

Hepatoprotective effects of efruxifermin in the GAN diet-induced obese and biopsy-confirmed mouse model of MASH

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Background & Aim

Efruxifermin (EFX, long-acting FGF21 analogue) is currently in phase-3 clinical development for the treatment of metabolic dysfunction-associated steatohepatitis (MASH). The present study aimed to investigate the therapeutic benefits of EFX on metabolic, biochemical, histopathological and transcriptome profile in the Gubra Amylin NASH (GAN) diet-induced obese (DIO) and biopsy-confirmed mouse model of MASH with liver fibrosis.

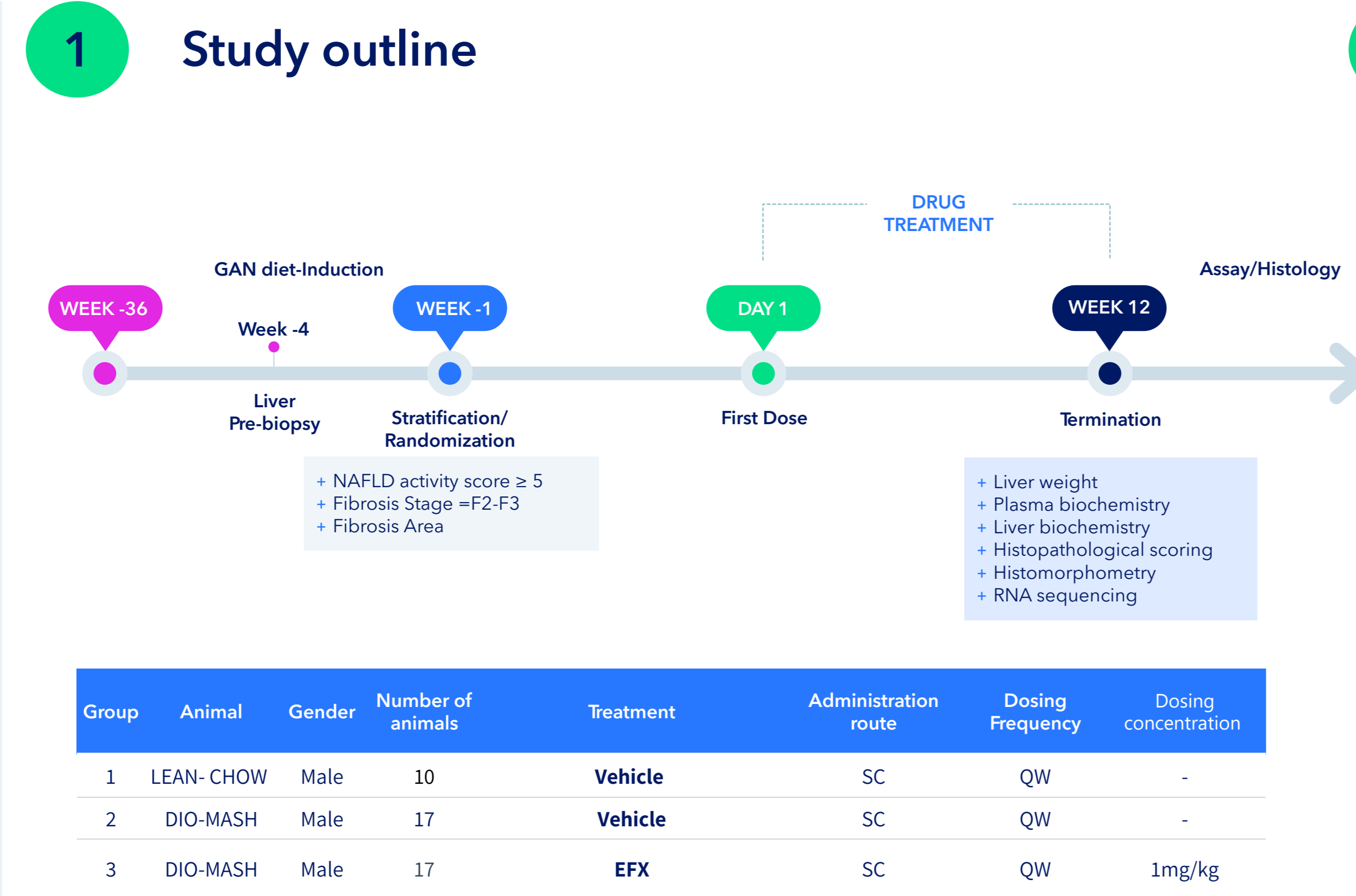


Figure 1. Study outline. SC; subcutaneous, QW; Once Weekly; GAN; Gubra Amylin NASH.

