

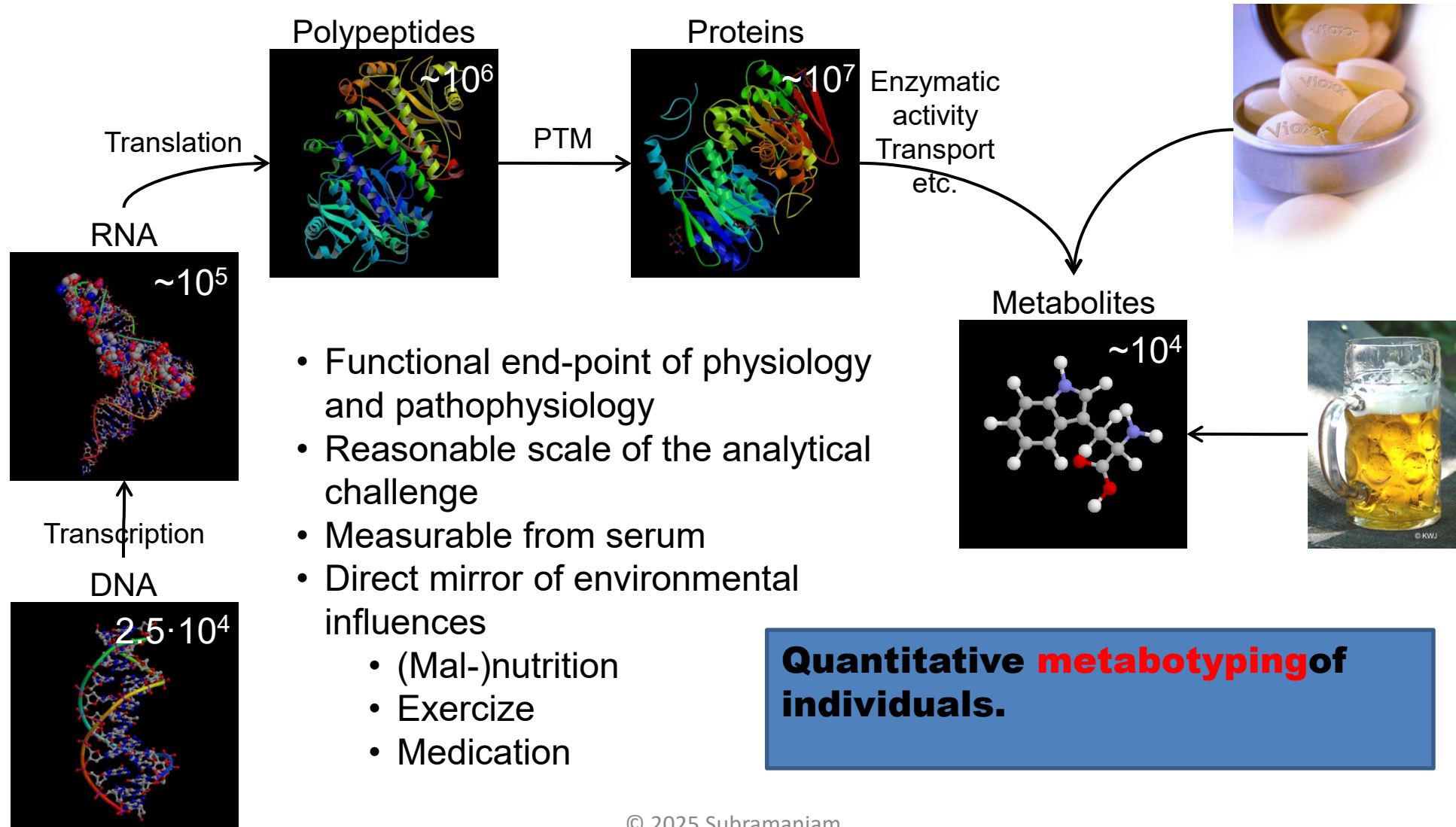
Systems Biology Approaches to Metabolic Health

Shankar Subramaniam
University of California San Diego



NASEM- Precision Medicine: Promoting Knowledge Exchange and Collaboration between Kuwait and the United States – Workshop Series. Oct 15, 2025

Why metabolomics?



Metabolomics Workbench and LIPIDMAPS – A 20-year journey

Acknowledgments

LIPIDMAPS – NIH NIGMS GLUE GRANT
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LIPIDMAPS Glue Grant Teams
LIPIDMAPS UK Teams
Metabolomics Common Fund Project Teams

METABOLOMICS WORKBENCH AND INFRASTRUCTURE: A GATEWAY TO MULTIOMICS INTEGRATION AND DISEASE BIOLOGY



Metabolomics Workbench website

<https://www.metabolomicsworkbench.org>



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Welcome to the UCSD Metabolomics Workbench, a resource sponsored by the Common Fund of the National Institutes of Health.

National Metabolomics Data Repository

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As of 02/27/25 a total of 3674 studies have been processed by the National Metabolomics Data Repository (NMDR). There are 3312 publicly available studies and the remainder (362) will be made available subject to their embargo dates.

