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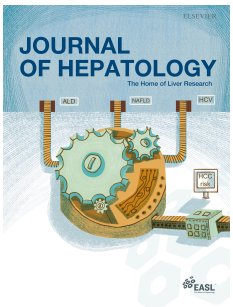

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PII: S0168-8278(21)02254-6

DOI: https://doi.org/10.1016/j.jhep.2021.12.012

Reference: JHEPAT 8540

To appear in: *Journal of Hepatology*

Received Date: 26 March 2021

Revised Date: 5 December 2021

Accepted Date: 7 December 2021

Please cite this article as: Govaere O, Petersen SK, Martinez-Lopez N, Wouters J, Van Haele M, Mancina RM, Jamialahmadi O, Bilkei-Gorzo O, Lassen PB, Darlay R, Peltier J, Palmer JM, Younes R, Tiniakos D, Aithal GP, Allison M, Vacca M, Göransson M, Berlinguer-Palmini R, Clark JE, Drinnan MJ, Yki-Järvinen H, Dufour JF, Ekstedt M, Francque S, Petta S, Bugianesi E, Schattenberg JM, Day CP, Cordell HJ, Topal B, Clément K, Romeo S, Ratziu V, Roskams T, Daly AK, Anstee QM, Trost M, Härtlova A, Macrophage Scavenger Receptor 1 mediates lipid-induced inflammation in non-alcoholic fatty liver disease, *Journal of Hepatology* (2022), doi: https://doi.org/10.1016/j.jhep.2021.12.012.

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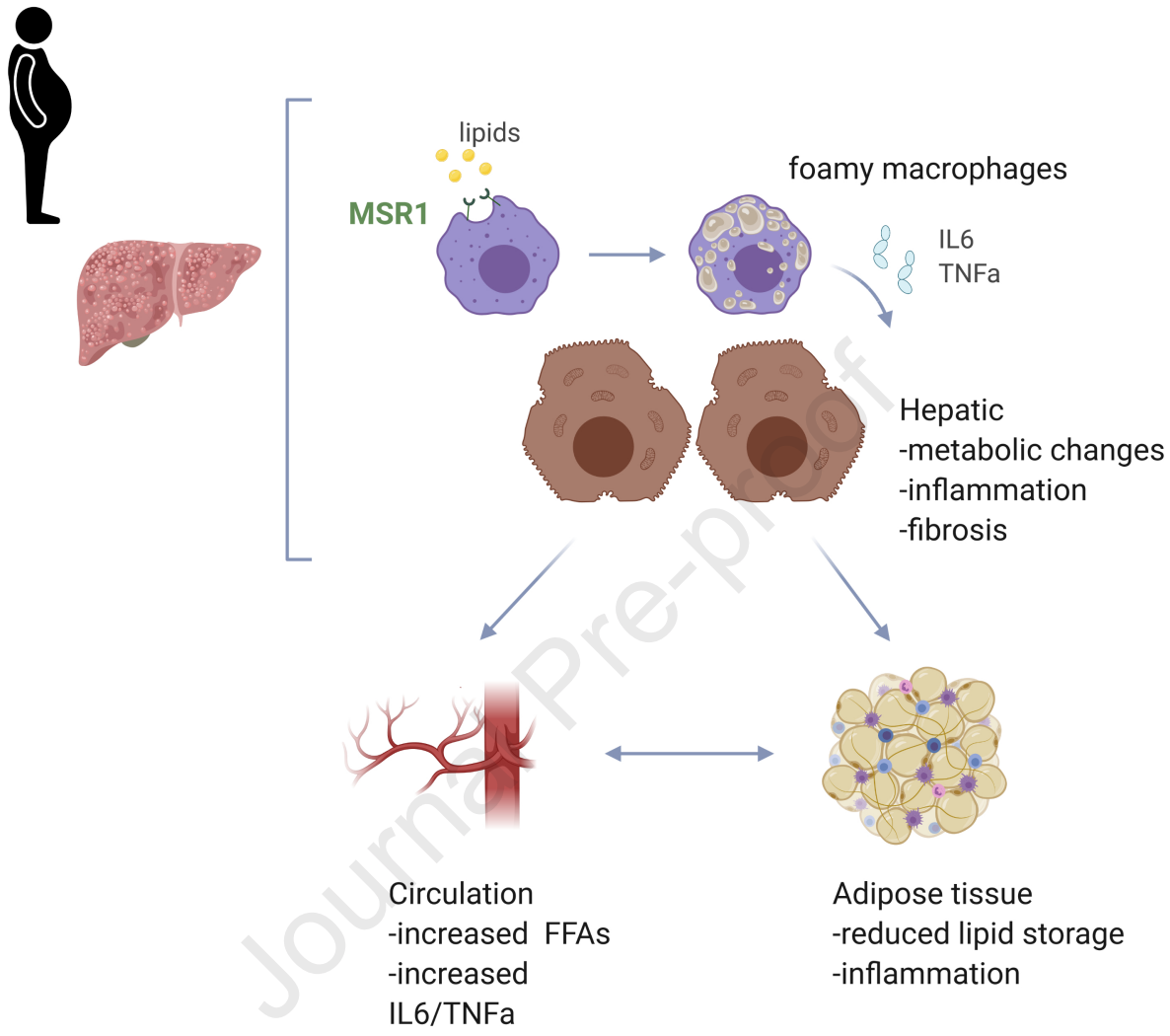

Macrophage Scavenger Receptor 1 mediates lipid-induced inflammation in non-alcoholic fatty liver disease

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Key words: macrophages, immunometabolism, NASH, inflammation

Word counts: 6,098 (including abstract, references, table, figure legends)

Number of figures and tables: 6 figures and 1 table

Conflict of interest: The authors have no potential conflicts (financial, professional or personal) directly relevant to the manuscript.

Funding: This study has been supported by the EPoS (Elucidating Pathways of Steatohepatitis) consortium funded by the Horizon 2020 Framework Program of the European Union under Grant Agreement 634413, the LITMUS (Liver Investigation: Testing Marker Utility in Steatohepatitis) consortium funded by the Innovative Medicines Initiative (IMI2) Program of the European Union under Grant Agreement 777377, which receives funding from the EU Horizon 2020 programme and EFPIA, and the Newcastle NIHR Biomedical Research Centre (to QMA), the Newcastle University start-up funding and the Wellcome Trust Investigator Award (215542/Z/19/Z) (to MT), Knut och Alice Wallenberg Foundation Wallenberg Centre for molecular and translational medicine, University of Gothenburg, Sweden and Åke Wirbergs Research funding #M18-0121 (to AH), Cancerfonfen # 19 0352 Pj (2020-2022) (to AH), the Belgian Federal Science Policy Office (Interuniversity Attraction Poles Program) grant Network P7/83-HEPRO2 (to TR), Rosetrees Trust (to NML), Flemish Cancer Society Kom op tegen Kanker, and Belgian Cancer Society Stichting tegen Kanker (to J.W).

Author contributions: OG and AH conceived the study. Study design, manuscript drafting and funding: AH, OG, MT and QMA. Manuscript preparation: AH, OG, SKP, MT, QMA. *In vivo* experiments: AH, SKP, OBG and NML. *In vitro* experiments: AH, OG and SKP. Human *ex vivo* experiments: OG, MVH, TR. Histopathology: OG, MVH, TR and DT. Nanostring analysis: OG. Bioinformatics: OG and JW. GWAS analysis: RD, HJC, AKD. eQTL UKBiobank data: RMM, OJ, SR. All authors contributed to data collection and interpretation, and critically revised the manuscript for intellectual content.

Data and materials availability:

To review GEO accession GSE163471:
Go to https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE163471
Enter token khehmemolruhbcj into the box

Lay summary

Non-alcoholic fatty liver disease (NAFLD) is a chronic disease primarily caused by excessive consumption of fat and sugar combined with a lack of exercise or a sedentary life style. Here we show that the macrophage scavenger receptor MSR1, an innate immune receptor, mediates lipid uptake and accumulation in Kupffer cells resulting in liver inflammation, and thereby promoting the progression of NAFLD in human and in mice.

Abstract:

Background & Aims: Obesity-associated inflammation is a key player in the pathogenesis of non-alcoholic fatty liver disease (NAFLD). However, the role of macrophage scavenger receptor 1 (MSR1, CD204) remains incompletely understood.

