Supplementary Information

Regulation of monocyte induced cell migration by the RNA binding protein, FXR1

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1. Supplemental Figures S1-S2

2. Supplemental Figure legends

3. Supplemental Table legends

4. Supplemental Tables S1-S3 (related to Figs. 2-3, excel files)

S1

Type	Gene Ontology category description	number of genes	Benjamini
Cluster 1 (Enrichment Score: 6.98)			
BP	response to wounding	58	7.10E-05
BP	defense response	63	9.40E-05
BP	inflammatory response	39	7.20E-04
Cluster 2 (Enrichment Score: 3.81)			
CC	extracellular region	137	9.00E-03
CC	extracellular region part	75	7.30E-03
CC	extracellular space	57	1.00E-02
Cluster 3 (Enrichment Score: 3.41)			
CC	intrinsic to plasma membrane	91	9.80E-03
CC	integral to plasma membrane	89	8.00E-03
CC	plasma membrane	232	9.80E-03
CC	plasma membrane part	136	1.50E-01

S2

GOTERM	Term	Count	%	P-Value	Benjamini
BP_FAT	Defense response	62	6.4	5.1E-8	1.4E-4
BP_FAT	Response to wounding	56	5.8	5.3E-8	7.5E-5
BP_FAT	Immune response	64	6.6	6.0E-7	5.7E-4
BP_FAT	Inflammatory response	38	3.9	9.6E-7	6.8E-4
CC_FAT	Intermediate filament cytoskeleton	25	2.6	1.4E-5	5.1E-3
CC_FAT	Intermediate filament	24	2.5	3.0E-5	5.3E-3
MF_FAT	Chemokine activity	11	1.1	5.9E-5	4.5E-2
CC_FAT	Extracellular region	135	13.9	6.7E-5	8.0E-3
CC_FAT	External side of plasma membrane	22	2.3	8.4E-5	7.5E-3
CC_FAT	Extracellular region part	74	7.6	9.2E-5	6.6E-3
BP_FAT	Cell surface receptor linked signal transduction	124	12.7	9.3E-5	5.2E-2
MF_FAT	Chemokine receptor binding	11	1.1	1.0E-4	4.0E-2
CC_FAT	Intrinsic to plasma membrane	88	9.0	1.6E-4	9.4E-3
CC_FAT	Plasma membrane	227	23.3	1.6E-4	8.2E-3
MF_FAT	Endopeptidase activty	36	3.7	1.8E-4	4.6E-2
CC_FAT	Extracellular space	56	5.8	1.8E-4	8.3E-3
CC_FAT	Integral to plasma membrane	86	8.8	2.0E-4	7.9E-3

Supplemental Figure Legends

Figure S1 Gene Ontology (GO) analysis of the differential gene expression profiling of FXR1 regulated mRNAs in control and FXR1 knockdown THP1 monocytes GO analysis of genes that are deregulated in FXR1 depleted cells compared with control shRNA cells, grown in 24 h serum-starvation (S- 24h) conditions was performed using the DAVID tool, as previously conducted[1]. BP, biological pathway; CC, cellular component; MF, molecular function.

Figure S2 Immune response genes, including cytokines and chemokines, are regulated by FXR1 GO analysis for differentially expressed immune and signaling genes in serum-starved cells (S-24 h) was performed using the DAVID tool, as previously conducted[1]. Immune response associated genes in serum-starved cells (S-24 h) are observed to be significantly affected by FXR1 depletion (highlighted in yellow) (Tables S2B, S3).

Supplemental Table Legends (Supplemental Tables are separate excel files)

Table S1 Microarray comparison of RNAs affected by FXR1 knockdown compared to control shRNA in serum grown and 24 h serum-starved THP1 cells (related to Figs. 2-3)

Table S1 is the microarray dataset comparing the RNAs from shFXR1 cells to shCtrl cells in S+ and S-24 h conditions. Total RNA was extracted from these samples. The synthesized cDNA probe (WT Expression Kit; Ambion) was hybridized to GeneChip Human Gene ST 2.0 Arrays (Affymetrix) by the Partners Healthcare Center for Personalized Genetic Medicine Microarray facility. A 1.5 fold change in expression was used as the cutoff to determine differentially regulated genes.

Table S2A-B Differentially regulated mRNAs upon FXR1 depletion in S+ and S-24 h conditions (related to Figs. 2-3)

Table S2A and S2B are the microarray results of mRNAs that are differentially regulated in FXR1 knockdown compared with shCtrl cells, grown in S+ (Table S2A) and S-24 h (Table S2B) conditions respectively. A 1.5 fold change in expression was used as the cutoff to determine differentially regulated genes.

Table S3 Immune response genes are affected in FXR1 knockdown compared with control shRNA THP1 cells in 24 h serum-starvation conditions (related to Figs. 2-3)

Table S3 is the microarray results of mRNAs encoding immune response genes that are significantly affected in FXR1 knockdown compared with shCtrl cells in S-24 h serum-starvation conditions (from Table S2B). A 1.5 fold change in expression was used as the cutoff to determine differentially regulated genes. Gene Ontology (GO) analysis for differentially expressed genes was performed with the DAVID tool as previously conducted[1].

Reference List

1. Lee,S. *et al.* Upregulation of eIF5B controls cell-cycle arrest and specific developmental stages. *Proc. Natl. Acad. Sci. U. S. A* **111**, E4315-E4322 (2014).