroenterol. Hepatol.* **5**, 17–30 (2020).

7. Gajendran, M. et al. A comprehensive review and update on ulcerative colitis. *Dis. Mon.* **65**, 100851 (2019).

8. Abraham, C. & Cho, J. H. Inflammatory bowel disease. *N. Engl. J. Med.* **361**, 2066–2078 (2009).

9.   Beaugerie, L. & Itzkowitz, S. H. Cancers complicating inflammatory bowel disease reply.

N. Engl. J. Med. **373**, 195–195 (2015).

10.   Nakase, H. et al. Evidence-based clinical practice guidelines for inflammatory bowel

disease 2020. *J. Gastroenterol.* **56**, 489–526 (2021).

11.   Singh, S., Murad, M. H., Fumery, M., Dulai, P. S. & Sandborn, W. J. First- and second-

line pharmacotherapies for patients with moderate to severely active ulcerative colitis: an

updated network meta-analysis. *Clin. Gastroenterol. Hepatol.* **18**, 2179–2191.e6 (2020).

12.   Mowat, C. et al. Guidelines for the management of inflammatory bowel disease in adults.

Gut **60**, 571–607 (2011).

13.   Peyrin-Biroulet, L. & Lémann, M. Review article: remission rates achievable by current

therapies for inflammatory bowel disease. *Aliment. Pharmacol. Ther.* **33**, 870–879

(2011).

14.   Okayasu, M., Ogata, H. & Yoshiyama, Y. Use of corticosteroids for remission induction

therapy in patients with new-onset ulcerative colitis in real-world settings. *J. Mark.*

Access Health Policy **7**, 1565889 (2019).

15.   Kayal, M. & Shah, S. Ulcerative colitis: current and emerging treatment strategies. *J.*

Clin. Med. **9**, 12 (2020).

16.   Bhattacharya, A. & Osterman, M. T. Biologic therapy for ulcerative colitis.

Gastroenterol. Clin. N. Am. **49**, 717–729 (2020).

17.   Hirten, R. P. & Sands, B. E. New therapeutics for ulcerative colitis in *Annual Review of*

Medicine (ed M. E. Klotman) 199–213 (Annual Reviews, 2021).

18. Mulloy, B., Hogwood, J., Gray, E., Lever, R. & Page, C. P. Pharmacology of heparin and

related drugs. *Pharmacol. Rev.* **68**, 76–141 (2016).

19. Oduah, E. I., Linhardt, R. J. & Sharfstein, S. T. Heparin: past, present, and future.

Pharmaceuticals (Basel, Switzerland) **9**, 38 (2016).

20. Cui, J. et al. Highly sensitive and selective detection of heparin in serum based on a long-

wavelength tetraphenylethylene-cyanopyridine aggregation-induced emission luminogen.

Anal. Chem. **92**, 7106–7113 (2020).

21. Gray, E., Hogwood, J. & Mulloy, B. The anticoagulant and antithrombotic mechanisms of

heparin in *Heparin - A Century of Progress. Handbook of Experimental Pharmacology*

(eds R. Lever, B. Mulloy, & C. Page) 43–61 (Springer, 2012).

22. Ang, Y. S. et al. Randomized comparison of unfractionated heparin with corticosteroids

in severe active inflammatory bowel disease. *Aliment. Pharmacol. Ther.* **14**, 1015–1022

(2000).

23. Ludwig, R. J. et al. The ability of different forms of heparins to suppress P-selectin

function in vitro correlates to their inhibitory capacity on bloodborne metastasis in vivo.

Thromb. Haemost. **95**, 535–540 (2006).

24. Kim, S. Y. et al. Glycosaminoglycan compositional analysis of relevant tissues in Zika

virus pathogenesis and in vitro evaluation of Heparin as an antiviral against Zika virus

infection. *Biochemistry* **58**, 1155–1166 (2019).

25. Gaffney, P. R. et al. Paradoxical response to heparin in 10 patients with ulcerative-colitis.

Am. J. Gastroenterol. **90**, 220–223 (1995).

26. Törkvist, L. et al. Low molecular weight heparin as adjuvant therapy in active ulcerative

colitis. *Aliment. Pharmacol. Ther.* **13**, 1323–1328 (1999).

27. Zezos, P. et al. Low-molecular-weight heparin (enoxaparin) as adjuvant therapy in the

treatment of active ulcerative colitis: a randomized, controlled, comparative study.

Aliment. Pharmacol. Ther. **23**, 1443–1453 (2006).

28. Chande, N., MacDonald, J. K., Wang, J. J. & McDonald, J. W. D. Unfractionated or low

molecular weight heparin for induction of remission in ulcerative colitis: a cochrane

inflammatory bowel disease and functional bowel disorders systematic review of

randomized trials. *Inflamm. Bowel Dis.* **17**, 1979–1986 (2011).

29. Huang, L. et al. "Two-birds-one-stone" oral nanotherapeutic designed to target intestinal

integrins and regulate redox homeostasis for UC treatment. *Sci. Adv.* **10**, eado7438

(2024).

30. Darwish, N. H. E., Godugu, K. & Mousa, S. A. Sulfated non-anticoagulant low molecular

weight heparin in the prevention of cancer and non-cancer associated thrombosis without

compromising hemostasis. *Thromb. Res.* **200**, 109–114 (2021).

31. Hirano, A. et al. Comparison of the microbial community structure between inflamed and

non-inflamed sites in patients with ulcerative colitis. *J. Gastroenterol. Hepatol.* (2018).

32. Zhao, X. et al. Porphyromonas gingivalis exacerbates ulcerative colitis via

Porphyromonas gingivalis peptidylarginine deiminase. *Int. J. Oral Sci.* **13**, 31 (2021).

33.   Malagola, E. et al. Isthmus progenitor cells contribute to homeostatic cellular turnover

and support regeneration following intestinal injury. *Cell* **187**, 3056–3071.e17 (2024).

34.   Yin, X. et al. Niche-independent high-purity cultures of Lgr5+ intestinal stem cells and

their progeny. *Nat. Methods* **11**, 106–112 (2014).

35.   Hirten, R. P. & Sands, B. E. New therapeutics for ulcerative colitis. *Annu. Rev. Med.* **72**,

199–213 (2021).

36.   Tang, S. et al. Sustained release of 5-aminosalicylic acid from azoreductase-responsive

polymeric prodrugs for prolonged colon-targeted colitis therapy. *J. Nanobiotechnology*

22, 468 (2024).