Recently released studies on NMDR

ST003703 - NAD Depletion in Skeletal Muscle does not Compromise Muscle Function or Accelerate Aging; *Mus musculus*; [University of Copenhagen](#)

ST003704 - Hyperglycemia leads to BMSC(bone marrow mesenchymal stromal cells) impaired osteogenesis, enhanced adipogenesis, and altered metabolism; *Homo sapiens*; [University of Adelaide](#)

ST003707 - Reprogramming the metabolome of *Centella asiatica* (L.) Urban callus: Profiling of newly synthesized cryptic anthocyanins triggered by LED light exposure; *Centella asiatica*; [University of Johannesburg](#)

Quick Links - Key Resources

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NMDR Summary table as of 10/13/25		
Category	All studies	Public studies
Number of studies in NMDR	4197	3780
Number of human studies in NMDR	1726	1547
Number of samples	465783	396074
Number of named metabolites submitted to NMDR	975274	869086
Number of named metabolites mapped to RefMet	810058	731092
Number of data points for named metabolites	75416830	67823501
Number of unknown MS features (m/z, rt values) in NMDR	12249351	11058183
Number of Sample sources in NMDR studies	310	284
Number of Species in NMDR studies	404	383
Number of Disease associations in NMDR studies	244	232
Number of Countries represented	51	49
Number of Institutes represented	678	642
Number of studies with LC-MS data	3276	2909
Number of studies with GC-MS data	555	528
Number of studies with NMR data	299	281
Number of metabolite species names in RefMet	190562	
Number of metabolite structures in the Metabolite structure database	175415	
Number of raw files (approximate)	500000	

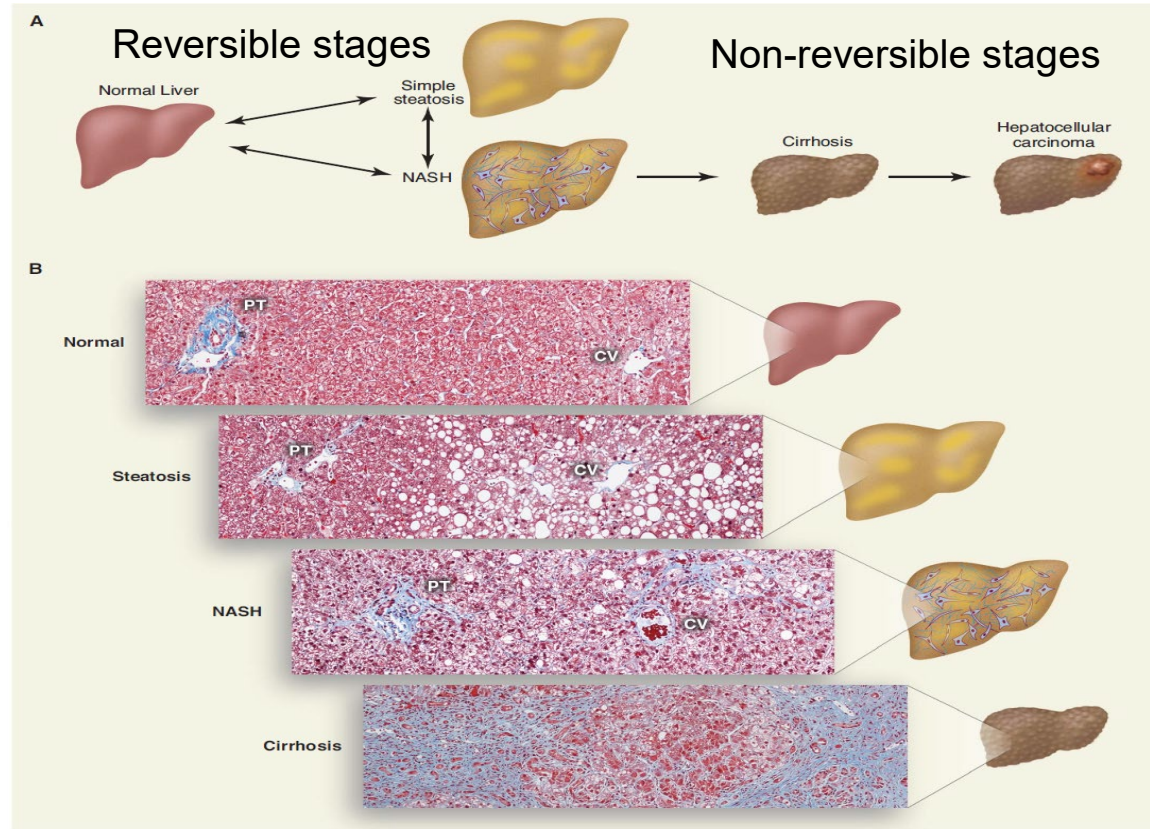
Integration of Metabolomics with other Omics

A study of fatty liver disease

Gorden DL, Myers DS, Ivanova PT, Fahy E, Maurya MR, Gupta S, Min J, Spann NJ, McDonald JG, Kelly SL, Duan J, Sullards MC, Leiker TJ, Barkley RM, Quehenberger O, Armando AM, Milne SB, Mathews TP, Armstrong MD, Li C, Melvin WV, Clements RH, Washington MK, Mendonsa AM, Witztum JL, Guan Z, Glass CK, Murphy RC, Dennis EA, Merrill AH Jr, Russell DW, Subramaniam S, Brown HA. Biomarkers of NAFLD progression: a lipidomics approach to an epidemic. *J Lipid Res.* 2015 Mar;56(3):722-36.

Zarrinpar A, Gupta S, Maurya MR, Subramaniam S, Loomba R. Serum microRNAs explain discordance of non-alcoholic fatty liver disease in monozygotic and dizygotic twins: a prospective study. *Gut.* 2015 May 22. pii: gutjnl-2015-309456.