Methods: 170 NAFLD liver biopsies were processed for transcriptomic analysis and correlated with clinicopathological features. $Msr1^{-/-}$ and WT mice were submitted to a 16 week high-fat and high-cholesterol diet. Therapeutic intervention with monoclonal antibody against MSR1 was performed in mice and *ex vivo* human liver slices. Genetic susceptibility was assessed using GWAS data from 1,483 NAFLD patients and 430,101 participants of the UKBiobank.

Results: MSR1 expression was associated with the occurrence of hepatic lipid-laden foamy macrophages and correlated with the degree of steatosis and steatohepatitis in NAFLD patients. Mice lacking Msr1 were protected against diet-induced metabolic disorder, showing fewer hepatic foamy macrophages, less hepatic inflammation, improved dyslipidemia and glucose tolerance, while showing altered hepatic lipid metabolism. MSR1 induced a pro-inflammatory response via the JNK signalling pathway upon triggering by saturated fatty acids. *In vitro* blockade of the receptor prevented the accumulation of lipids in primary macrophages which inhibited the switch towards a pro-inflammatory phenotype and the release of cytokines such as TNF-α. Targeting MSR1 using monoclonal antibody therapy in an obesity-associated NAFLD mouse model and human liver slices resulted in the prevention of foamy macrophage formation and inflammation. Moreover, we identified that rs41505344, a polymorphism in the upstream transcriptional region of *MSR1*, was associated with altered serum triglycerides and aspartate transaminase levels in a cohort of over 400,000 patients.

Conclusions: Taken together, our data suggest a critical role for MSR1 in lipid-induced inflammation and a potential therapeutic target for the treatment of NAFLD.

Introduction

With the increasing prevalence of obesity, non-alcoholic fatty liver disease (NAFLD) has become the most common chronic liver disease globally.[1] NAFLD is characterised by excessive hepatic triglyceride accumulation and represents a series of diseased states ranging from isolated steatosis (non-alcoholic fatty liver, NAFL) to non-alcoholic steatohepatitis (NASH), identified by the presence of necro-inflammation and hepatocyte ballooning, with varying degrees of fibrosis. NAFLD is strongly linked with metabolic syndrome, i.e. dyslipidemia, hypertension, obesity and type 2 diabetes mellitus (T2DM), and currently affects 20 to 30% of the global population.[1] Importantly, not all patients progress from NAFL to NASH and although gene signatures of more advanced fibrosing-steatohepatitis have been identified, the exact pathogenic pathways involved in the initiating phases of the disease, especially the transition from NAFL to NASH, are not fully understood.[2]

Growing evidence supports the view that Kupffer cells, the endogenous hepatic macrophages, are initiators of inflammation and hence contribute to NAFLD development, whilst recruited monocyte-derived macrophages are often observed in advanced stages of the disease.[3] Hepatic macrophages are responsive to a variety of stimuli including bacterial endotoxins (such as lipopolysaccharide) but also free fatty acids (FFAs) or cholesterol.[4] Excess of FFAs and cholesterol can cause the formation of hepatic foamy macrophages, and leads to Kupffer cell aggregates and lipogranulomas during steatohepatitis.[5] Specifically, the intake of saturated fat has been shown to induce insulin resistance, and to enhance intrahepatic triglyceride accumulation and steatohepatitis.[6]

Palmitic acid (PA), rather than non-saturated fatty acids (non-SFA), has been shown to be a strong inducer of inflammation in immortalised cell lines through activation of the downstream JNK signalling pathway.[7] Recent data show that pro-inflammatory activation of murine bone marrow-derived macrophages by PA is independent of Toll-like receptor 4, yet the receptor that is responsible is still not known.[8] Recently, we have shown that *in vitro* activation of the phagocytic receptor, macrophage scavenger receptor 1 (MSR1, also known as SR-A or CD204), results in pro-inflammatory macrophage polarisation through JNK activation.[9] MSR1 is a key macrophage receptor for the clearance of circulating lipoproteins and has been implicated in atherogenesis.[10] In irradiated low-density lipoprotein receptor-deficient mice, transplantation of *Msr1*$^{-/-}$/*CD36*$^{-/-}$ monocytes proved to reduce dietary-induced inflammation.[11] However, the molecular mechanisms underlying hepatic macrophage activation and/or the formation of foamy macrophages in NAFLD remain poorly understood. We therefore hypothesised

that MSR1 might be involved in inflammatory responses in the context of lipid overload during obesity-induced NAFLD.

Materials and Methods

Patient selection

Cases were derived from the European NAFLD Registry (NCT04442334), approved by the relevant Ethical Committees in the participating centres, and all patients having provided informed consent.[12] For the histopathological and nanoString® study, 194 formalin-fixed paraffin-embedded (FFPE) or frozen liver biopsies samples were obtained from patients diagnosed with histological proven NAFLD at the Freeman Hospital, Newcastle Hospitals NHS Foundation Trust, Newcastle-upon-Tyne, UK and at the Pitié-Salpêtrière Hospital, Paris, France (**Table S1**). For the Genome Wide Association Study, 1,483 patients with histological proven NAFLD were included as previously described.[13] All liver tissue samples for the histopathological and nanoString® study were centrally scored according to the semi-quantitative NASH-CRN Scoring System by an expert liver pathologist (DT).[14] Fibrosis was staged from F0 through to F4 (cirrhosis). Alternate diagnoses and etiologies such as excessive alcohol intake, viral hepatitis, autoimmune liver diseases and steatogenic medication use were excluded. Viable human normal liver tissue for the *ex vivo* slices was obtained after resection from two adult patients treated at the University Hospitals Leuven, Leuven, Belgium. Samples were assessed by an expert liver pathologist (TR).

Animals

Male *Msr1*$^{-/-}$ or *Msr1*$^{+/+}$ (wild type, WT) C57BL/6 mice were either kindly provided by Prof. Siamon Gordon, University of Oxford or obtained from Jackson Laboratories and bred in a conventional animal facility under standard conditions. Animals received human care and experimental protocols were approved by the institutional animal ethics committees at Newcastle University (PC123A338) and University of Gothenburg (2947/20). Mice had free access to water and were fed either standard chow (n=10, 5 WT and 5 *Msr1*$^{-/-}$) or 45%-high-fat and high-cholesterol diets (HFD; 820263, Special Diet Services; n=10, 5 WT and 5 *Msr1*$^{-/-}$) ad libitum. For the therapeutic intervention, WT mice were put on a 12 week HFD and intravenously injected with monoclonal rat anti-mouse Msr1 antibody (n=8 animals, MAB1797-SP, R&Dsystems) or IgG control (n=9 animals, MAB0061, R&D systems) at week 10 and 11 (0.25 mg antibody/animal).

Statistical analysis

Kolmogorov-Smirnov or the Shapiro-Wilk normality test, unpaired Student's t-test or Mann-Whitney U test, one way ANOVA or Kruskal-Wallis test with respectively Tuckey's or Dunn's post hoc multiple comparison test or Chi-Square test were performed using IBM SPSS statistics 26 or GraphPad Prism 8.4.3. A p-value<0.05 was considered significant. Binary logistic regression analysis was performed in SPSS using Backward Stepwise Likelihood Ratio model. The model predicting high disease activity NAS≥4 was calculated as follows: MSR1_model=-1.296883 + (0.003020**MSR1*_mRNA).

Additional Material and Methods can be found in the Supplementary Materials.

Results

MSR1 expression correlates with steatohepatitis activity in human NAFLD

To investigate the role of MSR1 in human NAFLD, we first analysed gene expression in a cohort of 170 histologically characterised human adult liver biopsies. The cohort was stratified according to histopathological disease grade and stage, i.e. NAFL and NASH with fibrosis ranging from F0 to F4 (**Table S1**). Univariate analysis indicated that *MSR1* transcript was significantly associated with high steatosis, hepatocyte ballooning, lobular inflammation, presence of NASH and a NAFLD Activity Score ≥ 4 (NAS, defined as the sum of steatosis, ballooning and lobular inflammation) (**Fig.1a-b** and **Table S2**).[14] Interestingly, *CD68* mRNA, a marker for monocytes/macrophages, was only significantly associated with NAS≥4 but not with any other clinicopathological features (**Table S2**). To further explore whether *MSR1* transcript was independently associated with high disease activity, we performed binary logistic regression analysis including the clinical variables sex, body mass index (BMI), age, T2DM, alanine aminotransferase (ALT) and aspartate aminotransferase (AST), together with *MSR1* and *CD68* mRNA levels. Backward Stepwise Likelihood Ratio modelling showed that *MSR1* transcript levels predicated NAS≥4 independently from *CD68* mRNA or other clinical variables with an Area Under the Curve of 0.735 (**Fig.1c**).