37.   Schlegel, N. Promoting mucosal healing by targeting TMEM219-dependent intestinal

epithelial stem cell defects in inflammatory bowel disease. *J. Clin. Invest.* **135**, e192640

(2025).

38.   Sarvestani, S. K. et al. Induced organoids derived from patients with ulcerative colitis

recapitulate colitic reactivity. *Nat. Commun.* **12**, 262 (2021).

39.   Wu, J. et al. EFHD2 suppresses intestinal inflammation by blocking intestinal epithelial

cell TNFR1 internalization and cell death. *Nat. Commun.* **15**, 1282 (2024).

Methods

Preparation of deanticoagulated HP derivatives[3]

The preparation process of deanticoagulated HP derivatives was described previously. Briefly,

pharmaceutical-grade HP sodium was purchased from Changshan Biochemical Pharmaceutical

Co., Ltd. (Hebei, China). To eliminate anticoagulant activity, HP was dissolved in water at a

concentration of 33 mg/ml. The solution was reacted with an equal volume of 0.2 M periodate

sodium solution at 4 °C for 22 hr prior to neutralization reactions with 4 ml of glycol and 1.4 g of

sodium borohydride per gram of HP at 4 °C for 1 hr and 16 hr, respectively. The resulting

solution was adjusted to pH 7.0, filtered through a membrane, desalted using a 3 kDa Pellicon 2

Mini Cassette (Millipore, Germany), and lyophilized to obtain deanticoagulated HP (NAHP).

NAHP was subsequently subjected to further enzymolysis with heparinase I (Beijing Bio-Cell

Technology Co., Ltd., China). NAHP was dissolved in a reaction buffer consisting of 20 mM

Tris, 200 mM NaCl, and 5 mM $CaCl_2$ at pH 7.4. The increase in the absorbance at 232 nm was

recorded immediately after heparinase I was added to the NAHP solution. Low-molecular-weight

NAHP (NALHP) and ultra-low-molecular-weight NAHP (NAULHP) were obtained when the

absorbance increased to 45 and 100, respectively. The excess heparinase I was inactivated once

the increase reached the endpoint by heating the solution at 100 °C for 10 min. The solution was

filtered, precipitated with alcohol, and lyophilized to obtain NALHP and NAULHP. The HP

derivative NAI45 was prepared through the enzymolysis of HP using heparinase I, allowing the

increase in the absorbance to reach 45, followed by periodate sodium oxidation and sodium

borohydride reduction. The nonanticoagulant enoxaparin (NAEno) was prepared from

commercial enoxaparin (Changshan Biochemical Pharmaceutical Co., Ltd., Hebei, China) using

the same preparation process used for the oxidation of HP to NAHP.

Molecular Weight Determination of deanticoagulated HP Derivatives

The molecular weight of each HP derivative was determined using gel penetration

chromatography (GPC) as described previously. In short, an HPLC system (Waters, America)

with a binary pump module, an autosampler, and a refractive index detector was used. The

mobile phase consisted of 0.2 M sodium sulfate solution at pH 5.0. HP derivatives, the HP

sodium molecular weight calibrant (USP, America), and low-molecular-weight HP for molecular

weight calibration (NIBSC, America) were dissolved in the mobile phase at a concentration of 20

mg/ml. The samples were subsequently injected onto a 300×7.8-mm TSK Gel G2000SW$_{XL}$

column (Tosoh, Japan) in a volume of 25 μl. The column was eluted at a flow rate of 0.5 ml/min

and a temperature of 35 °C. The data were collected and analyzed in Breeze 2 (Waters, America)

software. The molecular weight distributions of the HP derivatives were calculated based on the

standard curve generated from the calibrant with a general third-order calibration method.

Fine separation of the NALHP

Fine separation of the HP derivatives was performed using a HiPrep 16/60 Sephacryl S-100 HR

column (GE Healthcare, America) with a ÄKTA prime purification system (GE Healthcare,

America). The mobile phase consisted of 0.2 M sodium chloride solution at pH 5.0. The HP

derivative NALHP was dissolved in the mobile phase at a concentration of 120 mg/ml. The

sample was subsequently injected onto the column using a 5 ml injection loop. The column was

eluted at a flow rate of 0.5 ml/min at room temperature. Fractions were collected every 10 min

from 70 min to 180 min after sample injection and were designated S1 to S11 according to the

order of retention time. Afterward, the samples were lyophilized and reconstituted in water at

30% of the original volume to enrich polysaccharides, and alcohol precipitation and another

lyophilization step were then performed to obtain the separated components.

Mouse model of DSS-induced colitis

Male C57BL/6J mice (18–22 g, 6–8 weeks) were purchased from Vital River Laboratories

(Beijing, China). The mice were housed under specific pathogen-free conditions in the laboratory

animal facility of Tsinghua University. The animal protocols 17-XXH1 and 20-XXH1 were

carried out with the approval of the Institutional Animal Care and Use Committee (IACUC) of

Tsinghua University. The laboratory animal facility was accredited by AAALAC (Association

for Assessment and Accreditation of Laboratory Animal Care) International.

Evaluation of the anti-UC efficacy of the HP derivatives was performed using a 7-day mouse

model of acute colitis. All the mice were pre-fed for one week prior to any subsequent

experiments. The mice were given 3% DSS (dextran sulfate sodium; colitis grade, MP

Biomedicals, America) solution instead of water for 7 consecutive days. The HP derivatives and

5-aminosalicylic acid (5-ASA) were dissolved in saline at a concentration of 3 mg/ml. Starting 3

days post-DSS induction, the mice were orally administered the drug solution daily at a dosage

of 30 mg/kg/d. The mice were euthanized by CO_2 inhalation after DSS induction for 7 days. The

serum was separated from the cardiac blood of the mice, while the spleens and the colons were

excised and measured. The colon tissue was cut in the longitudinal direction, washed with ice-

cold PBS, rolled with the Swiss-rolling technique, fixed, and embedded in paraffin for further

investigations.

Multiomics analyses were performed in a 14-day mouse colitis model to evaluate the systemic

changes in mice with colitis caused by drugs. The mice were allowed to drink 3% DSS solution

for 3 days, after which they received standard drinking water and drug treatment for 4 days.

Afterward, the mice were allowed to drink 2% DSS solution for another 3 days, after which they

received standard drinking water and drug treatment for another 4 days. Fresh feces were

collected prior to euthanasia by CO_2 inhalation. After the mice were sacrificed, the colons were

removed. The colonic contents were collected while the colonic epithelial tissue was scraped and

collected in 1.5 ml centrifuge tubes containing TRIzol reagent (Invitrogen, America).