Non Alcoholic Fatty Liver Disease (NAFLD)



Liver Study

	Normal (n = 31)	Steatosis (n = 17)	NASH (n = 20)	Cirrhosis (n = 20)	P (Over Four States)	Post hoc (Steatosis vs. NASH)	Post hoc (NASH vs. Cirrhosis)
Gender (% female)	80.6	70.6	55.0	25.0	8.0E-04	NS	NS
Ethnicity (% white)	67.7	100.0	80.0	90.0	NS	NS	NS ^a
BMI (kg/m ²)	40.1 ± 1.7	46.4 ± 2.7	47.5 ± 2.9	31.8 ± 1.5	2.3E-05	NS	^b
Age (years)	48.1 ± 2.6	48.4 ± 2.8	47.6 ± 2.7	58.1 ± 2.0	1.8E-02	NS	^c
Glucose (mg/dl)	110.3 ± 4.7	118.2 ± 10.9	128.9 ± 8.7	122.5 ± 10.6	NS	NS	NS
AST (U/l)	30.3 ± 4.6	26.4 ± 3.8	26.8 ± 2.2	62.7 ± 11.1	4.5E-03	NS	NS
ALT (U/l)	28.5 ± 4.5	24.5 ± 2.9	31.0 ± 4.0	36.4 ± 4.6	NS	NS	NS
AlkP (U/l)	83.7 ± 5.8	74.1 ± 4.4	76.8 ± 5.1	116.6 ± 14.9	2.9E-02	NS	^c
Total bilirubin (mg/dl)	0.45 ± 0.05	0.53 ± 0.04	0.43 ± 0.06	6.3 ± 2.0	3.8E-03	NS	^c

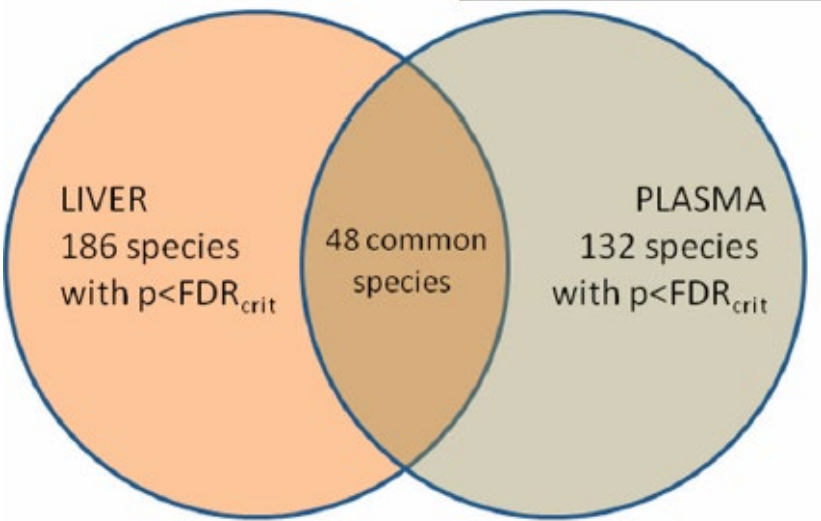
Data are expressed as mean ± SEM. Indicators, such as aspartate aminotransferase (AST), alanine aminotransferase (ALT), alkaline phosphatase (AlkP), and total bilirubin failed to show a strong difference between steatosis and NASH. Statistical testing across all four histological types was by chi-squared test for gender and ethnicity and ANOVA for all others. Post hoc testing of steatosis versus NASH and NASH versus cirrhosis for clinical data was conducted by Welch test (to control for unequal variances) for continuous variables and by chi-squared test for gender and ethnicity. Bonferroni corrected significance of the post hoc tests is indicated.

^a*P* < 0.001.

^b*P* < 0.01.

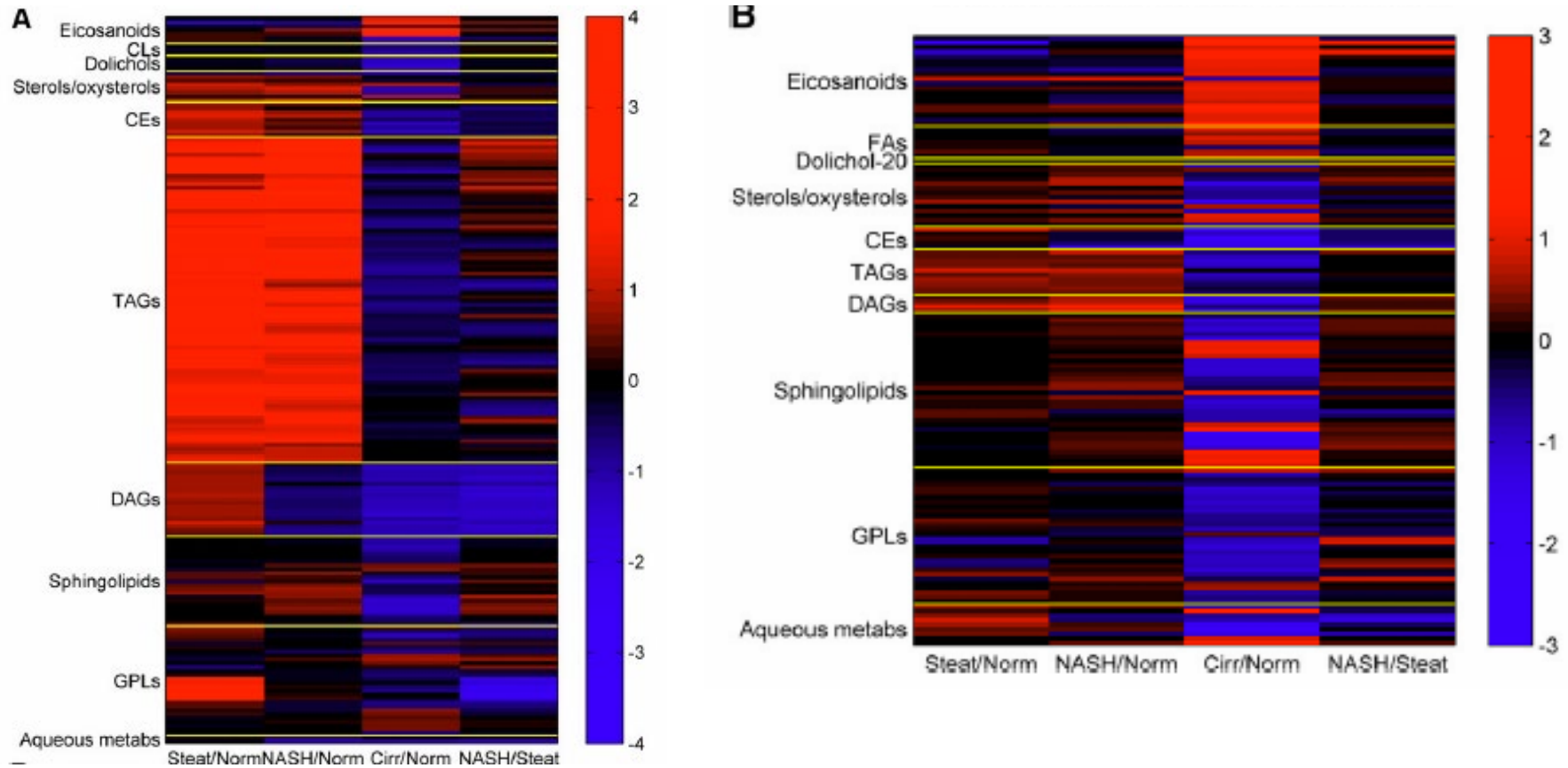
^c*P* < 0.05.