2 Metabolic and biochemical parameters

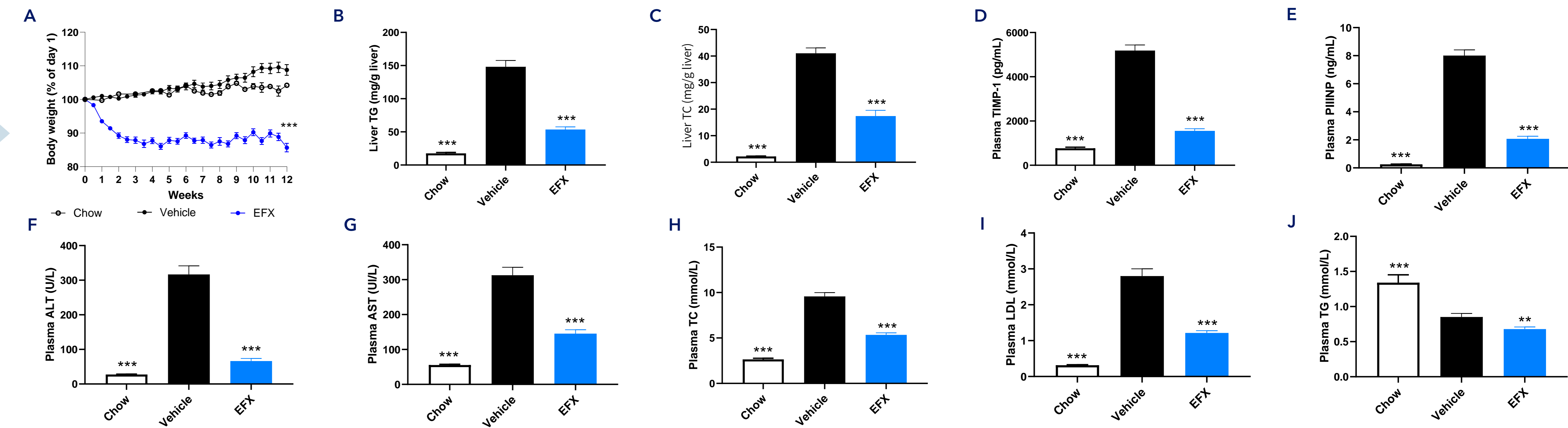


Figure 2. Metabolic and biochemical effects of EFX. (A) Relative body weight during study period. (B) Liver triglycerides (TG). (C) Liver total cholesterol (TC). (D) Plasma TIMP-1. (E) Plasma PIINP (F) Plasma alanine aminotransferase (ALT). (G) Plasma alanine transaminase (AST). (H) Plasma total cholesterol (TC). (I) Plasma LDL cholesterol. (J) Plasma triglycerides (TG). ** $p < 0.01$, *** $p < 0.001$ compared to vehicle control (Dunnett's test one-factor linear model).