ELISA

The concentrations of interleukin-6 (IL-6) and tumor necrosis factor-alpha (TNF-α) in serum and

cell culture medium were measured using an IL-6 Mouse ELISA Kit (Invitrogen, America) and a

TNF-α Mouse ELISA Kit (Invitrogen, America), respectively, according to the manufacturer's

instructions.

Principal Component Analysis (PCA)

The data matrix was standardized to unit variance to prevent scale bias. A covariance matrix was

computed and decomposed into eigenvalues and eigenvectors. Principal components

explaining >70–80% cumulative variance, or meeting Kaiser's criterion (eigenvalue >1), were

retained. Component scores were calculated by projecting data onto eigenvectors, and loadings

were computed to interpret trait contributions. A biplot visualized sample clustering and trait

relationships in the first two or three PCs. Analyses used the vegan (v.2.5–7) and ggplot2

(v.3.3.5) packages, with standard PCA functions post-preprocessing.

Biolayer interferometry

The molecular interactions between DSS and the HP derivatives were evaluated using an Octet

Red96 instrument (FortéBIO, America). DSS and the HP derivatives were dissolved in HBS-EP

buffer containing 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, and 0.005% Tween 20 at pH

7.4. The streptavidin sensors were loaded with DSS washed in HEB-EP buffer and exposed to

the HP derivatives.

RNA isolation and qPCR

Total RNA was extracted using TRIzol reagent (Invitrogen) and reverse transcribed to cDNA

using a FastKing RT Kit (TIANGEN, China). All qPCRs were run in a CFX96 Touch Real-Time

PCR Detection System (Bio-Rad, America) using Talent qPCR PreMix (TIANGEN, China) with

the specific primers listed in the extended data.

FTIR spectroscopy

The infrared absorption spectra of the HP derivatives were generated using a Nicolet 6700 FTIR

spectrometer (Thermo Electron Corporation, Shanghai, China) with the potassium bromide tablet

method. The spectral data were collected in a 4000–400 cm^{-1} range for all the samples.

NMR analysis

For 1D (^1H, ^{13}C) and 2D-NMR analyses, HP derivatives (50–60 mg) were dissolved in 0.6 mL of

deuterium oxide and lyophilized repeatedly to remove exchangeable protons. The thoroughly

dried samples were then dissolved in 0.5 mL of deuterium oxide with 0.002% 3-(trimethylsilyl)

propionate sodium salt (TSP) and transferred into 25 × 0.5-cm NMR tubes (Wilmad Lab Glass,

America). 1D (^1H, ^{13}C) and 2D-NMR experiments were performed at 298 K on a Bruker

Advance 600 MHz spectrometer (Germany) equipped with a 5 mm helium-cooled cryoprobe

using the following parameters: Proton—number of scans, 16; number of dummy scans, 2;

relaxation delay, 1.0 s; spectral width, 20 ppm; and transmitter offset, 6.0 ppm. One-dimensional

^{13}C spectra were obtained with proton decoupling during acquisition at 298 K over 5000 scans.

All the spectra were Fourier transformed, phased and baseline corrected. The chemical shift

values were calibrated with TSP at 0.00 ppm. HSQC spectra were recorded with carbon

decoupling during acquisition with 256 increments of 16 scans. The polarization transfer delay

was set for a $^1J_{C-H}$ coupling value of 145 Hz.

Microbiome analysis

Sample preparation and DNA extraction

Fresh fecal samples from colitis model mice were collected in 1.5-ml centrifuge tubes and stored

immediately at –80 °C until further analysis. Microbial genomic DNA samples were extracted

using a DNeasy PowerSoil Kit (QIAGEN, Germany) following the manufacturer's instructions.

The DNA concentrations in the samples were subsequently quantified using a NanoDrop ND-

1000 spectrophotometer (Thermo Fisher Scientific, America), and the samples were then

qualified by agarose gel electrophoresis.

16S rRNA amplicon sequencing

The V3–V4 region of the bacterial 16S rRNA gene was amplified by PCR using the forward

primer 338F (5'-ACTCCTACGGGAGGCAGCA-3') and the reverse primer 806R (5'-

CGGACTACHVGGGTWTCTAAT-3'). Sample-specific 7-bp barcodes were added to the

primers for further multiplex sequencing. PCR amplicons were purified using VAHTS™ DNA

Clean Beads (Vazyme, China) and quantified using a PicoGreen dsDNA Assay Kit (Invitrogen,

America) prior to manipulation to achieve equal amounts of DNA. Afterward, paired-end 2 ×

250 bp sequencing was performed on the MiSeq platform (Illumina, America) with a NovaSeq

6000 SP Reagent Kit.

Microbiome data analysis

The raw sequence data were processed with QIIME2 2019.4 (Bolyen *et al*. 2018) with slight

modifications based on the official tutorials (https://docs.qiime2.org/2019.4/tutorials/). In brief,

the raw data were demultiplexed with the demux plugin, and primers were removed with the cut

adapt plugin. Afterward, the data were subjected to quality filtering, denoising, merging, and

chimera removal with the DADA2 plugin. A count table without rarefaction was used for further

analysis. The following analysis was carried out using an in-house-developed R script in Rstudio

software (v.2021.09.1, R version 4.1.2). Alpha diversity analysis and principal coordinate

analysis (PcoA) were performed using the vegan (v.2.5-7) package. Enterotyping was performed

with the Dirichlet multinomial mixture model with the DirichletMultinomial (v.1.36.0) package.

Data visualization was performed using the ggplot2 (v.3.3.5) and ggalluvial (v.0.12.3) packages.

In addition, LefSe analysis was performed on the Genescloud platform

(https://www.genescloud.cn/home).

Metabolome analysis

Sample preparation and extraction

Samples of the colonic contents were thawed on ice. Aqueous homogenates were obtained by

mixing 100 mg of each sample with 300 µl of ice-cold water and steel balls for 5 min prior to

incubation on ice for 10 min. Then, 500 µl of methanol was added, and the homogenates were

mixed by vortexing for 5 min prior to incubation on ice for another 10 min. The homogenates

were centrifuged (12,000 rpm, 4 °C, 10 min), and 600 µl of the supernatant was transferred to

1.5-ml centrifuge tubes for further concentration. The concentrated dry products were dissolved

in 100 µl of 5% methanol–water, vortexed, and centrifuged (12,000 rpm, 4 °C, 10 min). Finally,

the supernatants were collected for LC–MS/MS analysis.