Common metabolites between liver and plasma. Major lipid classes, DAGs, TAGs, CEs, and GPLs are almost all polyunsaturated while sphingolipids are primarily longer chain species

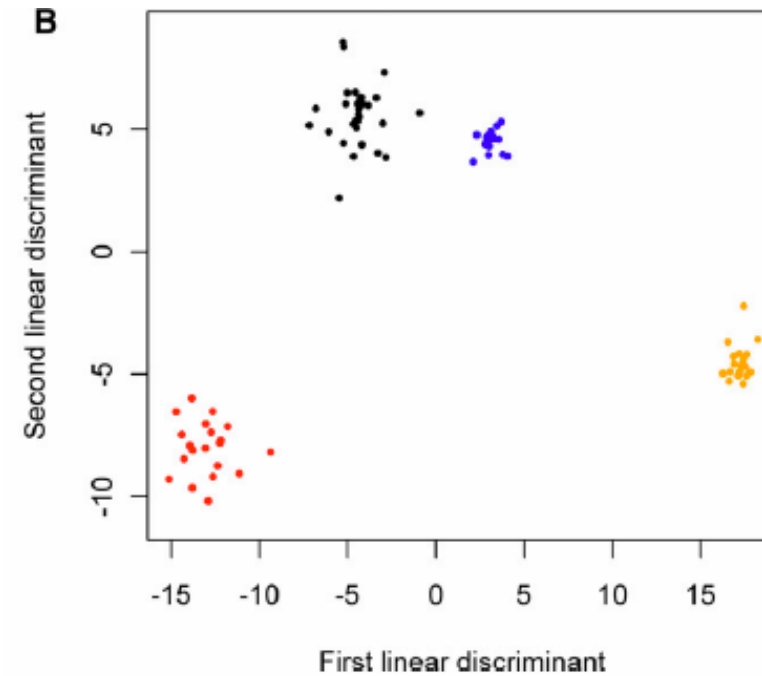
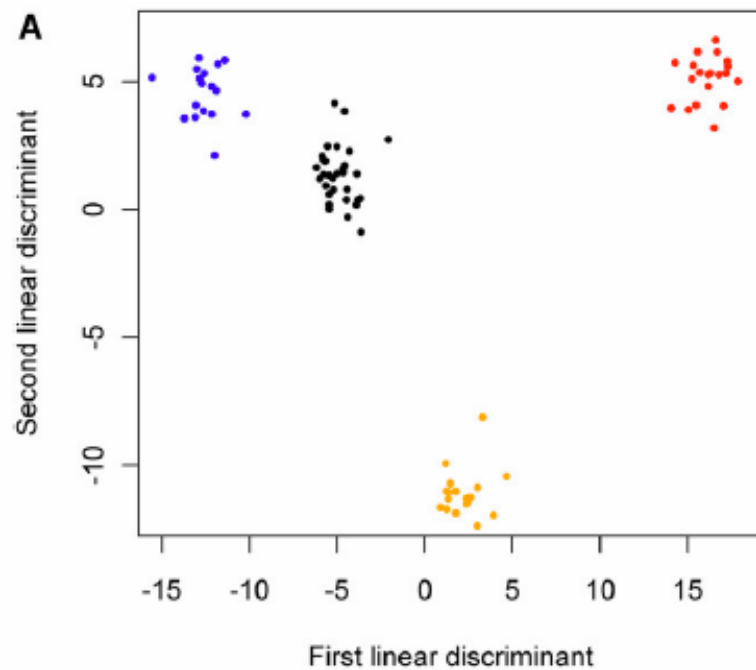