Histopathological analysis showed that MSR1 was predominantly expressed in resident liver macrophages, the Kupffer cells, rather than infiltrating monocyte-derived macrophages located in the portal tract, as visualised by the MSR1 and CD68 immunostaining (**Fig.1d and Fig.S1a-b**). This was confirmed by immunofluorescent double staining (**Fig.S1c**). While the number of infiltrating portal CD68-immunopositive cells increased with disease progression (p<0.05), no significant differences were found

for infiltrating MSR1-positive cells (**Fig.1d**). These results were supported by publicly available single cell RNA sequencing data indicating that *MSR1* expression was mainly restricted to the Kupffer cell population whereas *CD68* was also expressed in monocyte populations (**Fig.S2a-b**).[15] Moreover, when differentiating monocytes from healthy individuals towards mature macrophages, we observed an increase in MSR1 protein expression (**Fig.1e**). Notably, MSR1 immunopositivity was also seen in lipogranulomas and lipid laden macrophages throughout the spectrum of NAFLD (**Fig.1d and Fig.S1a**). Using the marker Perilipin 2 (PLIN2) to visualise intracellular lipid droplets, immunofluorescence analysis showed that lipid droplets accumulate in the Kupffer cells (**Fig.1f**). Furthermore, a significant increase in parenchymal CD68+_PLIN2+ cells was observed in NAFLD patients stratified based on NAS≥4 or steatosis grade≥2 (**Fig.1f**).

Taken together, these human data demonstrate a positive correlation of *MSR1* transcript and protein levels with NAFLD disease activity and the occurrence of hepatic-resident lipid-laden macrophages in the presence of excessive lipids.

Msr1 deficiency protects against diet-induced metabolic dysregulation and liver damage in mice

To further investigate how MSR1 functionally contributes to the development of obesity-related NAFLD, we subjected *Msr1*$^{-/-}$ mice (n=5) and their corresponding *Msr1*$^{+/+}$ (n=5 WT) age-matched male counterparts to a high-fat and high-cholesterol diet (HFD) for 16 weeks. Upon HFD feeding, *Msr1*-deficient mice displayed increased total body weight, an increase in liver and epididymal white adipose tissue (eWAT) weight and increased food intake compared to WT (**Fig.2a-b, Fig S3a-b**). Furthermore, HFD-fed *Msr1*$^{-/-}$ mice exhibited improved glucose uptake from blood, higher serum leptin, lower concentrations of circulating FFAs and enhanced fatty acid accumulation in the adipocytes (**Fig.2c, FigS3c-d**). Consistently the adipocytes in HFD-fed *Msr1*$^{-/-}$ mice were larger compared to WT, suggesting an increased adiposity and fat storage in the absence of *Msr1* (**Fig.2d-e**). Although no murine models accurately recapitulate all histological features of human steatohepatitis, histological and transcriptomic features of liver fibrosis were clearly attenuated by *Msr1* deficiency upon HFD feeding (**Fig.2d-f**). Sixteen weeks of regular diet did not result in any histological differences between the livers of WT and *Msr1*$^{-/-}$ mice (**Fig.S3e**), while WT mice on HFD displayed a significant higher hepatic fibrosis stage, sinusoidal fibrosis and increased collagen deposition (**Fig.2d-f, Fig.S3f**) compared to the *Msr1*$^{-/-}$ mice. Next, we characterised the livers of HFD-WT and HFD- *Msr1*$^{-/-}$ mice by high-throughput RNA sequencing analysis. The analysis revealed 728 differentially expressed genes (**Table S3**). Gene Ontology analysis of differentially expressed genes highlighted an enrichment for genes correlating to biological processes

including “innate immune response”, “phagocytosis” and “lipid metabolic process” (**Fig.2g**, **Fig.S3g-h**). HFD-*Msr1*$^{-/-}$ mice displayed a reduced hepatic transcript expression of inflammatory cytokines (including *Axl*, *Ccl6*, *Il1b*, *Spp1*), pro-inflammatory immune cell markers (*Ccr5*, *Cd14*, *Cd44*, *S100a8*, *S100a9*), markers for hepatic stellate cell activation (*Sox9*, *Pdgfb*) and members of the *Tnfa* signalling pathway (*Ripk3*, *Tnfaip2*, *Tnfaip8l2*) when compared with WT mice (**Fig.2g**). Furthermore, *Msr1*$^{-/-}$ mice on HFD showed a shift in gene expression associated with lipid metabolism, with genes including *Acox1*, *Acox2*, *Apoe*, *Ces1d*, *Hsd17b11*, *Pla2g6* and *Ppara* increasing, and genes such as *Fabp5*, *Lpcat2*, *Lpl*, *Pla2g7* and *Pnpla3* decreasing (**Fig.2g**). Functionally, the measured mitochondrial oxygen consumption rate in viable liver samples of HFD-*Msr1*$^{-/-}$ mice was approximately 50% higher compared to the WT, indicating enhanced metabolic function (**Fig.2h**). Taken together, these results demonstrate that *Msr1* deficiency increases the body weight but protects against features of the metabolic syndrome, including liver inflammation and fibrosis, while modulating hepatic lipid metabolism.

Msr1 deficiency prevents formation of pro-inflammatory foamy macrophages in vivo

Next, we asked whether the lipid-laden environment is a proximal stimulus leading to Msr1-mediated inflammation in the liver and adipose tissue, which may explain the observed metabolic dysfunction. In agreement with our human data, histopathological analysis of the liver and adipose tissue from HFD-fed *Msr1*$^{-/-}$ mice showed no hepatic lipogranuloma and very few foamy macrophages compared to their WT counterparts, demonstrated by F4/80 immunostaining (**Fig.3a**). Moreover, *Msr1*$^{-/-}$ mice displayed lower Il6 and Tnfα serum levels and reduced *Tnfa* and *Il6* gene expression in the liver and eWAT (**Fig.3b-d**). Furthermore, *Msr1* deficiency impaired pro-inflammatory activation of isolated adipose tissue- (ATMs) and hepatic-associated macrophages as shown by lower gene transcripts of *Tnfa* and *Il6* (**Fig.3e-g**). Altogether, these results show that Msr1 mediates HFD-induced hepatic and adipose tissue inflammation and facilitates macrophage activation toward a pro-inflammatory phenotype.

Triggering of Msr1 by lipids induces JNK-mediated pro-inflammatory activation of macrophages

We next investigated the underlying mechanism of Msr1-mediated lipid-induced inflammation. We reasoned that Msr1 is directly responsible for lipid uptake in macrophages, leading to an inflammatory response independent from other cell types. In this regard, we measured the uptake of SFA (palmitic acid, PA) and non-SFA (oleic acid, OA) in *Msr1*$^{-/-}$ and WT bone marrow-derived macrophages (BMDMs) by quantifying Oil-red-O staining using confocal microscopy (**Fig.4a-c, FigS4a**). The analysis revealed that Msr1 facilitates the uptake of both SFA as well as non-SFA but only SFA induced enhanced levels of *Tnfa*

and *Il6* transcripts in BMDMs (**Fig.4d)**. Furthermore, blocking of Msr1 receptor with a monoclonal antibody reduced the expression of *Tnfa* and *Il6*, and reduced the phosphorylation of JNK in response to SFA treatment (**Fig.4e-f**). In line with these data, pharmacological inhibition of JNK phosphorylation abrogated the induction of *Tnfa* and *Il6* pro-inflammatory gene expression upon SFA treatment (**Fig.S4b**). Similarly, using primary *Msr1*$^{-/-}$ hepatic macrophages or WT ones treated with monoclonal antibody resulted in reduced lipid uptake, reduced expression of *Tnfa* and reduced JNK phosphorylation (**Fig.4g-j**). To extend these findings, we co-cultured Hepa1-6 cells with BMDMs or primary hepatocytes with hepatic macrophages which resulted in a comparable response (**Fig.S5a-b**). These data indicate that SFA-induced triggering of Msr1 regulates JNK-mediated pro-inflammatory activation of macrophages in the absence of lipopolysaccharide.