LC–MS analysis

A combination of positive ion mode MS and negative ion mode MS was applied to identify the

metabolites in the colonic contents. Data were acquired with an LC–MS system comprising a

1290 Infinity LC System (Agilent, America) coupled to a 6545 LC/Q-TOF mass spectrometer

(Agilent, America). The method details are summarized as follows. The supernatants were

injected onto a 100 × 2.1-mm ACQUITY UPLC HSS T3 C18 column (Waters, America) in a

volume of 2 µl. The column was eluted at a flow rate of 400 µl/min and a temperature of 40 °C.

Mobile phase A (water with 0.1% formic acid) and mobile phase B (acetonitrile with 0.1%

formic acid) were used with the following gradient program: 95:5 V/V A:B at 0 min, 10:90 V/V

at 11.0 min, 10:90 V/V at 12.0 min, 95:5 V/V at 12.1 min, 95:5 V/V at 14.0 min. In positive ion

mode, MS analysis was carried out using the following settings: ion spray voltage, 250; gas flow,

8; fragmentor, 135; gas temperature, 325 °C; sheath temperature, 325 °C; sheath flow, 11; and

nebulizer, 40. In negative ion mode, MS analysis was carried out using the following settings:

ion spray voltage, 1,500; gas flow, 8; fragmentor, 135; gas temperature, 325 °C; sheath

temperature, 325 °C; sheath flow, 11; nebulizer, 40.

Metabolome data analysis

The raw data obtained by LC–MS analysis were first converted into mzML format with

ProteoWizard software. Peak extraction, alignment, and retention time correction were carried

out with the XCMS program, while the peak area was corrected using the "SVR" method. Peaks

with a deletion rate of $> 50\%$ were filtered out in each group of samples. Next, metabolic

identification information was obtained by searching the laboratory's in-house-built database and

integrating the public database and the metDNA tool. Finally, statistical analysis was carried out

using an in-house-developed R script in RStudio software (v.2021.09.1, R version 4.1.2).

Metabolites at the MS2 confidence level were selected for the following analysis. Principal

component analysis (PCA) was performed and the results were visualized using the vegan

(v.2.5–7) and ggplot2 (v.3.3.5) packages, respectively. Orthogonal partial least squares

discriminant analysis (OPLS-DA) was carried out using the ropls (v.1.26.0) package, and

metabolites with a VIP > 1, $p < 0.05$, and $|logFC| > 1$ were identified as differentially abundant

metabolites. The abundances of the differentially abundant metabolites in each group were

visualized using the ComplexHeatmap (v.2.10.0) package. Spearman correlation analysis was

performed on the the metabolome and microbiome data, and the results were visualized using the

WGCNA (v.1.70-3) and pheatmap (v.1.0.12) packages, respectively. The Mantel test was

performed between the metabolome and microbiome data using the ggcor (v.0.9.4.3) package.

Transcriptome analysis

RNA-seq library construction and sequencing

Total RNA from the colonic epithelial tissue of colitis model mice was extracted using TRIzol

reagent (Invitrogen, America). The RNA-seq libraries were constructed using a TruSeq RNA

Sample Prep Kit (Illumina, America) according to the manufacturer's instructions. The polyA+

RNA was enriched, fragmented, and reverse transcribed to obtain cDNA, and end repair, PCR

amplification, purification, and quantification were then performed. The libraries were

subsequently sequenced on the Illumina NovaSeq 6000 platform.

RNA-seq data analysis

The raw data were quality filtered using fastx_toolkit (v.0.0.14), mapped to the mouse genome

GRCm39 using Bowtie2 (v.2.4.1), assembled with cufflinks (v.2.2.1), and quantified with RSEM

(v.1.1.3).

The transcripts per million (TPM) values were used in the following analysis. Low-abundance

data were filtered based on the mean TPM values. The differentially expressed genes were

defined as those whose p value was <0.05 with the DESeq2 (v.1.34.0) package, and GO and

KEGG enrichment analyses were then performed with the clusterProfiler (v.4.2.1) package. The

results were visualized using the ggplot2 (v.3.3.5) and ComplexHeatmap (v.2.10.0) packages.

Cell culture

All the cells were maintained at 37 °C in 5% CO_2 in a Heracell 150i incubator (Thermo Fisher

Scientific, America). Human NCM460 cells (ATCC) were cultured in RPMI 1640 medium

(Gibco, America) supplemented with 10% fetal bovine serum (Gemini, America). Mouse

RAW264.7 cells (ATCC) were cultured in DMEM (Gibco, America) supplemented with 10%

fetal bovine serum.

To assess the anti-inflammatory effects of the HP derivatives, RAW264.7 cells were seeded in

96-well plates, stimulated with 100 ng/ml lipopolysaccharide (Sigma–Aldrich, America) for 15

min, and treated with the HP derivatives at a concentration of 1 mg/ml for 24 hr. The

supernatants were collected and subjected to ELISA.

UC organoid culture

Human UC patient-derived colonoids were cultured as previously described[40,41] with slight

modifications. Colon tissue samples were obtained from biopsies taken from male and female

UC patients aged 20 to 80 years (inclusive); in all patients, UC had been clearly diagnosed for

more than 3 months through clinical manifestations and endoscopic examination. All samples

were graded as mild to moderate active ulcerative colitis (Mayo score: 3–10) and were collected

at Tsinghua Changgung Hospital (22111–4-02) in Beijing, washed in ice-cold PBS, incubated

with 10 mM DTT for 15 min, and disassociated in PBS containing 20 mM EDTA for 60 min at

4 °C. The crypts were isolated by vortexing, collected by centrifugation, embedded in growth

factor-reduced Matrigel (Corning), and cultured in complete medium consisting of advanced

DMEM/F12 (Thermo Fisher Scientific, America) supplemented with 1% penicillin and

streptomycin (Thermo Fisher Scientific, America), 10 mM HEPES (Thermo Fisher Scientific,

America), 2 mM GlutaMAX (Thermo Fisher Scientific, America), 1 × B-27 supplement (Thermo

Fisher Scientific, America), 1 mM N-acetylcysteine (Sigma–Aldrich, America), 100 ng/ml

recombinant mouse EGF (Thermo Fisher Scientific, America), 100 ng/ml recombinant human

Noggin (PeproTech, America), 1 µg/ml recombinant human R-spondin-1 (PeproTech, America),

500 nM A83-01 (Tocris, England), 10 µM SB202190 (Sigma–Aldrich, America) and 10%

Afamin/WNT3A conditioned medium (JSR Life Sciences, Japan). To prevent anoikis, 10 mM Y-

27632 (STEMCELL Technologies, Canada) was added to the complete medium for the first day

of culture. The colonoids were passaged every 6 to 7 days by mechanical disassociation, and the

medium was changed every day to ensure their rapid growth.