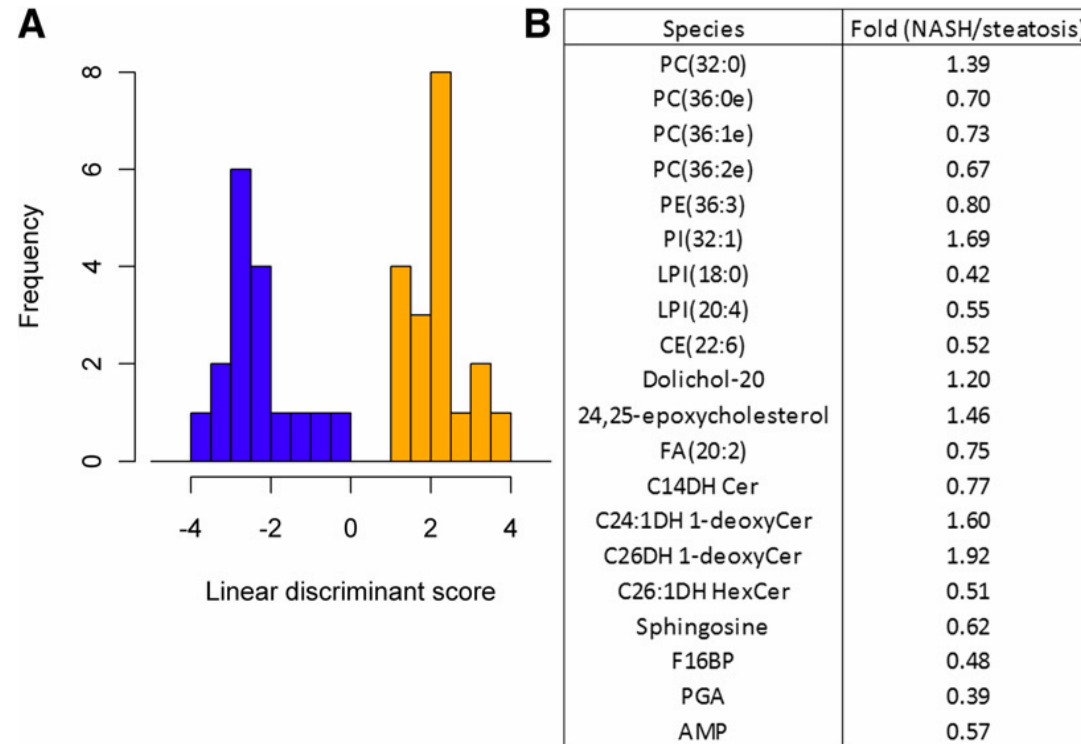
1,2-DAG(34:2)	Lanosterol	C18 Cer
1,2-DAG(36:2)	14-desmethyl-14-dehydrolanosterol	C20 Cer
1,2-DAG(36:3)	27-hydroxycholesterol	C22 Cer
TAG(50:2)	3-oxo,7 α -hydroxycholesterol	C24 Cer
TAG(52:1)	7 α -hydroxycholesterol	C18DH 1-deoxyCer
TAG(52:3)	12-HETE	C20DH 1-deoxyCer
TAG(52:4)	15-HETrE	C22DH 1-deoxyCer
TAG(52:5)	LTE4	C24DH 1-deoxyCer
TAG(54:3)	LPC(18:0)	C24:1DH Cer
TAG(54:4)	PC(36:4)	C24 GlcCer
TAG(54:5)	PC(38:4)	C24 HexCer
TAG(56:6)	PE(36:3)	C22 Sphingomyelin
CE(18:2)	PE(38:4p)	Sphingosine
CE(20:3)	PE(38:6)	Sphingosine-P
CE(20:4)	PE(40:6)	F16BP
CE(22:6)	PI(36:3)	Dolichol-20

Fold changes (log2) for species with FDR-adjusted significant P-values A. Liver, B. Plasma



LDA on plasma (A) liver species (B) with top 80 ANOVA scores classified samples by disease status. Blue: steatosis, black: normal; orange: steatohepatitis; red: cirrhosis

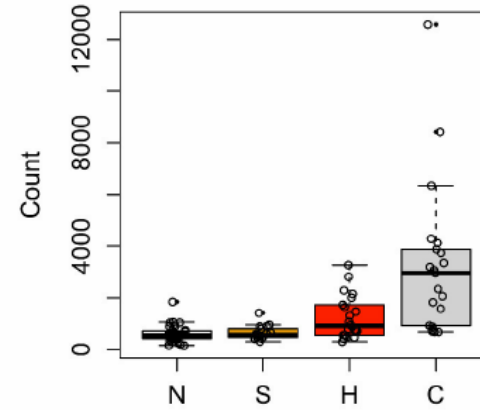




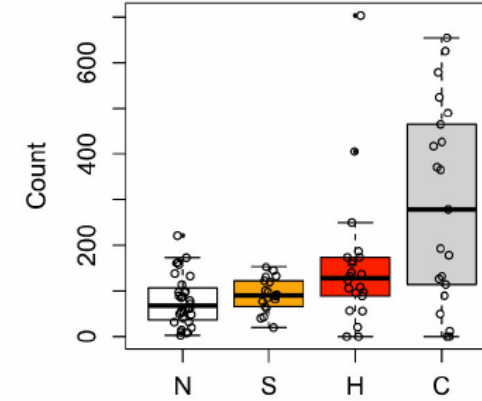
A: Histogram of LDA results from the 20 plasma metabolites having the most statistically significant differences between NASH and steatotic samples as demonstrated by *P* values. When these species are used for classification, the two disease states are clearly distinguished. Blue, steatosis; orange, steatohepatitis. **B:** The list of 20 species used in (A) shows that a diverse spectrum of lipids and aqueous metabolites make up the signature distinguishing steatosis and NASH.