3 NAFLD Activity Score and Fibrosis Stage

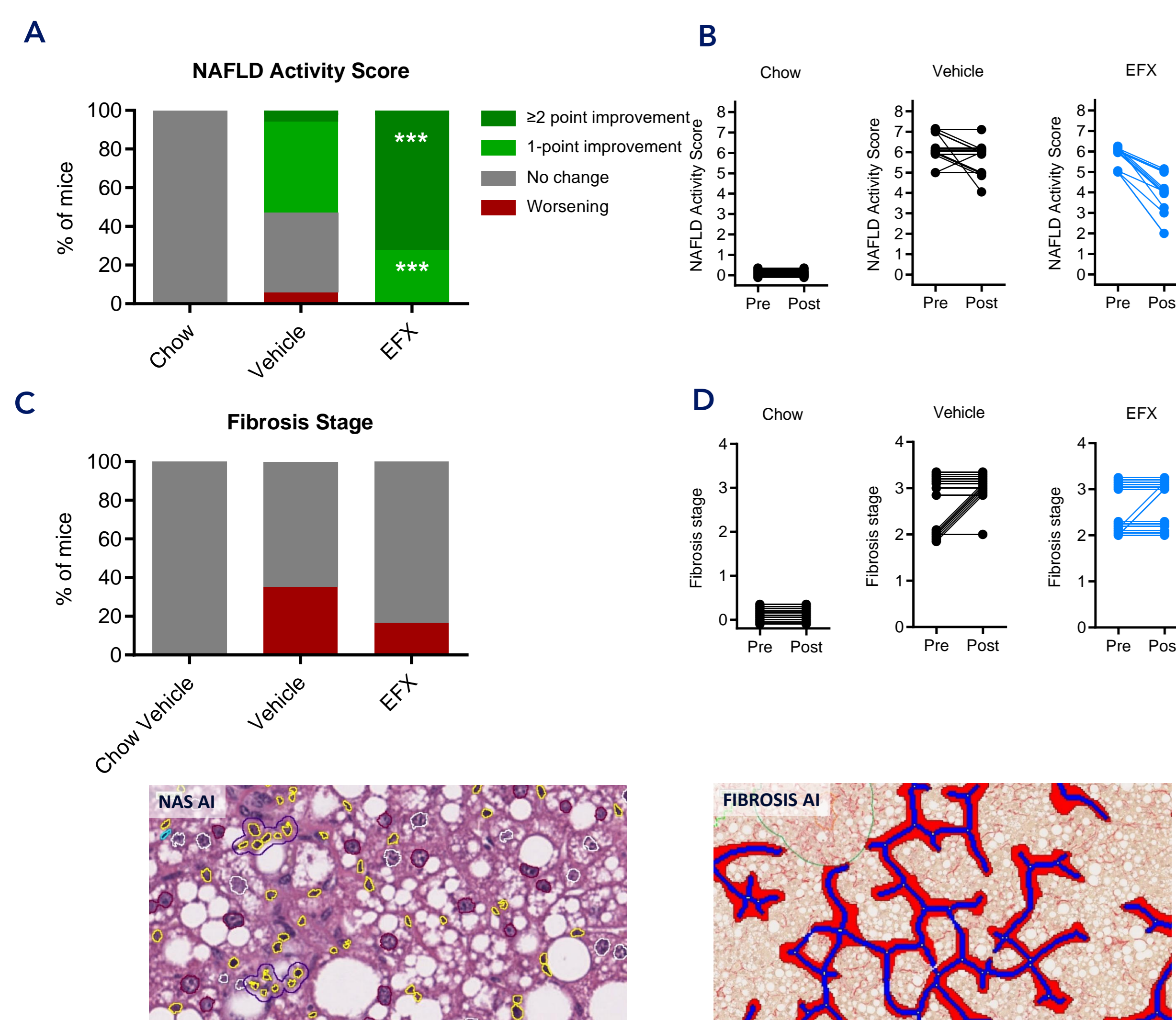


Figure 3. EFX improves NAFLD Activity Score in GAN DIO-MASH mice. Histopathological scores were determined by Gubra Histopathological Objective Scoring Technique (GHOST) deep learning-based image analysis. (A) NAFLD Activity Score (NAS). (B) Individual pre-post NAS. (C) Fibrosis stage. (D) Individual pre-post fibrosis stage. *** $p < 0.001$ compared to vehicle control (one-sided Fisher's exact test).