EdU labeling

EdU labeling of proliferating cells in the colonic epithelia of colitis model mice was performed

on 3-μm sections of paraffin-embedded tissues with a Click-iT EdU Imaging Kit (Invitrogen,

America) according to the manufacturer's protocol.

Immunohistochemical and immunofluorescence staining

Paraffin-embedded sections (3 μm thick) were deparaffinized, washed with PBS containing

0.01% Tween 20, and subjected to antigen retrieval by immersion in Tris-EDTA buffer (pH 9.0)

at 100 °C for 20 min.

For immunohistochemical staining, the samples were blocked using peroxidase-blocking

solution (Dako, Denmark) and incubated with specific primary antibodies at 4 °C overnight. The

fluorescence signals were detected using a REAL EnVision Detection System (Dako, Denmark)

and observed using AxioScan. Z1 Slide Scanner (Zeiss, Germay).

For immunofluorescence staining, the samples were blocked with 1% BSA/PBS for 1 hr,

incubated with specific primary antibodies at 4 °C overnight, and then incubated with secondary

antibodies; nuclei were then stained, and the samples were mounted with ProLong Gold Antifade

Mountant (Thermo Fisher Scientific, America) and observed using inverted confocal microscopy

(Nikon, Japan).

Single-cell RNA sequencing[42]

Preparation of single-cell suspensions from UC organoids

The UC organoids grown on filter paper were placed on an ice-cold plate and allowed to cool for

2–3 minutes. The sample wells containing the tissue spheroids to be analyzed were confirmed,

the culture medium in the wells was discarded, and the solid Matrigel^{TM} was left. One milliliter

of precooled (4 °C) advanced DMEM/F12 culture medium supplemented with 1% HEPES, 1%

P/S and 1% GlutaMAX was added to each well, the Matrigel^{TM} surrounding the UC organoids

was gently disrupted by pipetting to break it down and dissolve it, and the organoids were

collected in 15 mL centrifuge tubes. This procedure was repeated 3 times until all the tissue

spheroids were disrupted by pipetting and collected. The mixture was centrifuged at 300 × g and

4 °C for 5 minutes, the supernatant was removed, 3 mL of precooled (4 °C) advanced

DMEM/F12 culture medium was added to resuspend the pellet, and the mixture was centrifuged

again at 200 × g and 4 °C for 5 minutes to remove the supernatant to obtain the colon tissue

spheroids. Two milliliters of 0.25% trypsin was added to the suspension, which was subsequently

incubated at 37 °C in a water bath for 5 minutes, after which an equal volume of RPMI-1640

medium containing 10% fetal bovine serum (FBS) was added to terminate the enzymatic

digestion. A 1 mL pipet was used to pipet the suspension ten times. The suspension was

centrifuged at 300 × g and 4 °C for 5 minutes, and the supernatant was removed. Then, 2 mL of

0.0005% Y-27632/TrypLE was added to generate a suspension, which was incubated at 37 °C in

a water bath for 15 minutes and pipetted ten times at 5-minute intervals. After the incubation was

complete, an equal volume of RPMI-1640 medium containing 10% FBS was added to terminate

the reaction. The suspension was centrifuged at 400 × g and 4 °C for 5 minutes, and the

supernatant was removed. Then, 50–200 μL of RPMI-1640 medium containing 10% FBS was

added to generate a suspension so that the cell concentration was within the range of 700–1200

cells/μL. This suspension was disrupted by vigorous pipetting ten to twenty times to obtain

single cells from the UC organoids.

Single-cell RNA sequencing and library construction for colonic organoids

The concentration and viability of the cells in the single-cell suspensions of colonic organoids

were measured with a cell counter. Samples with a cell viability greater than 80%, an

agglomeration rate of less than 5% and a lack of obvious cell debris or impurities were

considered suitable for library construction. Using microfluidic technology, gel beads and

individual cells with specific cell barcodes and reverse transcription information were coated

with oil droplets. The cells were solubilized and released mRNA in this system, and the mRNA

was captured by the gel beads and reverse transcribed to generate the full-length cDNA

sequence. The oil droplets were then disrupted and purified, the amount of cDNA was increased

by PCR amplification, and the sequencing primers were ligated. The cDNA was cleaved into

fragments of approximately 200~300 bp by a chemical method, end repair was carried out, P7

adapters were connected, sample barcodes were introduced, and the sequence fragments were

screened. The library was sequenced on the Illumina NovaSeq platform with a PE150

sequencing strategy.

The unique molecular identifiers (UMIs) in the off-machine data were preprocessed using

CellRanger software, an official tool of 10x Genomics. Loupe Browser 6 software, an official

tool of 10x Genomics, was used to delete the multicell data, low-quality data, and apoptotic cell

data. The corresponding data barcode criteria were a UMI count of greater than 60,000, a feature

count of less than 210, and a percentage of mitochondrial UMIs of greater than 25%. Afterward,

the uniform manifold approximation and projection (UMAP) method was used for

dimensionality reduction. After dimensionality reduction, the CellRanger off-machine data were

imported into R Studio, and Seurat was used for dimensionality reduction classification.

Data availability

All the data supporting the results of this study are available within the paper and its

Supplementary Materials. Additional processed data are available from the corresponding

authors upon request.

Methods references

40.   Fujii, M., Matano, M., Nanki, K. & Sato, T. Efficient genetic engineering of human

949   intestinal organoids using electroporation. *Nat. Protoc.* **10**, 1474–1485 (2015).

950   41.   Sato, T. et al. Long-term expansion of epithelial organoids from human colon, adenoma,

951   adenocarcinoma, and Barrett's epithelium. *Gastroenterology* **141**, 1762–1772 (2011).

952   42.   Hao, Y. et al. Dictionary learning for integrative, multimodal and scalable single-cell

953   analysis. *Nat. Biotechnol.* **42**, 293–304 (2024).

Acknowledgments

We thank the National Center for Electron Microscopy in Beijing, School of Materials Science, Tsinghua University, for assistance with electron microscopy imaging; the Laboratory Animal Resources Center, Tsinghua University, for technical support; and the Center of Biomedical Analysis, Tsinghua University, for assistance with imaging technology and flow cytometry; Key Research and Development Program of the Ministry of Science and Technology (2023YFA0914300) and Shenzhen Medical Research Fund (SMRF, B2302009), for regarding financial assistance.

