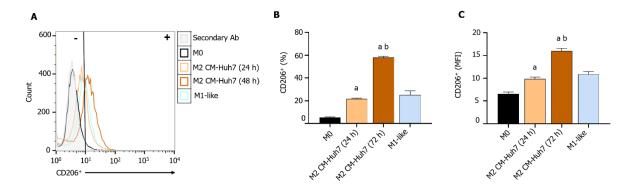
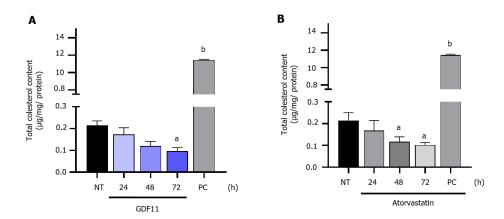


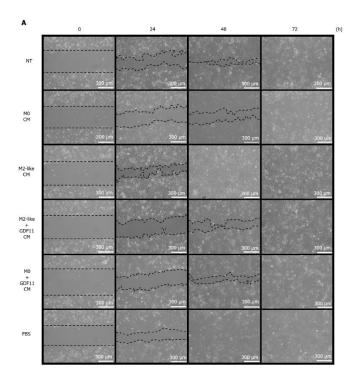
Supplementary Figure 1 Experimental design of the study. Image created using Biorender. PMA: Phorbol myristate acetate; ATCC: American Type Culture Collection; IL: Interleukin; GDF11: Growth differentiation factor 11; CM: Conditioned media; CD206: Cluster of differentiation 206; ROS: Reactive oxygen species.

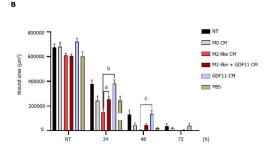


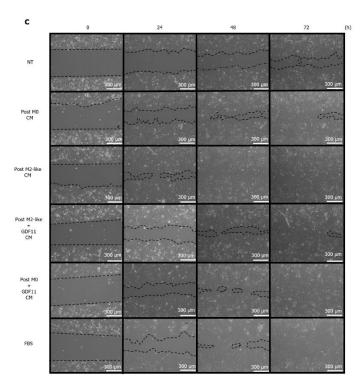
Supplementary Figure 2 Effects of the conditioned media (CM) derived from Huh7 cells on macrophages. Flow cytometry analysis was performed to evaluate cluster of differentiation 206 (CD206⁺) subsets. Macrophages were treated with conditioned media derived from HCC cells, as stated in the Materials and Methods section. A: Fluorescence histogram; B: percentage (%) of CD206⁺ cells; C: Median fluorescence intensity of CD206⁺ subset. Each column represents the mean \pm SEM of at least three independent experiments. $aP \le 0.01 \ vs \ MO$; $bP \le 0.05 \ vs \ M2$ conditioned media-Huh7 (24 hours). CM: Conditioned media; CD206: Cluster of differentiation 206.

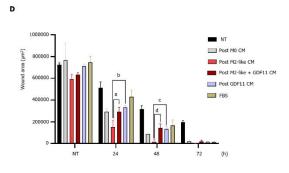


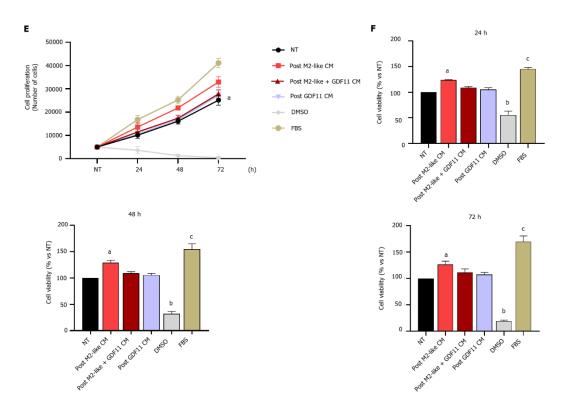
Supplementary Figure 3 Growth differentiation factor 11 decreases cholesterol content in macrophages. Cholesterol was biochemically quantified. A: Cholesterol content from growth differentiation factor 11-treated macrophages; B: Cholesterol from Atorvastatin-treated macrophages. Liver tissue from a mouse fed a high cholesterol diet (2%) for eight months. Each column represents the mean \pm SEM of at least three independent experiments in triplicate. ${}^{a}P \leq 0.05 \ vs$ not treated cells; ${}^{b}P \leq 0.0001 \ vs$ not treated cells. NT: Not treated cells; GDF11: Growth differentiation factor 11.