Liver transcripts for all collagen genes showing upregulation with progression of disease

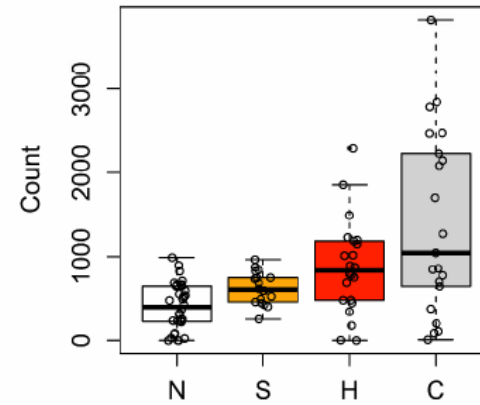
(A) ENST00000225964 : COL1A1 : 1277



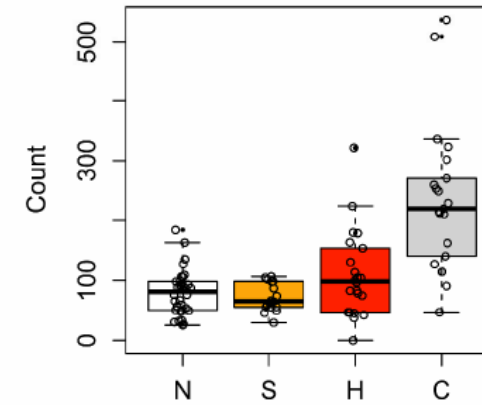
(B) ENST00000464916 : COL1A2 : 1278



(C) ENST00000317840 : COL3A1 : 1281



(D) ENST00000396625 : COL4A4 : 1286



Liver transcripts for IL1b, TGFb1, CCL2, CXCL1, MMP9 show upregulation with disease progression. MMP14 shows upregulation between cirrhosis and other disease stages

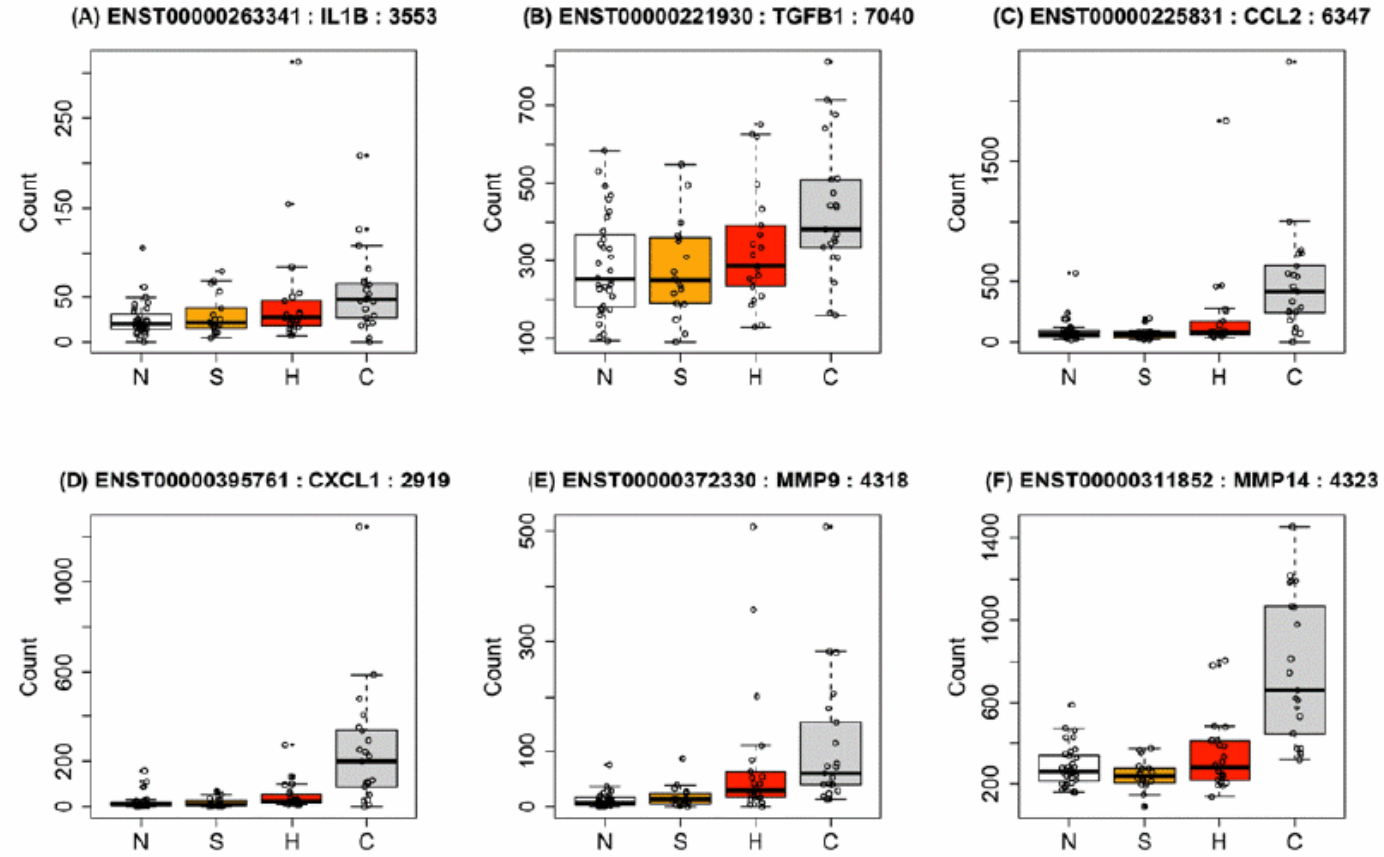


Table S3. Single nucleotide polymorphisms with $P < 0.001$ for steatosis vs. NASH, assessed using PLINK.