Author contributions

XH. X., Y. W. and X. J. oversaw the research. W. H., L. H., Y. W., W. Z. and XH. X. designed the research strategy. W. H., XY. R and W. Z. established the ulcerative colitis organoids. W. H., L. H., ZK. L., QX. Z., W. Z, and XY. R. performed the experiments. W. H., Y. W., and ZQ. Z. analyzed the experimental data. W. H., Y. W., and XH. X. prepared the manuscript. YS. Y., HC. Z and Y. C. provided the materials needed for the experiments. All the authors approved the manuscript.

Competing interests

XH. X., W. H. and Y. W. are inventors on related patents filed by Tsinghua University describing the materials reported in this study. The other authors declare that they have no competing

975   interests.

   Extended Data

   Extended Data Fig.1| Therapeutic efficacy evaluation of the library of non-anticoagulated

   heparin derivatives.

a, 3%DSS was added to the drinking water for 7 days to induce acute colitis in mice (n=10). The

control group of mice was given regular drinking water (n=10), and the drug treatment group was

given 30mg/kg heparin (HP), Enoxaparin (Eno), Nonanticoagulant heparin (NAHP),

Nonanticoagulant Enoxaparin (NAEno), Heparin digested by heparinase I(I-45), Heparin digested

by heparinase II and heparinase III(III-II-2) on the third day (n=10). **b,** Changes in weight **c-f,** Mice

were scarified on day 7 and colon (**c**) and spleen (**d**) were collected, Colon length (**e**) and Spleen

index (**f**) were quantitated. **g,** Representative images of colons stained with Hematoxylin and eosin,

Scale bar, 100μm. Shown (**b, e, f**) are representative images or quantitative analysis from at least

n=5 biologically independent samples. Data represent mean ±SD. * $p < 0.05$, ** $p < 0.01$, *** $p <$

0.001, **** $p < 0.0001$ and ns (no significance) $p > 0.05$, analyzed by ordinary one-way ANOVA

(**b**) multiple comparisons test.

Extended Data Fig.2| Therapeutic efficacy evaluation of different molecular weight NAHP.

a, Changes in weight **b-e,** Mice were scarified on day 7 and colon (**b**) and spleen (**c**) were collected,

Colon length (**d**) and Spleen index (**e**) were quantitated. **f,** Representative images of colons stained

with Hematoxylin and eosin, Scale bar, 100μm. **g,h,** The concentration of Serum IL-6 (**g**) and

TNF-α (**h**) were determined by ELISA when mice were scarified on day 7. **i,** The death status of

mice after being modeled with DSS and treated with NAHP, NALHP and NAULHP. **j,** The

adsorption(A) and desorption(D) response curves among HP, NAHP, NALHP, NAULHP and DSS

by Bio-Layer Interferometry (BLI), blue line represents the blank contrast, orange line represents

the sample.

Shown (**a, d, e, g-l**) are representative images or quantitative analysis from at least n=5 biologically

independent samples. Data represent mean ±SD. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p <$

0.0001 and ns (no significance) $p > 0.05$, analyzed by ordinary one-way ANOVA (**a**) multiple

comparisons test.

1008

1009 **Extended Data Fig. 3| The physicochemical properties of heparin derivatives.**

1010

a, Gel chromatograms of four batches production of NALHP. **b,** The morphology and

solubility of NALHP prepared by four batches (#1-#4). **c,** The concentration of IL-6 factor in the

cell supernatant of RAW264.7 cells after treatment with the four batches of NALHP. **d**, Gel

exclusion chromatograms of the separated components from two batches (BATCH-1 and -2).

Shown (**c**) are representative images or quantitative analysis from n=4 biologically independent

samples. Data represent mean ±SD. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$ and

ns (no significance) $p > 0.05$, analyzed by ordinary one-way ANOVA (**g**) multiple comparisons

test.

Extended Data Fig.4 | Therapeutic efficacy evaluation of different non-anticoagulated

heparin derivates.

1021

a, Changes in weight. **b-e,** Mice were scarified on day 7 and colon (**b**) and spleen (**c**) were collected,

Colon length (**d**) and Spleen index (**e**) were quantitated. **f,** Representative images of colons stained

with Hematoxylin and eosin, and Histological score (**g**) were quantified. Scale, 100μm. **h,i,** The

concentration of Serum IL-6 (**h**) and TNF-α (**i**) were determined by ELISA when mice were

scarified on day 7. j, Principal component analysis of phenotypes pertaining to UC treatment by

HP, NAHP, NALHP, NAULHP, S4, S6 and S10.

Shown (**d, e, g-i**) are representative images or quantitative analysis from n=6 biologically

independent samples. Data represent mean ±SD. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p <$

0.0001 and ns (no significance) $p > 0.05$, analyzed by ordinary one-way ANOVA (**a**) multiple

comparisons test. The data obtained from the PCA analysis represent the improvement in the

characteristics of UC mice (including body weight, colon length, spleen index, serum IL-6 and

TNF-α levels, and histological scores) treated with drugs of different molecular weights (HP,

NAHP, NALHP, NAULHP, S4, S6 and S10).

1035

1036

1037 **Extended Data Table.1** The molecular weight size and distribution of NALHP and its fine
1038 fragments

Name	Separation(mg)	Content (%, w/w)	M_w （Da）	P	M_w （Da） Distribution （%）			
					>8k	5k~8k	3k~5k	<3k
NALHP	650	100	6224	2.33	28.04	27.87	19.11	24.95
NAULHP	-	-	2974	3.22	5.21	14.96	20.05	59.77
S1	37.7	5.8	12121	1.036	99	1		
S2	44.2	6.8	9557	1.037	80	20		
S3	42.9	6.6	7686	1.038	38	60	2	
S4	37.7	5.8	6254	1.041	8	78	13	
S5	89.7	13.8	5094	1.055	1	50	46	2
S6	99.5	15.3	4115	1.076		19	68	13
S7	71.5	11.0	3227	1.117		5	50	45
S8	78.65	12.1	2426	1.172		1	23	76
S9	62.4	9.6	1736	1.188			7	93
S10	48.1	7.4	1282	1.153			1	99
S11	37.7	5.8	812	1.073				100

1039

1040

1041
1042

1043

1044 **Extended Data Fig. 5| Therapeutic efficacy evaluation of the library of S6.**

1045

a, The body weight changes of mice under different administration methods (Intravenous

injection(i.v.), intraperitoneal injection(i.p.), hypodermic injection(i.h.)). **b,** The body weight

changes of mice under different administration methods. **c-f,** Mice were scarified on day 7 and

colon (**c**) and spleen (**d**) were collected, Colon length (**e**) and Spleen index (**f**) were quantitated.

g, The concentration of Serum IL-6 was determined by ELISA when mice were scarified on day

7. Shown (**a, e-g**) are representative images or quantitative analysis from at least n=5 biologically

independent samples. Data represent mean ±SD. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p <$

0.0001 and ns (no significance) $p > 0.05$, analyzed by ordinary one-way ANOVA (**g**) multiple

comparisons test.