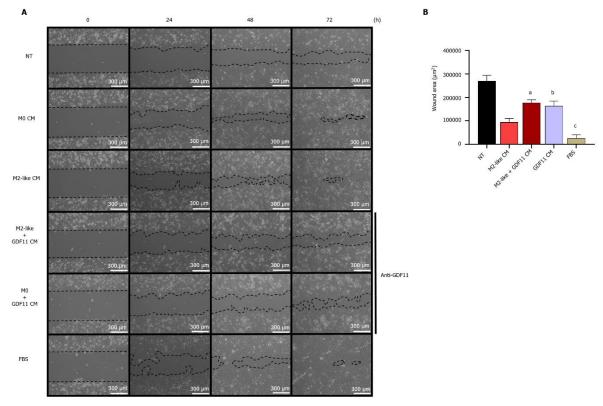




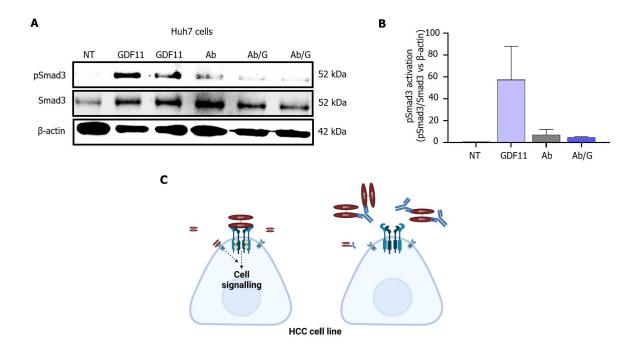




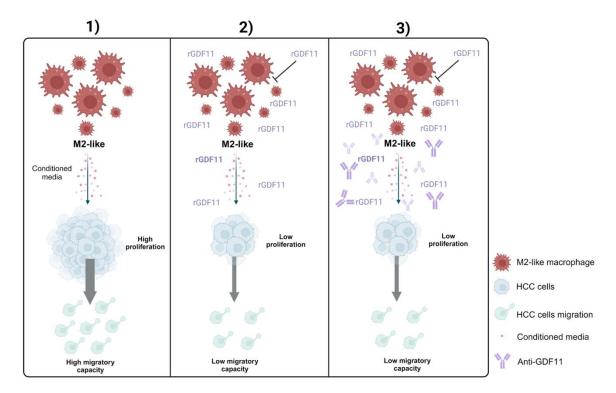
Supplementary Figure 4 Effects of the conditioned media derived from M2-like macrophages on hepatocellular carcinoma cells. Includes complete controls. A: Cell migration determined by a wound healing assay, representative images of at least three independent experiments. Scale bars: 300 µm (100×, original magnification); B: Wound area (µm²) quantification determined by Image J software; C: Cell migration determined by a wound healing assay. Scale bars: 300 µm (100×, original magnification); D: Wound area (µm²) quantification determined by Image J software. Each column represents the mean \pm SEM of at least three independent experiments in triplicate; E: Cell proliferation; F: Cell viability was assayed by the Cell Counting Kit-8. Fetal bovine serum was used as a control. Dimethyl sulfoxide was used as a negative control. Each column or point represents the mean \pm SEM of at least three independent experiments carried out in triplicate. $^aP \le 0.05 \ vs$ not treated cells; $^bP \le 0.05 \ vs$ not treated cells; $^cP \le 0.01 \ vs$ not treated cells. NT: Not treated cells; CM: Conditioned media; FBS: Fetal bovine serum; GDF11: Growth differentiation factor 11; DMSO: Dimethyl sulfoxide.