4 Histological markers of steatosis, inflammation, fibrosis and fibrogenesis

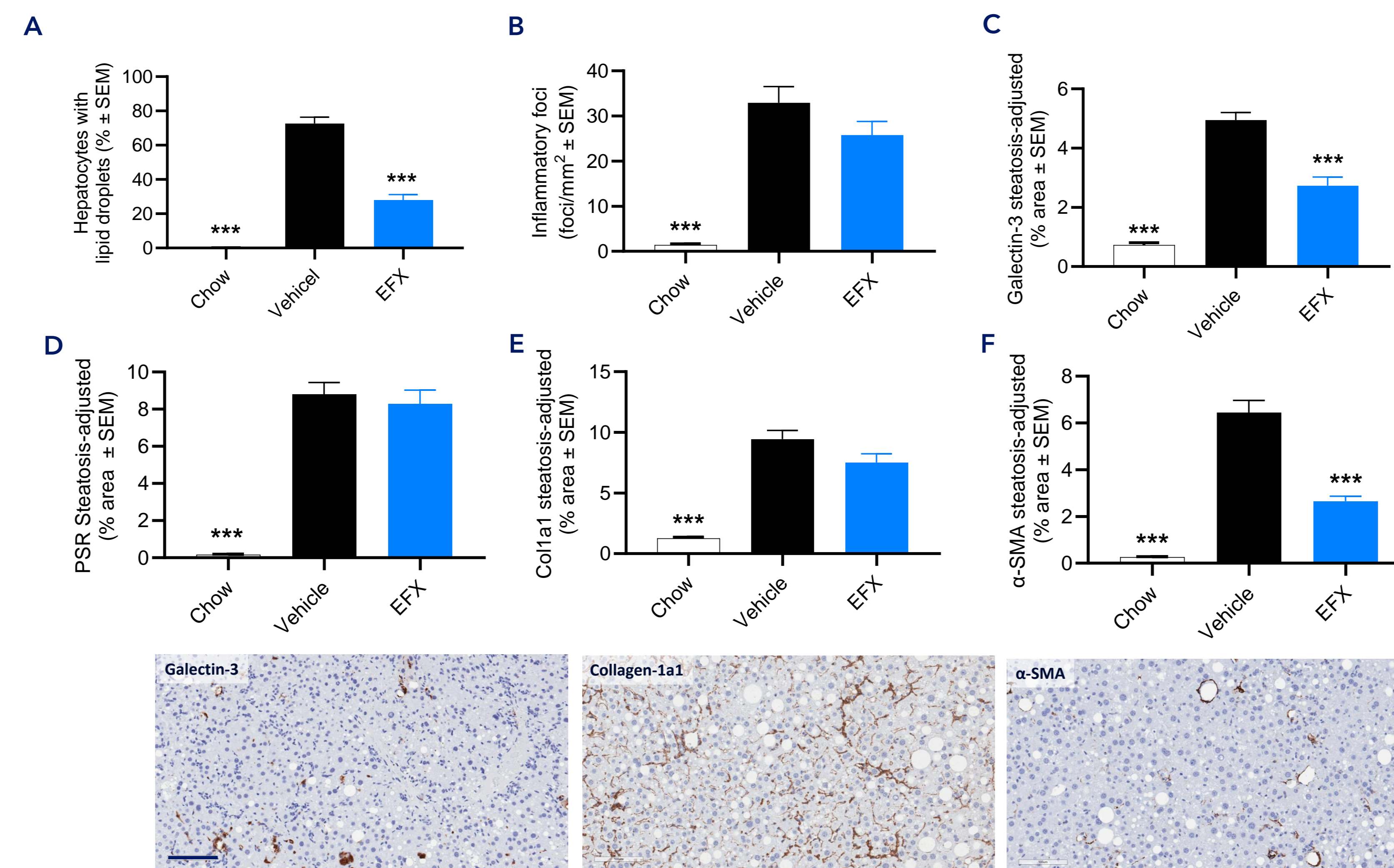


Figure 4. EFX improves quantitative histological endpoints. Histomorphometric assessments were performed by GHOST deep learning-based image analysis on scoring-associated variables (panels A-B) and conventional IHC image analysis (panels C-F). (A) % hepatocytes with lipid droplets. (B) Number of inflammatory foci. (C) % area of galectin-3 (steatosis-adjusted). (D) % area of PSR (steatosis-adjusted). (E) % area of collagen-1a1 (Col1a1, steatosis-adjusted). (F) % area of alpha-smooth muscle actin (α -SMA, marker of stellate cell activation; steatosis-adjusted). *** $p < 0.001$ compared to vehicle control (Dunnett's test one-factor linear model). Bottom panels: Representative photomicrographs of galectin-3, Col1a1 and α -SMA (scale bar, 100 μ m).

