FPR-1 is an important regulator of neutrophil recruitment and a tissue-specific driver of

pulmonary fibrosis

Jack Leslie<sup>1#</sup>, Ben JM Millar<sup>1#</sup>, Alicia del Carpio Pons<sup>1</sup>, Rachel A Burgoyne<sup>1</sup>, Joseph D Frost<sup>1</sup>,

Ben S Barksby<sup>1</sup>, Saimir Luli<sup>1</sup>, Jon Scott<sup>2</sup>, A John Simpson <sup>2,3</sup>, Jack Gauldie<sup>4</sup>, Lynne A Murray<sup>5</sup>,

Donna K Finch<sup>5</sup>, Alan M Carruthers<sup>5</sup>, John Ferguson<sup>5</sup>, Matthew A Sleeman<sup>5</sup>, David Rider<sup>5</sup>,

Rachel Howarth<sup>1</sup>, Christopher Fox<sup>1</sup>, Fiona Oakley<sup>1</sup>, Andrew J Fisher<sup>1,6</sup>, Derek A Mann<sup>1</sup>, Lee

A Borthwick<sup>1</sup>\*

<sup>1</sup> Newcastle Fibrosis Research Group, Biosciences Institute, Newcastle University, Newcastle

upon Tyne, UK.

<sup>2</sup> Biosciences Institute, Newcastle University, Newcastle upon Tyne, United Kingdom.

<sup>3</sup> Interstitial Lung Disease Clinic, Newcastle upon Tyne Hospitals NHS Foundation Trust,

United Kingdom.

<sup>4</sup> St Joseph's Healthcare and Department of Pathology and Molecular Medicine, Firestone

Institute for Respiratory Health, McMaster University Hamilton, Hamilton, Ontario, Canada.

<sup>5</sup> MedImmune Ltd., Cambridge, UK, CB21 6GH.

<sup>6</sup> Institute of Transplantation, Freeman Hospital, Newcastle upon Tyne, UK.

# authors contributed equally to this study

\* Correspondence author

Dr Lee Borthwick

Newcastle Fibrosis Research Group

**Biosciences Institute** 

1

4th Floor, William Leech Building

Newcastle University

Newcastle upon Tyne

NE2 4HH

Tel: 0191 208 3112

Email: <a href="mailto:lee.borthwick@ncl.ac.uk">lee.borthwick@ncl.ac.uk</a>

**Conflict of interest statement** 

DF and LM are employees of an AstraZeneca group company and may receive AstraZeneca

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2

## Figure S1- fpr1-/- mice are not protected from CCl4 induced acute liver injury

A) C57Bl/6 and fpr1-/- mice were challenged with a single intraperitoneal dose of carbon tetrachloride (CCl<sub>4</sub>) at 2µl/g body weight (CCl<sub>4</sub>:olive oil at 1:1 [vol/vol]) or olive oil as a control. Serum and liver tissue were harvested at 24, 48 and 72 hours. Serum AST (**B**) and ALT (**C**) levels (U/L) were quantified. Number of **D**) NIMP and **E**) CD68 positive cells and **F**) PCNA positive hepatocytes per x20 magnification field. Data represent the mean value of n=20 randomly selected non-overlapping x20 magnification fields per mouse. **G**) Percentage area positive of  $\alpha$ -smooth muscle actin ( $\alpha$ SMA). Data represents the mean value of n=20 randomly selected, non-overlapping fields at x10 magnification. No significant difference was seen between olive oil-treated C57Bl/6 and fpr1-/- mice and therefore olive oil treated mice were pooled and presented as mean (red hashed line). n=5-8 mice per group. Data were analysed using a Mann-Whitney U test and presented as box and whiskers plots. All p-values >0.05.

## Figure S2 - CCl4-induced liver damage is comparable in C57Bl/6 and fpr1-/- mice

C57Bl/6 and fpr1-/- mice were challenged bi-weekly for 8 weeks with intraperitoneal injection of CCl<sub>4</sub> at 2µl/g body weight (CCl<sub>4</sub>: olive oil at 1:3 [vol/vol]) or olive oil as a control. Mice were killed 24 hours after the last CCl<sub>4</sub> injection. Serum AST (**A**) and ALT (**B**) levels (U/L) were quantified. **C**) Number of PCNA positive cells per x20 magnification field. Data represent the mean value of n=20 randomly selected, non-overlapping fields per mouse. Relative gene expression of MMP-2 was assessed by qPCR (**D**). Gene expression was normalised to GAPDH as a loading control. No significant difference was seen between olive oil-treated C57Bl/6 and fpr1-/- mice and therefore olive oil-treated mice are grouped and presented as mean (red hashed line). n=5-9 mice per group. Data were analysed using Mann-Whitney U test and presented as box and whiskers plots. All p-values >0.05.

## Figure S3- fpr1-/- mice are not protected from MCD or BDL induced liver fibrosis

C57Bl/6 and fpr1-/- mice were fed a methionine/choline deficient diet (MCD) or control methionine/choline sufficient (MCS) diet and then harvested after 6 weeks. A) Representative αSMA stained liver sections in MCD fed mice. **B**) Serum aspartate aminotransferase (AST) and Alanine transaminase (ALT) levels expressed as units/litre (U/L). C) Relative gene expression of αSMA (i), Collagen 1A1 (ii), TGFβ1 (iii) and Timp1 (iv) in liver tissue was assessed by qPCR and normalised to GAPDH as a loading control. No significant difference was seen between MCS fed C57Bl/6 and fpr1-/- mice and therefore MCS-treated mice were pooled and presented as mean (red hashed line). C57Bl/6 and fpr1-/- mice also underwent bile duct ligation (BDL) and were harvested 10 days post-surgery. **D**) Representative αSMA stained liver section in BDL injured mice. E) Serum AST and ALT levels in BDL injured mice. F) Relative gene expression of αSMA (i), Collagen 1A1 (ii), TGFβ1 (iii) and Timp1 (iv) in liver tissue was assessed by qPCR and normalised to GAPDH as a loading control. No significant difference was seen between Sham C57Bl/6 and fpr1-/- mice and therefore sham mice were pooled and presented as mean (red hashed line). n=6-10 mice per group for panels A-F and n=5-9 mice per group for panels G-L. Data were analysed using a Mann-Whitney U test and presented as box and whiskers plots.

Gene target	Gene name	Forward primer sequence	Reverse primer sequence
Collagen 1a1	Collal	TTCACCTACAGCACGCTTGTG	GATGACTGTCTTGCCCCAAGTT
Fibronectin	Fn1	GAGCAAGAAGACAACAGAG	GGTCTGGGGTTGGTAAATAG
Elastin	Eln	CCCTGTCCCTGTTCCTTCTG	CGCTCCCTATCCTCTTGTTG
MMP2	Mmp2	CCGATGCTGATACTGACACT	GTCACTGTCCGCCAAATAAA
KC	Cxcl2	CTGGGATTCACCTCAAGAACATC	CAGG-GTCAAGGCAAGCCTC
MCP-1	Ccl2	AGGTCCCTGTCATGCTTCTG	TCTGGACCCATTCCTTCTTG
GAPDH	Gapdh	GCACAGTCAAGGCCGAGAAT	GCCTTCTCCATGGTGGTGAA

Table S1. Primer sequences