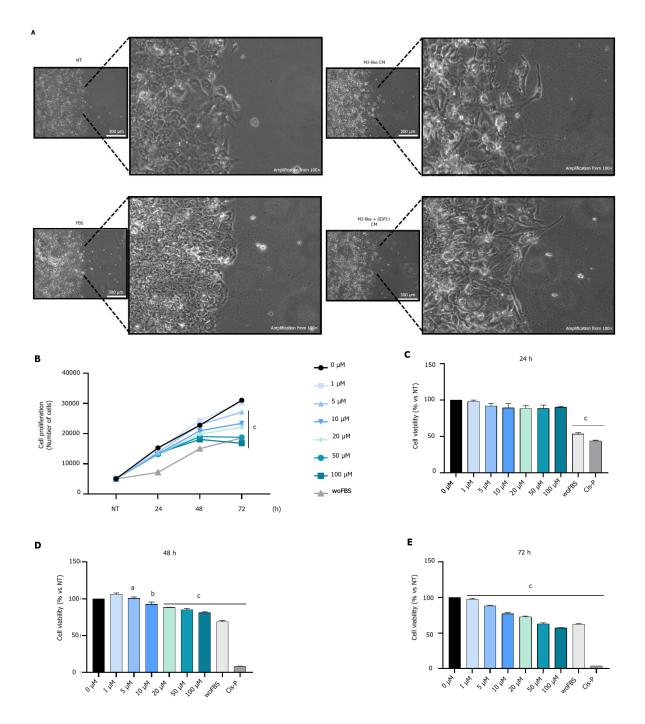
Supplementary Figure 5 Conditioned media from growth differentiation factor 11-treated macrophages decrease the migration capacity of Huh7 cells, even in the presence of anti-growth differentiation factor 11. Includes complete controls. A: Cell migration assay determined by a wound healing assay, representative images of at least three independent experiments. Scale bars: 300 µm (100×, original magnification). B: Wound area (µm²) quantification determined by Image J software at 72 hours. Each column represents the mean \pm SEM of at least three independent experiments in triplicate. $^aP \le 0.05 \ vs$ M2-like conditioned media; $^bP \le 0.05 \ vs$ M2-like conditioned media; and $^cP \le 0.01 \ vs$ not treated cells. Anti-growth differentiation factor 11 was used to inhibit the remnants of the recombinant growth differentiation factor 11. Fetal bovine serum was used as a control. NT: Not treated cells; CM: Conditioned media; FBS: Fetal bovine serum; GDF11: Growth differentiation factor 11.



Supplementary Figure 6. Anti-growth differentiation factor 11 repressed the phosphorylation of Smad3 protein. A: Representative images of western blot; B: Densitometries from A. C: Representation of the model. Image created using Biorender. β -actin was used as a loading control. Ab: anti-growth differentiation factor 11. NT: Not treated cells; GDF11: Growth differentiation factor 11; HCC: Hepatocellular carcinoma.