5 Liver transcriptome analysis

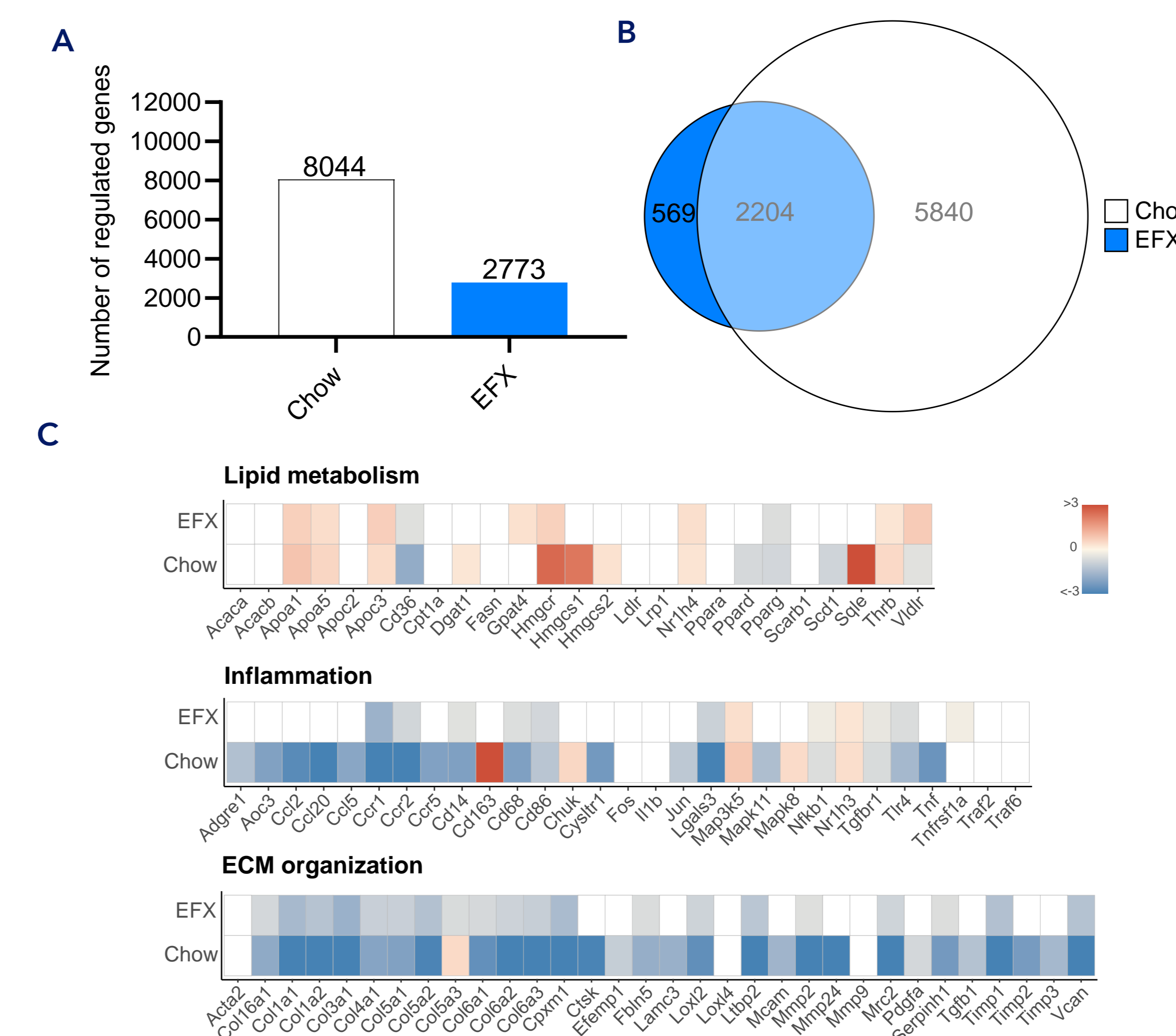


Figure 5. Hepatic transcriptome signatures following EFX therapy. (A) Total number of differentially expressed genes. (B) Venn diagram on overlapping gene expression signatures. (C) Regulation of gene expression markers of hepatic lipid metabolism, inflammation and extracellular matrix (ECM). Log2 fold change is indicated for significantly regulated genes ($p_{adj} < 0.05$ after correcting for multiple testing). Red and blue colours indicate up- and down-regulation, respectively, compared to Vehicle.

Conclusion

- + EFX improves body weight, hepatomegaly, plasma transaminases and lipid levels.
- + EFX improves NAFLD Activity Score, but not Fibrosis Stage.
- + Benefits on NAS are supported by quantitative histological markers for steatosis and inflammation.
- + EFX reduces quantitative histological markers for fibrogenesis and plasma markers of fibrosis.
- + EFX regulates hepatic transcriptomic profile, improving gene expression markers of lipid metabolism and fibrogenesis.
- + Longer treatment intervention might be needed for demonstrating histological anti-fibrotic effects of EFX.
- + The hepatoprotective effects observed for EFX further supports clinical translatability of the biopsy-confirmed GAN DIO-MASH mouse model.