1055

1056   **Extended Data Fig. 6| Infrared spectra of different heparin derivatives.**

1057

1058   **a,** Infrared full spectrum of heparin derivates. **b,** Infrared spectra between 2000 cm^{-1} and 500 cm^{-}

1059 ^{1} of heparin derivates.

1060

1061

1062

1063

1064   **Extended Data Table.2** The batch numbers of raw materials and products of 4 batches of
1065   NALHP production

Batch Number	#1	#2	#3	#4
HP	NHS210204	NHS200606	NHS200803	NHS180302
NAHP	BATCH-211019	BATCH-210401	BATCH-210319	BATCH-190304
NALHP	BATCH-211023	BATCH-210408	BATCH-210402	BATCH-190504

1066

1067

1068 **Extended Data Table.3** Preparation process parameter standards for 4 batches of NALHP
1069 production

Process Indicators	#1	#2	#3	#4	Process standard	Qualified or unqualified
anti-Xa （IU/mg）	19.4	18.1	18.5	19.0	<20	Qualified
A_{232}	19.0	12.2	28.1	23.4	<30	Qualified
ΔA_{232}	41.0	39.7	38.8	39.6	39.5±2.0	Qualified
A_{294}	0.167	0.134	0.189	0.245	<0.350	Qualified
A_{420}	0.018	0.019	0.015	0.022	<0.025	Qualified
NALHP ΔM_w （Da）	102	136	150	242	- 300~300	Qualified

1070

1071

Extended Data Table.4 The molecular weight size and distribution of 4 batches of NALHP production

Batch number	M_w （Da）	ΔM_w （Da）	P	M_w （Da） Distribution （%）			
				>8k	5k~8k	3k~5k	<3k
#1	6326	102	1.505	28	34	20	18
#2	6360	136	1.494	29	33	21	17
#3	6374	150	1.573	30	32	19	19
#4	6466	242	1.548	31	29	21	19
Standard	6224	0	1.531	28	32	21	19

1078 **Extended Data Fig.7 | ¹³C NMR spectrum of different heparin derivatives.**

1079

1080

Extended Data Table.5 ^{13}C NMR chemical shift attribution of HP and different non-
 anticoagulated heparin derivatives

Peak position	Test the chemical shift of the sample（ppm）							Chemical shift attribution
	HP	NAHP	NALHP	NAULHP	S4	S6	S10	
a	177.7	176.7	177.7	177.7	177.7	177.7	177.7	U, -**COOH**; GlcNAc6S / GlcNAc, **CH₃CO**-
b	-	-	172.1	172.1	172.1	172.1	172.1	ΔU / ΔU2S, -**COOH**
c	-	-	147.6	147.6	147.6	147.6	147.6	ΔU2S, **C5**
d	-	-	108.9	108.9	108.9	108.9	108.9	ΔU2S, **C4**
e	-	106.7	106.7	106.7	106.7	106.7	106.7	gsIdoA / gsGlcA, **C1**
f	102.3	102.3	102.3	102.3	102.3	102.3	102.3	IdoA2S, **C1**
g	99.9	99.9	99.9	99.9	99.9	99.9	99.9	ΔU2S / GlcNS6S / GlcNS / GlcNAc6S / GlcNAc, **C1**
h	-	99.1	99.1	99.1	99.1	99.1	99.1	**GlcNAc**-(gsIdoA)/ **GlcNAc**-(gsGlcA), **C1**
i	-	-	93.9	93.9	93.9	93.9	93.9	GlcNS-α-RE
j	24.8	24.8	24.8	24.8	24.8	24.8	24.8	-**CH₃CO**-

    Extended Data Fig.8| ¹H NMR spectrum of different heparin derivatives.

 Extended Data Table.6 ^{1}H NMR chemical shift attribution of HP and different non-
 anticoagulated heparin derivatives

Peak position	Test the chemical shift of the sample（ppm）							Chemical shift attribution
	HP	NAHP	NALHP	NAULHP	S4	S6	S10	
a	-	-	5.99	5.99	5.99	5.99	5.99	ΔU, **H4**
b	5.58	-	-	-	-	-	-	**GlcNS-(GlcA), H1**
c	5.53	5.53	5.53	5.53	5.53	5.53	5.53	GlcNS3S6S, **H1**
d	-	-	5.52	5.52	5.52	5.52	5.52	ΔU, **H1**
e	5.42	5.42	5.42	5.42	5.42	5.42	5.42	GlcNS6S / GlcNAc6X / **GlcNS6X**-(gsIdoA) / **GlcNS6X**-(gsGlcA), **H1**
f	5.35	-	-	-	-	-	-	**GlcNS6X**-(IdoA), **H1**
g	5.22	5.22	5.22	5.22	5.22	5.22	5.22	IdoA2S, **H1**
h	-	5.12	5.12	5.12	5.12	5.12	5.12	**GlcNAc**-(gsIdoA)/ **GlcNAc**-(gsGlcA), **H1**
i	5.01	-	-	-	-	-	-	**IdoA**-(GlcNS), **H1**
j	4.83	4.92	4.83	4.83	4.83	4.83	4.83	IdoA2S, **H5**
k	-	4.97	4.97	4.97	4.97	4.97	4.97	gsIdoA, **H1**
l	-	4.85	4.85	4.85	4.85	4.85	4.85	gsGlcA, **H1**
m	-	4.73	4.73	4.73	4.73	4.73	4.73	gsXyl, **H1**
n	4.64	4.64	4.64	4.64	4.64	4.64	4.64	Gal, **H1**
o	4.61	-	-	-	-	-	-	GlcA, **H1**
p	-	-	4.63	4.63	4.63	4.63	4.63	ΔU, **H2**
q	4.34	4.34	4.34	4.34	4.34	4.34	4.34	IdoA2S, **H2**
r	3.40	-	-	-	-	-	-	GlcA, **H2**
s	3.28	3.28	3.28	3.28	3.28	3.28	3.28	GlcNS6X, **H2**
t	2.05	2.05	2.05	2.05	2.05	2.05	2.05	-C**H₃**CO

1094   **Extended Data Fig.9| Heteronuclear singular quantum correlation (HSQC) of different**

1095   **heparin derivatives.**

1096

1097

1098   **a,** HP. **b,** NAHP. **c,** S4. **d,** NAULHP. **e,** S10. **f,** NAI45.