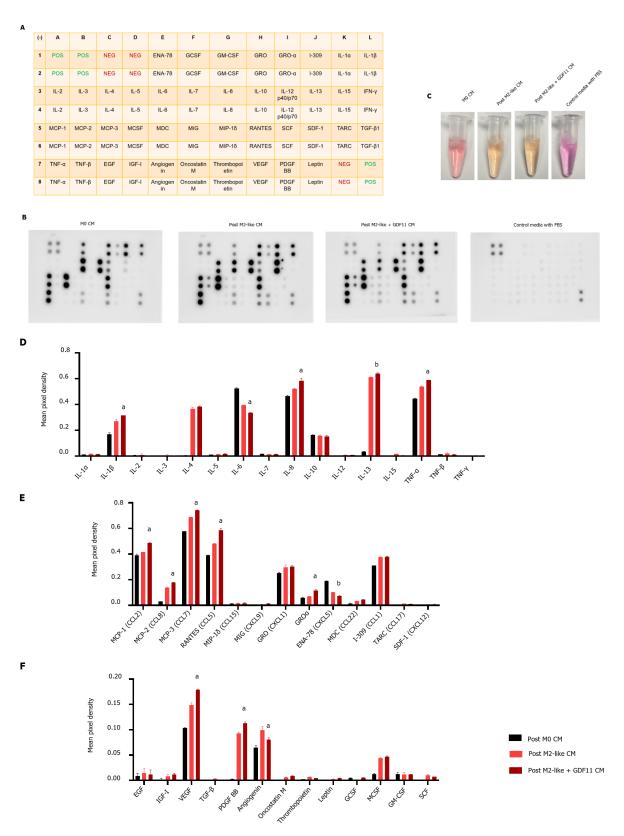
Supplementary Figure 7 The three scenarios of the model. M2-like macrophages exacerbate aggressively on hepatocellular carcinoma cells due to secretion factors (1); growth differentiation factor 11 alters and mitigates M2-like polarization, reducing aggressiveness (2), and using anti-growth differentiation factor 11 in conditioned media did not affect the previous results; hepatocellular carcinoma aggressiveness was reduced (3). Image created using Biorender. GDF11: Growth differentiation factor 11; HCC: Hepatocellular carcinoma.



Supplementary Figure 8 Evidence of the migratory morphologies of the cells. A:

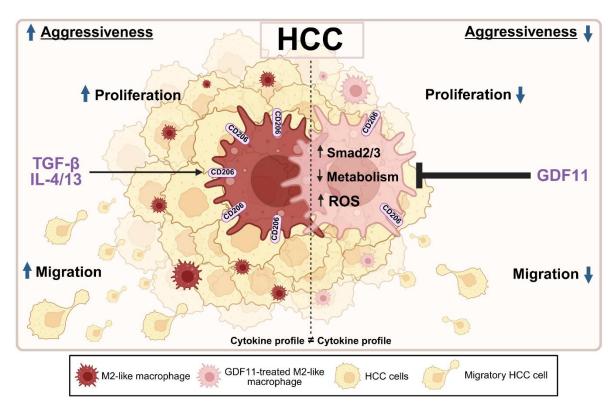
At the border of Huh7 wound healing culture, representative images of at least three independent experiments. Scale bars: 300 μ m (100×, original magnification); B: Proliferation assay using cytarabine at different concentrations; C-E: Cell viability using cytarabine at different concentrations, absence of fetal bovine serum and cisplatin were used as negative controls, respectively. Each column represents the

mean \pm SEM of at least three independent experiments in triplicate. ${}^{a}P \le 0.05 \ vs$ not treated cells, ${}^{b}P \le 0.001 \ vs$ not treated cells, and ${}^{c}P \le 0.0001 \ vs$ not treated cells. NT: Not treated cells; CM: Conditioned media; FBS: Fetal bovine serum.



Supplementary Figure 9 Cytokine profile changes induced by growth differentiation factor 11 on post M2-like macrophages. A: Map of interleukin's

location in the cytokine array membranes; B: Representative membranes or dot blots; C: Conditioned media quality derived from M0, post M2-like, and post M2-like + growth differentiation factor 11 macrophages; D: Interleukin and interferon family alteration by growth differentiation factor 11 on post M2-like macrophages, $^aP < 0.0001 \ vs$ post M2-like conditioned media, $^bP = 0.0012 \ vs$ post M2-like conditioned media; E: Chemokine family alteration by growth differentiation factor 11 on post M2-like macrophages, $^aP < 0.0001 \ vs$ post M2-like conditioned media, $^bP = 0.0050 \ vs$ post M2-like conditioned media; F: Growth factors alteration by growth differentiation factor 11 on post M2-like macrophages, $^aP \le 0.0001 \ vs$ post M2-like conditioned media. The mean pixel density in each column represents the mean \pm SEM of at least three independent experiments. CM: Conditioned media; GDF11: Growth differentiation factor 11; FBS: Fetal bovine serum.