Therapeutic inhibition of MSR1 reduces the release of TNFA

To investigate the therapeutic potential of targeting MSR1 in the treatment of NAFLD, we applied an antibody-based intervention using NAFLD mouse models and *ex vivo* human liver slices. WT mice were fed a HFD for 12 weeks and were administered two doses of monoclonal rat anti-mouse Msr1 antibody (n=8 animals) or isotype-matched IgG control (n=9 animals) at week 10 and 11 by intravenous injection. Antibody treatment did not result in any weight difference or changes in glucose or insulin levels at week 12 (**Fig.S6**). Notably, histological assessment did show reduced hepatic fibrosis and sinusoidal/peri-cellular fibrosis in anti-Msr1-treated mice compared to the IgG control mice, while steatosis grade, hepatocyte ballooning and lobular inflammation remained unchanged (**Fig.5a-b**). In addition, F4/80 immunostaining showed a reduction in occurrence of hepatic foamy macrophages and lipogranulomas upon treatment, which translated into reduced surface area positivity of F4/80-positive cells (**Fig.5b-c**). Furthermore, treated animals showed reduced expression of *Tnfa* transcript in liver samples and isolated hepatic macrophages (**Fig.5d**).

To further investigate whether inhibition of MSR1 prevents the formation of foamy macrophages and release of TNFA in humans, we collected human liver slices with normal morphology from two different patients (2 biological replicates per condition for each patient sample). The samples were incubated with a polyclonal anti-human MSR1 antibody prior to culturing them with a mixture of OA (2mM) and PA (1mM) combined with anti-MSR1 antibody for 16h (**Fig.5e**). Treatment with the antibody reduced the surface area positivity of Kupffer cells as shown by the CD68 immunostaining (**Fig.5f-g**). Moreover, lipid-induced release of TNF-α into the culture medium was reduced upon anti-MSR1 antibody treatment

(**Fig.5h**). Overall, our *in vivo* and *ex vivo* results show that therapeutic inhibition of MSR1 prevents the formation of foamy macrophages and the release of TNF-α.

Relevance of polymorphisms in *MSR1* region to NAFLD and metabolic traits

Next, we asked whether genetic variants in MSR1 are associated with susceptibility to NAFLD and if there is an association with transcriptional regulatory mechanisms controlling *MSR1* expression. Using previously published genomics data encompassing a cohort of 1,483 European Caucasian patients with histologically proven NAFLD and 17,781 European general-population controls [13], we identified 4 single nucleotide polymorphisms (SNPs) in or around the *MSR1* locus with p-values<$5*10^{-4}$, with rs41505344 as the most significant (p=$1.64*10^{-4}$) (**Fig.6a** and **Table S4**). Quantitative trait analysis for rs41505344 in 430,101 patients enrolled in the UKBiobank showed a significant correlation with serum triglycerides and AST levels, even after adjustment for age, gender, BMI, centre, batch and the first ten principal components (**Table 1**).

Our human data indicated that MSR1 is expressed in the liver on mature endogenous macrophages rather than on infiltrating monocyte-derived macrophages. To unravel transcriptional regulatory mechanisms of *MSR1*, we used publicly available RNA sequencing data comparing human monocytes with differentiated macrophages, which identified 1,208 differentially expressed genes, with *MSR1* mRNA expression increased in the macrophage population.[16] By motif enrichment analysis using iRegulon, we identified eight differentially expressed transcription factors, upregulated in human macrophages compared to monocytes, that are predicted to regulate the expression of *MSR1*: *BHLHE41*, *ETV5*, *HMGN3*, *MAF*, *MITF*, *NR1H3*, *THRA* and *ZNF562* (**Fig.6b**, **Table S5**). To verify whether these transcription factors bind any regulatory regions near the *MSR1* gene, and in particular the rs41505344 SNP locus, we investigated ChIP-sequencing data for these proteins. *MITF*, *MAF*, *THRA* and *NR1H3* proved to bind in the vicinity of the rs41505344 locus, suggesting an indirect role for the SNP in the transcriptional regulation of *MSR1* (**Fig.6c**). When assessing the rs41505344 genotype in our nanoString cohort, a significant increase in *MSR1* transcript was observed in patients carrying the SNP (**Fig.S7**). Taken together, these results suggest there is an increased frequency in NAFLD of variants potentially affecting *MSR1* expression during monocyte-macrophage differentiation, which thereby could influence features of obesity-related diseases.

Discussion

In this study, we provide evidence that MSR1 is important for the uptake of lipids in macrophages leading to an inflammatory response and metabolic changes throughout the body. In a setting of lipid overload, MSR1 deficiency not only led to reduced hepatic inflammation and changes in hepatic lipid metabolism but it also reduced circulating fatty acids, increased lipid storage in the adipose tissue and improved glucose tolerance, highlighting the importance of the liver-adipose tissue axis in NAFLD and the metabolic syndrome.[17] Our data demonstrated that MSR1 expression was observed in tissue-resident macrophages, the Kupffer cells, rather than in infiltrating monocytes, located in the portal tract, and that the expression increases when differentiating human monocytes towards mature macrophages.[16, 18] The association between *MSR1* mRNA and disease activity in our study would suggest that there is an ongoing differentiation from infiltrating monocytes towards macrophages during NASH. Although portal inflammation is associated with advanced NAFLD, lobular inflammation has been reported to predict fibrosis progression in human NAFLD, suggesting that disease progression is driven by tissue-resident macrophages rather than infiltrating monocytes.[19] Our results support this as *Msr1* deficiency in HFD-fed mice tempered the lipid-induced inflammatory response in the liver, by reducing the expression of *Axl*, *Il1b*, *S100a8/a9* and *Spp1* but also *Cd44*. Cd44 expression has been associated with NASH in human and mouse, and is crucial for homing of monocytes into the damaged liver, suggesting that lipid accumulation in tissue-resident macrophages via MSR1 is a trigger to recruit immune cells.[20] This is in line with previous reports where it was described that Kupffer cell depletion by clodronate liposomes in mice on a 22 week choline-deficient l-amino acid-defined diet suppresses infiltration of inflammatory cells, mainly monocytes, into the liver.[21] Furthermore, our results showed that the absence of Msr1 induced a change in hepatic expression of genes associated with lipid metabolism, including an increase in *Ppara*, with concordantly increased mitochondrial oxygen consumption and ameliorated glucose tolerance in HFD-fed mice. Peroxisome proliferator–activated receptors (PPAR) are nuclear receptors playing key roles in metabolic homeostasis and inflammation.[22] Selective Kupffer cell depletion has been reported to activate Ppara signalling in hepatocytes while resulting in overall reduced levels of hepatic triglycerides in mice fed a 45%-HFD.[23] Furthermore, hepatocyte-restricted *Ppara* deletion in mice impaired liver lipid metabolism, leading to increased plasma FFAs.[24] In human adult non-cirrhotic NASH patients, the pan-PPAR agonist lanifibranor proved to induce NASH resolution after 24 weeks of treatment in a Phase 2b randomised, placebo-controlled, double-blind study.[25] Taken together, the effects of Msr1 deficiency observed in this study on liver

metabolism, triglycerides and circulating FFAs could in part be explained by the changed Ppara signalling in the liver.

This study showed that MSR1 can facilitate the uptake of SFAs, such as palmitic acid, as well as non-SFAs, such as oleic acid, independent from other receptors. Yet, only SFAs could induce the release of TNFα through phosphorylation of JNK in macrophages, which is in line with previous reports.[7-9] In our *Msr1*$^{-/-}$ HFD-fed mice, we observed lower hepatic *Tnfa* expression as well as lower serum Tnfα. Furthermore, therapeutic blocking of MSR1 *in vivo* or *ex vivo* reduced foamy macrophage formation and the release of TNFα. TNFα has a pleiotropic effect as it can sensitise hepatocytes to apoptosis and as it can stimulate hepatic lipid synthesis while reducing *Ppara* expression.[26, 27] Furthermore, Tnfα affects glucose homeostasis in adipocytes and promotes lipolysis in cultured adipocytes, and could explain the obese phenotype in our *Msr1*$^{-/-}$ HFD-fed mice.[28]

Although current efforts to develop drug therapies for NAFLD primarily focus on ameliorating the specific histological features of the disease (i.e. steatohepatitis or fibrosis), it is important to remember that NAFLD is part of a multi-system metabolic disease state and so agents that offer more broad metabolic or cardiovascular benefits would be highly attractive . Our data indicate that by targeting MSR1, one would not only reduce lipid-induced inflammation in the liver but also improve dyslipidemia and affect improved lipid storage in the adipocytes. In addition, we demonstrated the feasibility of using targeted monoclonal antibody therapy to treat NASH by reducing hepatic inflammation. Moreover, we found some evidence that the genetic variant rs41505344 in *MSR1* was associated with serum triglycerides and ALT in a large cohort of over 400,000 patients. Though the SNP in *MSR1* was not strongly associated with susceptibility to NAFLD, we found that several transcription factors regulating the expression of *MSR1* bound in the locus and that the SNP was associated with changes in *MSR1* transcript, indicating a role for rs41505344 during macrophage differentiation.