SNP	Gene	P-value	Odds ratio	Alleles [WT/ mutation]	Mutation information
rs3747636	PIK3C2B	1.26E-04	0.09	[A/G]	Synonymous_N1198N
rs7257872	ZNF584	2.51E-04	20.67	[A/G]	Missense_T301A
rs2010834	KATNAL2	3.37E-04	6.23	[A/C]	Silent, Missense_C254F
exm110947	PEAR1	4.90E-04	18.60	[A/G]	Missense_R885H
rs882610	ZNF446	4.90E-04	18.60	[A/G]	Missense_R387H
rs17795400	EFHB	7.81E-04	0.12	[A/C]	Missense_G99V
exm529135	VAR2	9.35E-04	16.69	[A/G]	Missense_R777Q, Missense_R917Q, Missense_R947Q

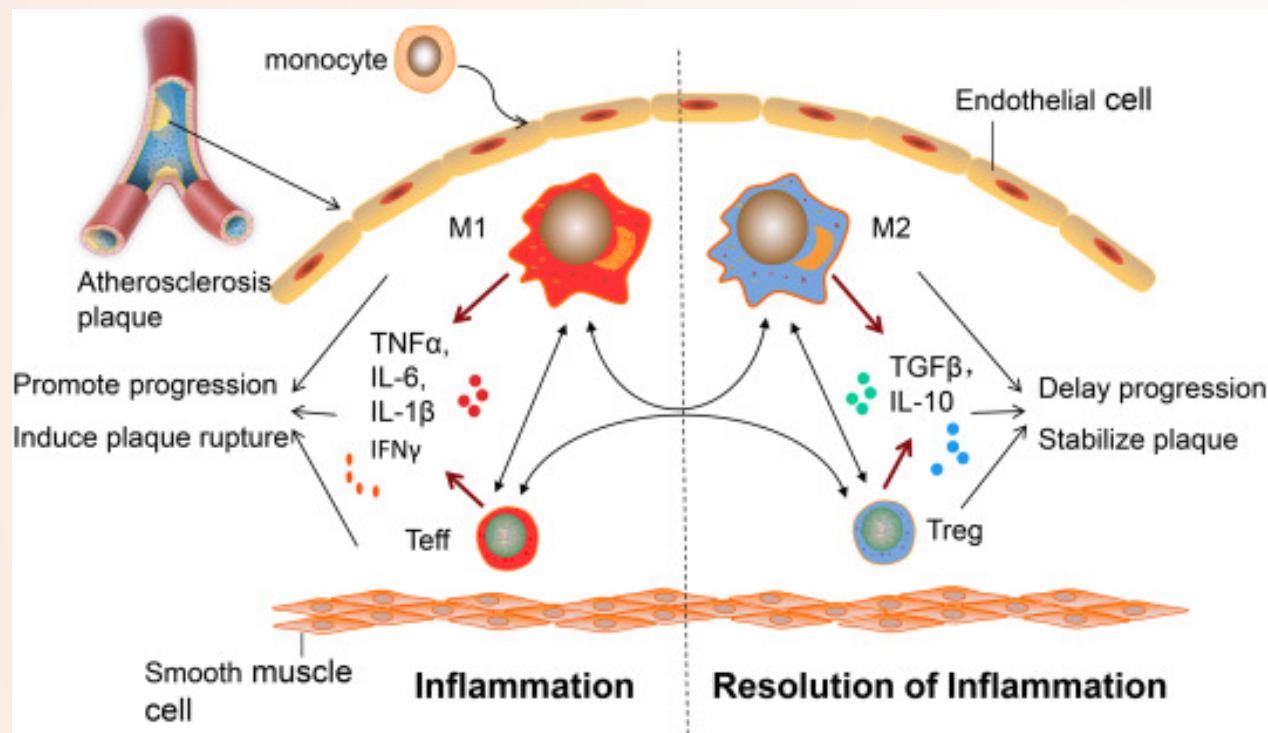
Table S4 . Single nucleotide polymorphisms with $P < 0.0001$ for normal vs. cirrhosis, assessed using PLINK.

SNP	Gene	P	Odds Ratio	Alleles	Mutation
rs738409	PNPLA3	1.77E-06	9.603	[C/G]	Missense_I148M
exm1032658	NUAK1	2.39E-05	11.8	[C/G]	Missense_P543R
exm8127	AJAP1	2.68E-05	0.143	[A/G]	Missense_G263R
rs185200	ARHGAP26	3.06E-05	0.136	[A/G]	Synonymous_R85R
rs9482	ATF6	3.27E-05	0.126	[A/G]	Synonymous_S632S
rs3761472	SAMM50	4.03E-05	7.636	[A/G]	Missense_D110G

Metabolomics, Transcriptomics, & Epigenomics in Atherosclerosis

“Atherosclerotic cardiovascular disease is the leading cause of mortality worldwide.”

Barquera, S., et al., Arch Med Res, 2015. **46**(5): p. 328-38.