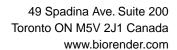
Supplementary Figure 10 Graphical abstract. Image created using Biorender. HCC: Hepatocellular carcinoma; TGF: Transforming growth factor; IL: Interleukin; ROS: Reactive oxygen species; CD206: Cluster of differentiation 206; GDF11: Growth differentiation factor 11.

Supplementary Table 1 Antibodies used in the study

Antibody	Dilution	Secondary	Catalog Number
pSmad3 (S423/425)	1:1000 WB	Rabbit mAb	Cell Signaling C25A9
Smad3	1:1000 WB	Rabbit mAb	Cell Signaling C67H9
pSmad2 (S465/467)	1:1000 WB	Rabbit mAb	Cell Signaling 138D4
Smad2	1:1000 WB	Rabbit mAb	Cell Signaling D43B4 XP(R)
Smurf1	1:200 WB	Mouse mAb	Santa Cruz Biotechnology sc-100616
CD206 (15-2)	0.6 μg FCM	Mouse mAb	Santa Cruz Biotechnology sc-58986
GDF11	30 ng WH	Mouse mAb	Santa Cruz Biotechnology sc-81952
β-actin	1:10000 WB	Rabbit mAb	Millipore-Sigma A3854
Alexa Fluor 488	1:500 FCM	Mouse mAb	Thermo Fisher A32723

CD206: Cluster of differentiation 206; GDF11: Growth differentiation factor 11; WB:

Western blot; FCM: Flow cytometry.





September 17th, 2025

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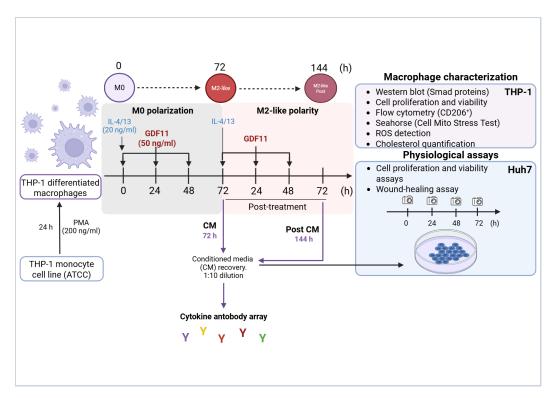
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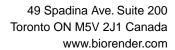
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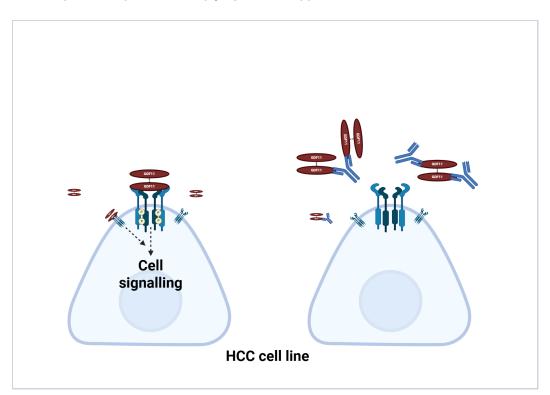
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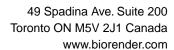
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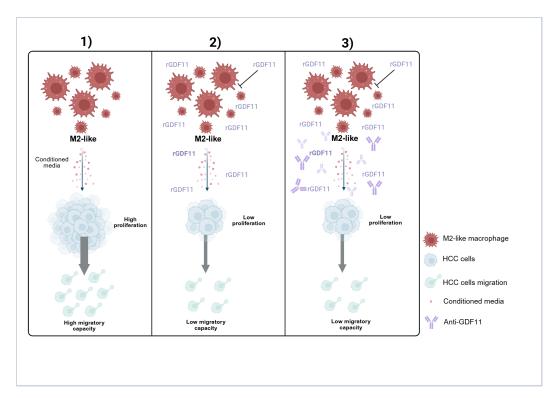
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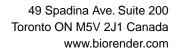
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