1099

1100

Extended Data Fig.10| Microbiological and metabolome analysis.

a, Intestinal type analysis under the action of different heparin derivatives. **b,** The distribution of

marker flora at the genus level in the DMM classification model. **c,** The composition of intestinal

flora at the genus level in each experimental group. **d,** Changes in metabolites among different

experimental groups**. e,** Spearman correlation analysis of the microbiome and metabolome. **f,**

Mantel analysis of the microbiome and metabolome.

 Extended Data Fig.11| Transcriptome analysis of the colons of UC and drug-treated mice.

1111

1112   **a,** Differential genes analysis. **b,** Enrichment analysis of differential genes. **c,** GO enrichment

1113   analysis of differential genes under the action of different heparin derivatives.

1114

1115　**Extended Data Fig.12| The expression level of TCF1 in the colonic submucosal layer of**

1116　**colitis model mice.**

1117

1118　Representative images of immunohistochemical staining for TCF1 in healthy and colitis mice

1119　treated by water, NALHP, S6, S4, S10, HP and 5-ASA. Scale bar, 100 μm. Representative

1120　images from n= 5 biologically independent samples are shown.

1121

1122

1123 **Extended Data Fig.13| The expression level of PCNA in the colonic submucosal layer of**

1124 **colitis model mice.**

1125

1126 Representative images of immunohistochemical staining for PCNA in healthy and colitis mice

1127 treated by water, NALHP, S6, S4, S10, HP and 5-ASA. Scale bar, 100 μm. Representative

1128 images from n= 5 biologically independent samples are shown.

1129

1130

1131

1132

1133

1134

1135 **Extended Data Fig.14| The expression levels of MUC2 and PCNA vary among human [1],**

1136 **mice, and organoids.**

1137

1138 Representative images of immunohistochemical staining for MUC2(a) and PCNA(b) in human,

1139 mice and organoids. Scale bar, 50 μm. Representative images from n= 3 biologically

1140 independent samples are shown.

1141

1142

1143

1144 [1] He, T., Wang, W., Li, L., Qiu, S., Sun, S., & Zong, L. (2022). PCNA, EGFR, MUC2

1145 expression levels and clinical significance in ulcerative colitis. *Journal of Medical Research*,

1146 *51*(3), 104-107.

1147

1148 **Extended Data Fig.15| Single-cell transcriptome analysis.**

1149

1150 **a,** The proportion of cells in different groups. **b,** The changes in cell types of organoids under the

1151   action of heparin derivatives. **c,** Cell typing criteria. **d,** The expression of genes in different cell

1152   types. **e,** Schematic diagram of cell type changes in UC organoids.

1153

1154

1155   **Extended Data Fig.16 | Pseudotime Analysis reveals the trajectory of stem cells**

1156   **differentiating into goblet cells in organoids**

1157

1158   The single-cell RNA-seq data from stem cells of UC-type organs were subjected to time-series

1159   analysis (using Monocle2) under different cell types **(a)** and different group **(b)**. The cells were

1160   arranged on a continuous trajectory based on their transcriptional status. The cells were sorted

1161   according to pseudo-time, and genes were clustered according to their expression patterns (blue:

1162   intestinal epithelial cells; yellow: intestinal stem cells; green: TA cells).

1163

1164

1165

1166 **Extended Data Fig.17 | U-map dimensionality reduction analysis.**

1167

1168 Dimensionality reduction of U-maps under the effects of NALHP, S6, and 5-ASA in three

1169 different UC patient derived UC organoids (UC1-UC3).

1170

1171

1172

1173

1174

1175 **Extended Data Fig.18 | NCM460 cell fluorescence staining image**

1176

1177 NCM460 cells were stimulated with IL-6 and treated with HP, NALHP, S4, S6, S10, 5-ASA (1

1178 mg/mL), scale bar=50 um. The expression level of ZO-1 protein was detected by fluorescent

1179 staining.

1180

1181   **Extended Data Fig.19 | Organoid transcriptomic analysis.**

1182

1183   **a,** GO enrichment analysis of differentially expressed genes in UC organoids after NALHP

1184   treatment. **b,c,** Bright-field diagram of untreated (UC)(**b**) and under the treatment of IWP-2 and

1185   DAPT (ID)(**c**), scale bar=200 um. **d,e,** Relative mRNA expression of MUC2(**d**) and LGR5(**e**)

1186 under the treatment of IWP-2 and DAPT (ID).

1187

1188 **Extended Data Fig.20 | Bright-field diagram**

1189

1190

1191 UC organoids under the treatment of NALHP(a2), S6(a3), CV(a4), CV+NALHP(a5),

1192 CV+S6(a6), scale bar=200 um

1193

1194 **Extended Data Fig.21 | Expression of key proteins after NALHP/S6 and CHIR99021(C)**

1195 **and VPA(V) were co-cultured with UC organoids.**

1196

1197

1198

1199

1200 **Extended Data Fig.22 | Expression of key proteins after NALHP/S6 and CHIR99021(C)**

1201 **were co-cultured with UC organoids.**

1202

1203

1204 **Extended Data Fig.23 | Expression of key proteins after NALHP/S6 and VPA(V) were co-**

1205 **cultured with UC organoids.**

1206

1207

1208

1209 **Extended Data Fig.24 | Expression of key proteins after fondaparinux (Fonda) and non-**

1210 **anticoagulated fondaparinux (gs-Fonda) were co-cultured with UC organoids.**

1211

1212

1213 Extended Data is available for this paper.

1214

1215 **Correspondence and requests for materials should be addressed to** Xin-Hui Xing, Tel: 86-

1216 10-62794771, Email: xhxing@tsinghua.edu.cn, Yi Wang, Tel: 86-10-62773004, Email:

1217 wangyi671@mail.tsinghua.edu.cn, Xuan Jiang, Email: jiangxuan68@126.com

1218

1219