There are several limitations to this study. We used a global knock-out mouse model and focused on the early phases of NAFLD by using a relative short-term diet of 16 weeks. To further investigate the liver-adipose tissue axis, a Kupffer cell-specific Msr1 knock-out or a conditional Msr1 knock-out mouse model challenged to a long term diet would provide more information on advanced NAFLD. Furthermore, we mainly explored the role of SFAs in macrophages, but this does not exclude that exosomes or oxLDL can have an additive effect in the inflammatory response, nor have we explored the synergetic function of other scavenger receptors such as CD36 or TREM2.

This study showed that the scavenger receptor MSR1, as part of the innate immune system, is a critical sensor for lipid homeostasis, highlighting the importance of the liver-adipose tissue axis. With the prevalence of obesity increasing globally, it is crucial that we understand how our immune system reacts when challenged with over-nutrition. Understanding and therapeutically influencing macrophage immunometabolism, could help us treat features of the metabolic syndrome, such as dyslipidemia, NAFLD and type II diabetes.

Abbreviations: FFA free fatty acids, NAFL non-alcoholic fatty liver, NAFLD non-alcoholic fatty liver, NASH non-alcoholic steatohepatitis, OA oleic acid, PA palmitic acid, SFA saturated fatty acids, SNP single nucleotide polymorphism

Acknowledgments: The authors would like to thank the Newcastle Bioimaging Unit, the Newcastle University Genomics Core Facility, the Newcastle NanoString Core Facility and the Newcastle Molecular Pathology Node Proximity Laboratory for their technical support.

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514 **Table 1.** Correlation rs41505344 SNP with clinical features using UK Biobank (n=430,101)
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			rs41505344_*MSR1*						Unadjusted	Adjusted for age, gender, BMI, PC 1-10, centre and batch		
			GG		GA		AA			Inverse normal rank transformation		
Characteristic	**Value**	**Range**	**Value**	**Range**	**Value**	**Range**	**Value**	**Range**	**p-value**	**p-value**	**Beta**	**CI**
n-value	430101		344142		81079		4880					
Age, y (mean ± SD)	56.8±8.03	39-73	56.8±8.03	39-72	56.8±8.02	39-73	56.7±8.06	40-70	0.80			
BMI (mean ± SD)	27.4±4.76	12.1-74.7	27.4±4.77	12.6-68.4	27.4±4.75	12.1-74.7	27.3±4.81	16.2-54.5	0.02			
Male, n (%)	196727 (45.7)		157394 (45.7)		37080 (45.7)		2253 (46.2)		0.80			
ALT (U/L)	23.5±14.1	3.01-495	23.6±14.1	3.1-495	23.5±14.3	3.01-472	23.3±13.1	3.82-286	0.01	0.063	-0.0060	
AST (U/L)	26.2±10.6	3.3-947	26.2±10.5	3.3-947	26.2±11	3.3-711	26±9.72	8.4-227	8.29E-04	0.003	-0.010	
Glucose (mM)	5.12±1.21	1-36.8	5.12±1.2	1.1-36.8	5.12±1.23	1-32.7	5.12±1.18	1.8-22.3	0.76	0.41	0.003	
Cholesterol (mM)	5.71±1.14	0.601-15.5	5.71±1.14	0.601-15.5	5.71±1.14	1.71-13.3	5.68±1.13	2.39-12.3	0.16	0.12	-0.005	
LDL (mM)	3.57±0.87	0.266-9.8	3.57±0.87	0.266-9.8	3.57±0.868	0.751-9.61	3.55±0.862	1.22-7.64	0.16	0.15	-0.0051	
HDL (mM)	1.45±0.382	0.219-4.4	1.45±0.382	0.226-4.4	1.46±0.382	0.219-4.13	1.45±0.38	0.628-3.22	0.03	0.071	0.006	
Triglycerides (mM)	1.75±1.02	0.231-11.3	1.76±1.03	0.233-11.3	1.74±1.02	0.231-11.3	1.72±1	0.375-11	8.27E-07	3.55E-06	-0.015	
Chronic liver disease, n (%)	6024 (1.401)		4807 (1.397)		1161 (1.432)		56 (1.148)		0.98	0.92	1.003	0.946-1.06
All-cause cirrhosis, n (%)	1709 (0.397)		1349 (0.392)		344 (0.424)		16 (0.328)		0.40	0.37	1.051	0.943-1.17

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Figure legends

Fig.1. Macrophage Scavenger Receptor 1 (MSR1) expression in human non-alcoholic fatty liver disease (NAFLD) correlates with steatosis and steatohepatitis. (a) mRNA levels of *MSR1* in a cohort of 170 histological proven NAFLD samples covering the different stages of the disease using nanoString (Mann-Whitney-U test and Kruskal-Wallis with correction for multiple testing). **(b)** *MSR1* transcript in patients stratified based on NAS≥4 and presence of NASH (Mann-Whitney-U test). **(c)** Receiver operating characteristic curve showing the binary logistic model based on *MSR1* transcript, MSR1 model, compared to other variables *CD68* transcript, ALT and AST. **(d)** Immunohistochemical analysis of MSR1 in human NAFLD biopsies (n=14), red arrows indicate lipogranuloma and lipid laden macrophages. Histopathological quantification of MSR1 and CD68 immunopositive cells in the parenchyma and portal tract (NAFL n=4; NASH F0-2 n=6; NASH F3-4 n=4; one-way ANOVA or Kruskal-Wallis with correction for multiple testing). **(e)** Differentiation of human monocytes obtained from 5 healthy volunteers towards mature macrophages. MSR1 protein expression was assessed using FACS (n=3, unpaired Student's t-test) and western blotting (n=2). **(f)** Representative image of PLIN2+CD68+ parenchymal macrophages. Quantification was done in a cohort of 10 NAFLD samples (unpaired Student's t-test). Data are presented as mean ± SEM (* p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001, *ns:* non-significant). Scale bars 100µm.

Fig.2. Msr1 deficiency protects against HFD-associated metabolic dysregulation and liver damage. (a) Body weight of *Msr1*$^{+/+}$ (Wild-type, WT) and *Msr1*$^{-/-}$ male aged-matched mice fed high fat/cholesterol diet (HFD) for 16 weeks (n=5 mice/experimental group). **(b)** Epididymal (eWAT) and liver mass of WT and *Msr1*$^{-/-}$ male mice fed with HFD. **(c)** Glucose tolerance test on overnight fasted mice during the 15th week of HFD feeding; AUC (area under curve). **(d)** Histological characterisation of livers specimens from WT and *Msr1*$^{-/-}$mice fed a HFD for 16 weeks. **(e)** Representative images of morphology of the eWAT and liver from HFD-fed WT and *Msr1*$^{-/-}$ mice. Scale bar 100µm. **(f)** Quantification of the adipocyte number per area and hepatic collagen deposition of WT and *Msr1*$^{-/-}$ HFD-fed mice (n = 5 mice/experimental group; Mann-Whitney-U test). **(g)** RNA sequencing data comparing *Msr1*$^{-/-}$ (n=5) with baseline WT (n=4) HFD-fed mice. Gene Ontology enrichment analysis was performed for biological processes and selected differentially expressed genes were visualised with corrected p-values. **(h)** Seahorse analysis of oxygen consumption rates (OCRs) of liver tissue from HFD-fed WT and *Msr1*$^{-/-}$ mice (n = 4/group). Data are presented as mean ± SEM (unpaired Student's t-test or Mann-Whitney-U test, or one-way ANOVA with

correction for multiple testing; p-values are shown for the comparisons WT and *Msr1*$^{-/-}$; *p< 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001, ns: non-significant).

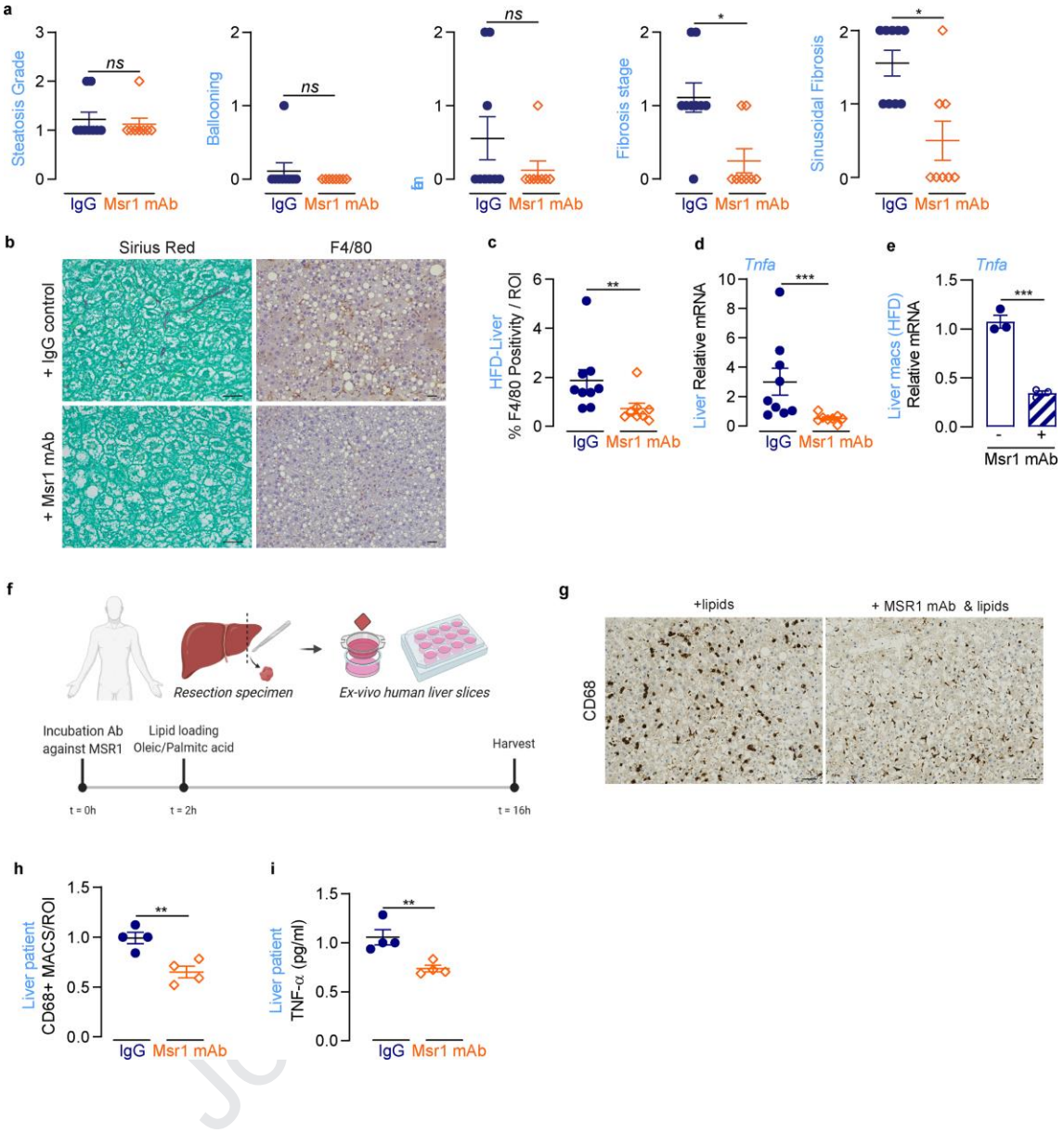
Fig.3. Msr1 mediates HFD-induced adipose tissue and hepatic inflammation and facilitates macrophage activation toward a pro-inflammatory phenotype. (**a**) Representative images for F4/80 immunostainings in eWAT and liver (scale bars 100µm) from WT and *Msr1*$^{-/-}$ HFD-fed mice (n=5/experimental group). Arrows indicate immunopositive cells. (**b**) Serum levels of Tnfa and Il-6 in NC- and HFD-fed mice (n=5/ group). **(c-d)** Quantification of mRNA levels of *Tnfa, Il6* inflammation markers in the eWAT and liver of NC- and HFD-fed mice (n=5/group). **(e-f)** Real-time PCR analysis for markers of inflammation in isolated F4/80^{+} adipose tissue (ATMs) and liver macrophages (n=5 mice/group). Data are presented as mean ± SEM (unpaired Student's t-test or Mann-Whitney-U test, or one-way ANOVA or Kruskal-Wallis with correction for multiple testing; p-values are shown for the comparisons WT and *Msr1*$^{-/-}$; *p< 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001, ns: non-significant).

Fig.4. Msr1 regulates JNK-mediated lipid-induced pro-inflammatory activation of macrophages. (a) Representative image of lipid uptake (mixture of 1mM Palmitic acid, saturated fatty acids (SFA), and 2mM Oleic, non-saturated fatty acids (non-SFA)) by WT and *Msr1*$^{-/-}$ bone marrow derived macrophages (BMDMs) visualised by Oil-red-O staining using confocal microscopy (n=3). **(b-c)** Quantification of SFA (palmitic acid 1mM) and non-SFA (oleic acid 2mM) uptake in WT and *Msr1*$^{-/-}$ BMDMs, or WT BMDMs pre-treated with or without anti-Msr1 antibody (n=5). Data are normalised to the average of the WT BMDM group. **(d)** Real-time PCR analysis for *Tnfa* and *Il6* in WT and *Msr1*$^{-/-}$ BMDMs stimulated or not either with SFA, non-SFA or bovine serum albumin (BSA) control for 6 hrs. **(e)** Real-time PCR analysis of BMDMs with or without SFA stimulation that were treated with 10 or 25µg/ml anti-Msr1 monoclonal antibody for 6 hrs. **(f)** Flow cytometry analysis and quantification of JNK1/2 phosphorylation in WT and *Msr1*$^{-/-}$ BMDMs stimulated with SFA or BSA control. **(g)** Quantification of SFA and non-SFA uptake in WT and *Msr1*$^{-/-}$ primary liver macrophages (n=3). Data are normalised to the average of the WT BMDM group. **(h)** Real time-PCR analysis and **(i)** flow cytometry analysis of phospho-JNK (Thr183/Tyr185) in WT and *Msr1*$^{-/-}$ primary liver macrophages treated either with control BSA or SFA or non-SFA for 6hrs (n=3). **(j)** Real time-PCR analysis of WT primary liver macrophages treated with or without monoclonal anti-Msr1 antibody (n=3). Data are shown as mean ± SEM (unpaired Student's t-test or one-way ANOVA/Kruskal-Wallis with correction for multiple testing; for panels d and f-i the p-values are shown

only for grouped comparisons per experimental condition; *p< 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001).

Fig.5. Therapeutic inhibition of MSR1 prevents formation of pro-inflammatory foamy macrophages. (**a**) Histological characterisation of livers specimens from WT male mice fed a HFD for 12 weeks and treated with anti-Msr1 antibody (n=8) or IgG control (n=9) at week 10 and 11. (**b**) Representative images of morphology of HFD-fed animals treated with anti-Msr1 antibody or IgG control. **(c)** Quantification of F4/80 staining from treated animals presented as percentage pixel positivity of the region of interest (ROI). **(d-e)** Real-time PCR analysis for *Tnfa* transcript in liver samples and isolated hepatic macrophages from HFD-fed animals treated with anti-Msr1 antibody (n=8) or IgG control (n=9). Isolated primary liver macrophages were pooled together before real-time PCR analysis (n=3). **(f)** Schematic overview of antibody-based treatment of *ex vivo* lipid-loaded human liver slices. Samples were loaded with a combination of oleic (2mM) and palmitic acid (1mM). **(g)** Immunohistochemical staining for CD68 on human lipid-loaded liver slices treated with or without anti-MSR1 antibody. **(h)** Quantification of CD68 staining presented as percentage pixel positivity of the region of interest (ROI). Normalisation was done to untreated reference. **(i)** TNF-α ELISA from human liver slices treated with lipids or anti-MSR1-antibody+lipids. Data are presented as mean ± SEM (unpaired Student's t-test or Mann-Whitney-U test; *p< 0.05, **p < 0.01, ***p < 0.001). Scale bars 50µm.

Fig.6. Regulatory mechanisms of *MSR1* expression in human NAFLD.
(**a**) Locus plot showing *MSR1* rs41505344 SNP based on case-control analysis comparing 1,483 histologically characterised NAFLD samples with 17,781 matched population controls. (**b**) Schematic overview of the workflow used to identify transcriptional regulatory mechanisms of *MSR1* from publicly available RNA sequencing data, comparing human monocytes with differentiated macrophages.[16] (**c**) Visualisation of chromatin immunoprecipitation sequencing data around *MSR1* rs41505344 SNP of the predicted transcription factors that are differentially expressed in the RNA sequencing data as identified by iRegulon. Bottom row indicates known transcriptional regulatory regions of *MSR1*.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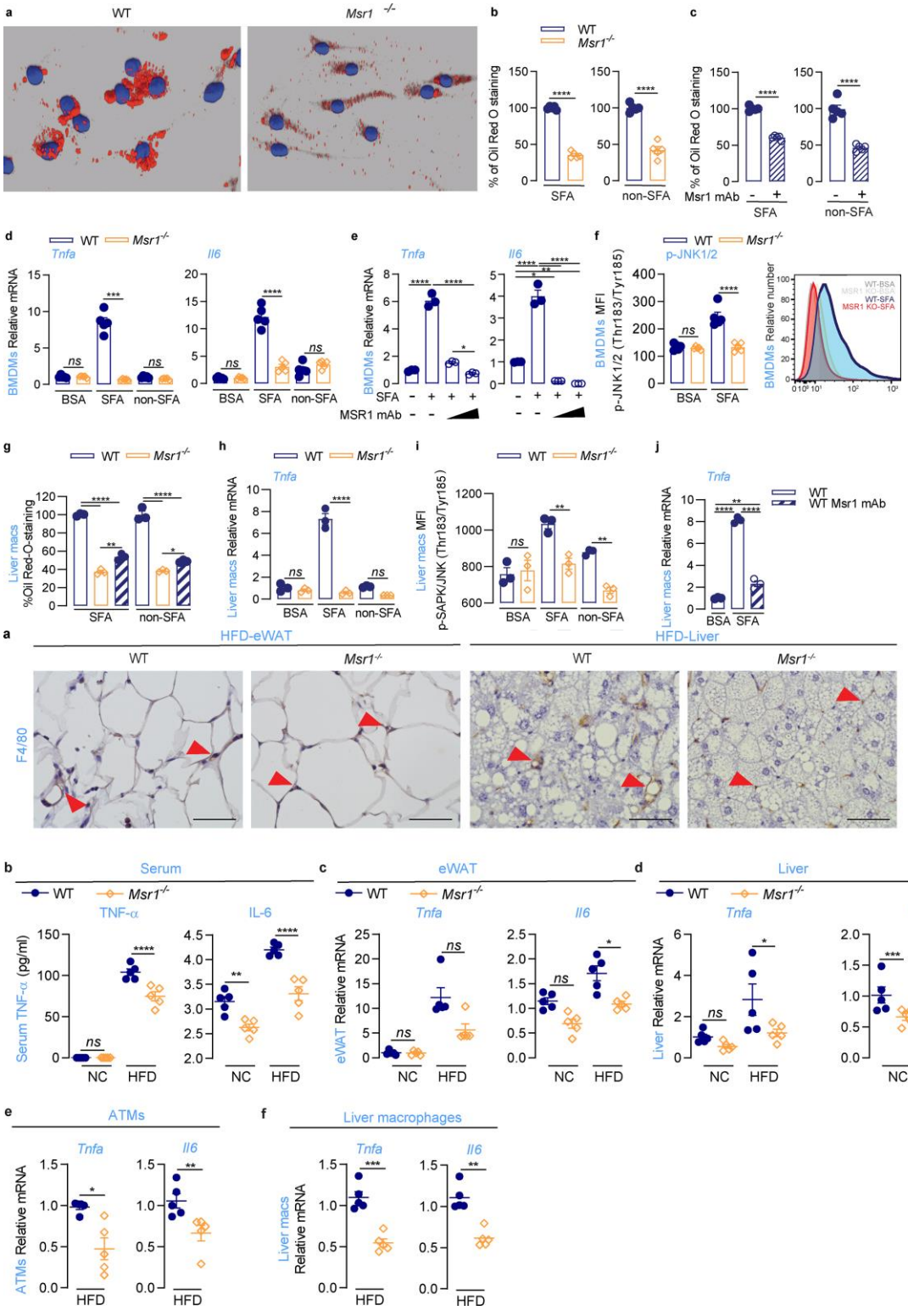
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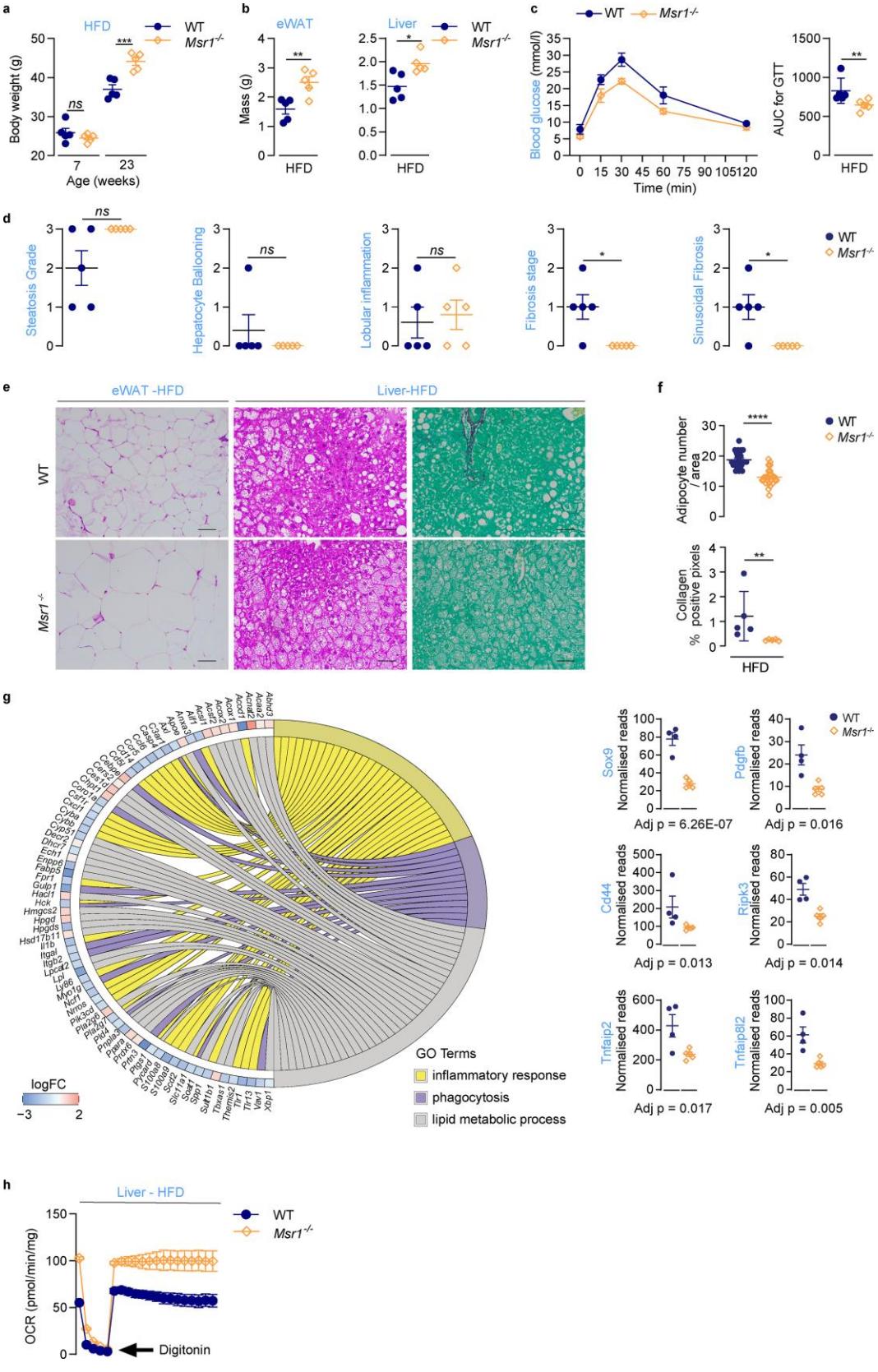
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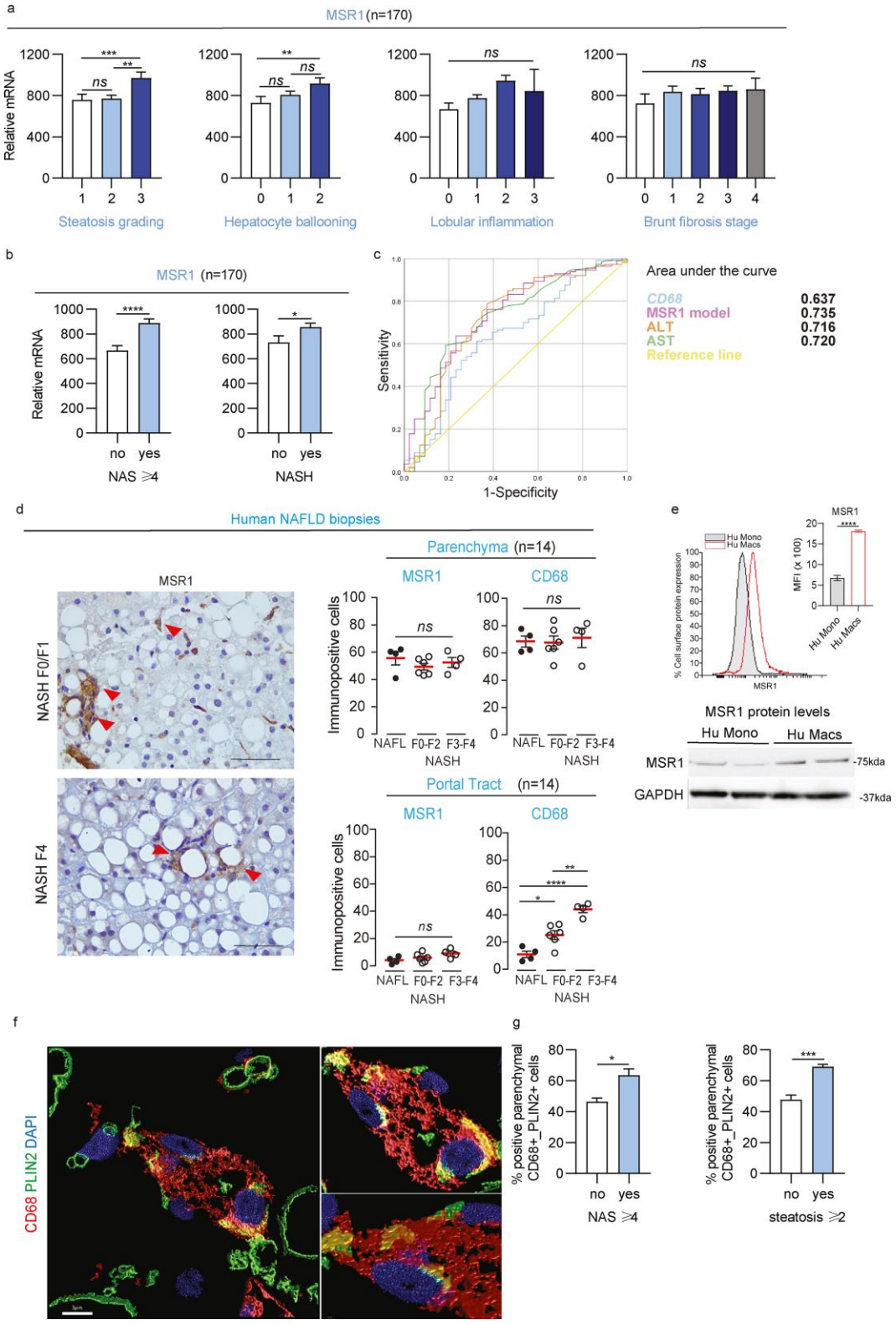
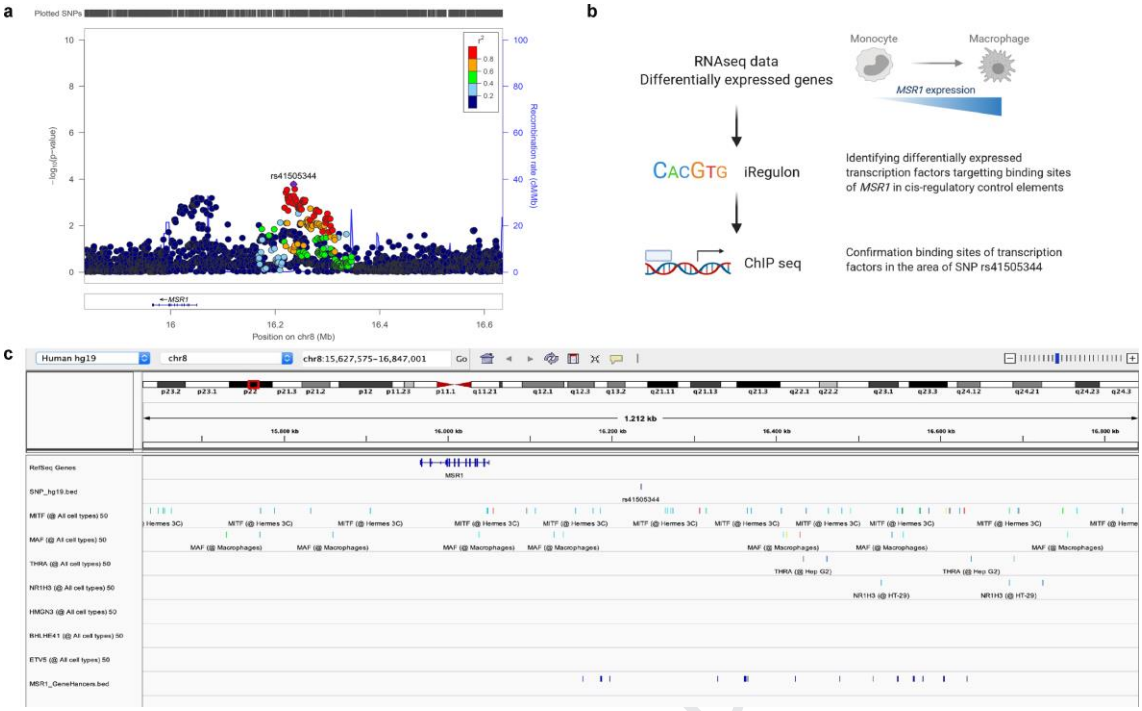
WT
Msr1-/-
Collagen % positive pixels
**
HFD
g
logFC
−3
2
GO Terms
inflammatory response
phagocytosis
lipid metabolic process
Sox9
Normalised reads
Adj p = 6.26E-07
Pdgfb
Adj p = 0.016
Cd44
Adj p = 0.013
Ripk3
Adj p = 0.014
Tnfaip2
Adj p = 0.017
Tnfaip8l2
Adj p = 0.005
h
Liver - HFD
WT
Msr1-/-
OCR (pmol/min/mg)
Digitonin


a
MSR1 (n=170)
Relative mRNA
Steatosis grading
Hepatocyte ballooning
Lobular inflammation
Brunt fibrosis stage
b
MSR1 (n=170)
Relative mRNA
NAS ⩾4
NASH
c
Sensitivity
1-Specificity
Area under the curve
CD68 0.637
MSR1 model 0.735
ALT 0.716
AST 0.720
Reference line
d
Human NAFLD biopsies
MSR1
NASH F0/F1
NASH F4
Parenchyma (n=14)
Portal Tract (n=14)
Immunopositive cells
NAFL F0-F2 F3-F4
NASH
e
MSR1
Hu Mono
Hu Macs
% Cell surface protein expression
MFI (x 100)
MSR1 protein levels
GAPDH
-75kda
-37kda
f
CD68 PLIN2 DAPI
g
% positive parenchymal CD68+_PLIN2+ cells
NAS ⩾4
steatosis ⩾2



Highlights

- In human NAFLD, MSR1 is expressed in mature Kupffer cells and foamy macrophages
- *MSR1* transcript levels are associated with disease activity in patients with NAFLD
- Mice lacking Msr1 are protected against diet-induced metabolic disorder
- MSR1 is essential for the uptake of lipids in mature macrophages
- Uptake of saturated fatty acids via MSR1 results in a pro-inflammatory response
- The SNP rs41505344 upstream of MSR1 is associated with altered serum triglycerides