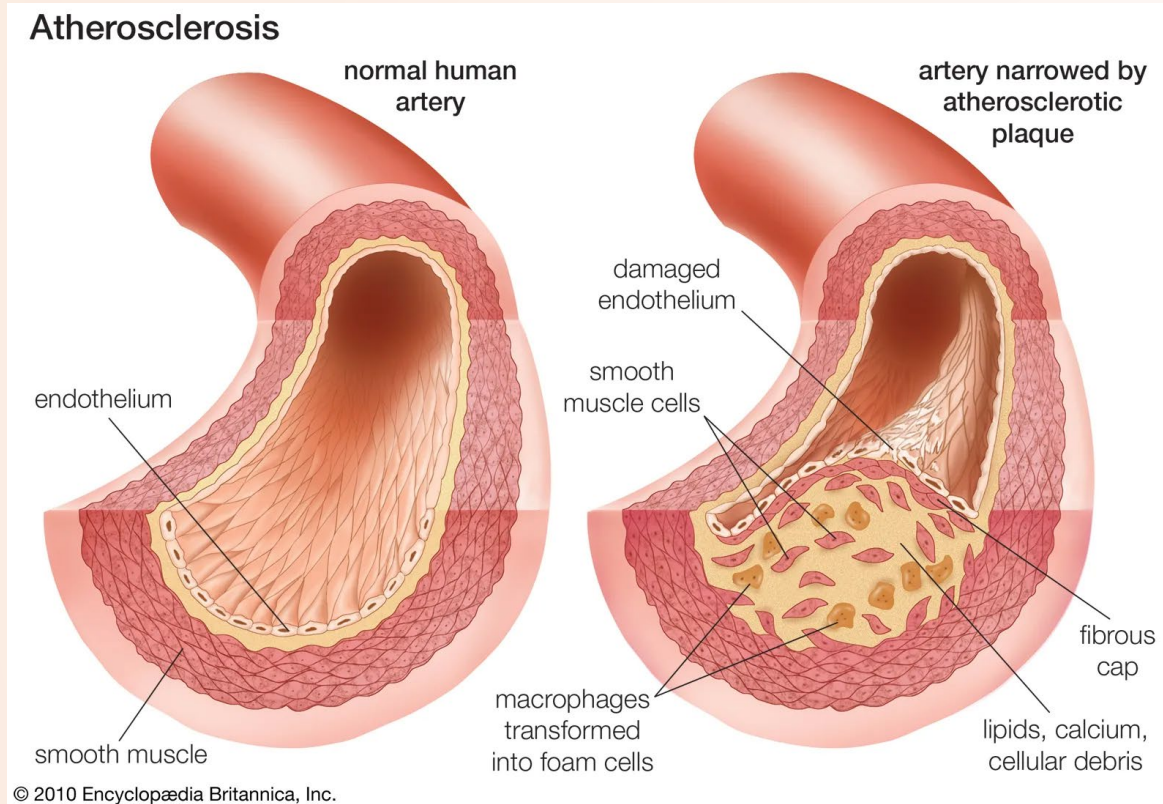


Song et al. Clinical Immunology Volume 202, May 2019, Pages 11-17

(Some) Causes of Plaque Formation

- Diet and other lifestyle choices
- Genetic predispositions
- Blood flow and shear stress

Metabolomics, Transcriptomics, & Epigenomics in Atherosclerosis



Britannica

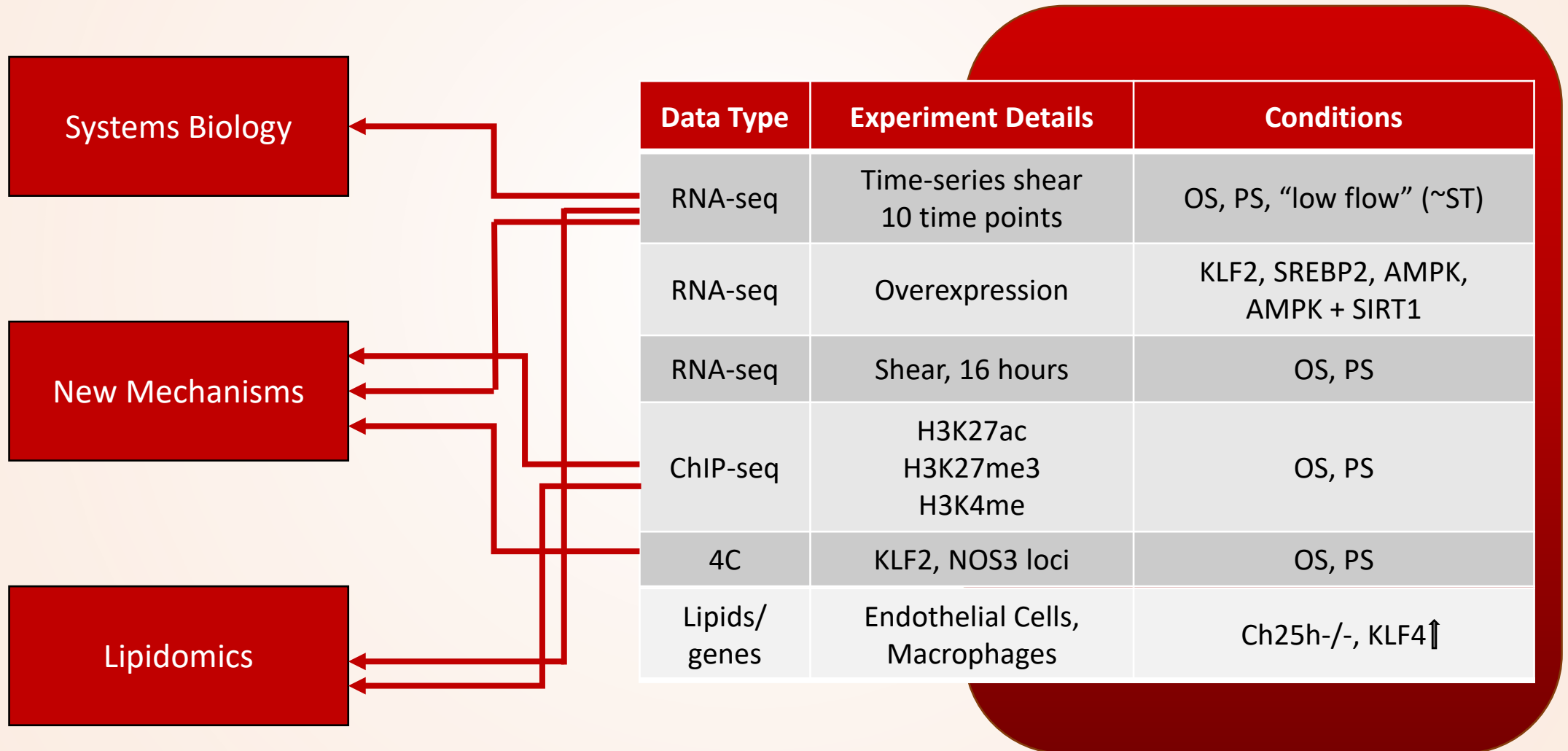
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(Some) Causes of Plaque Formation

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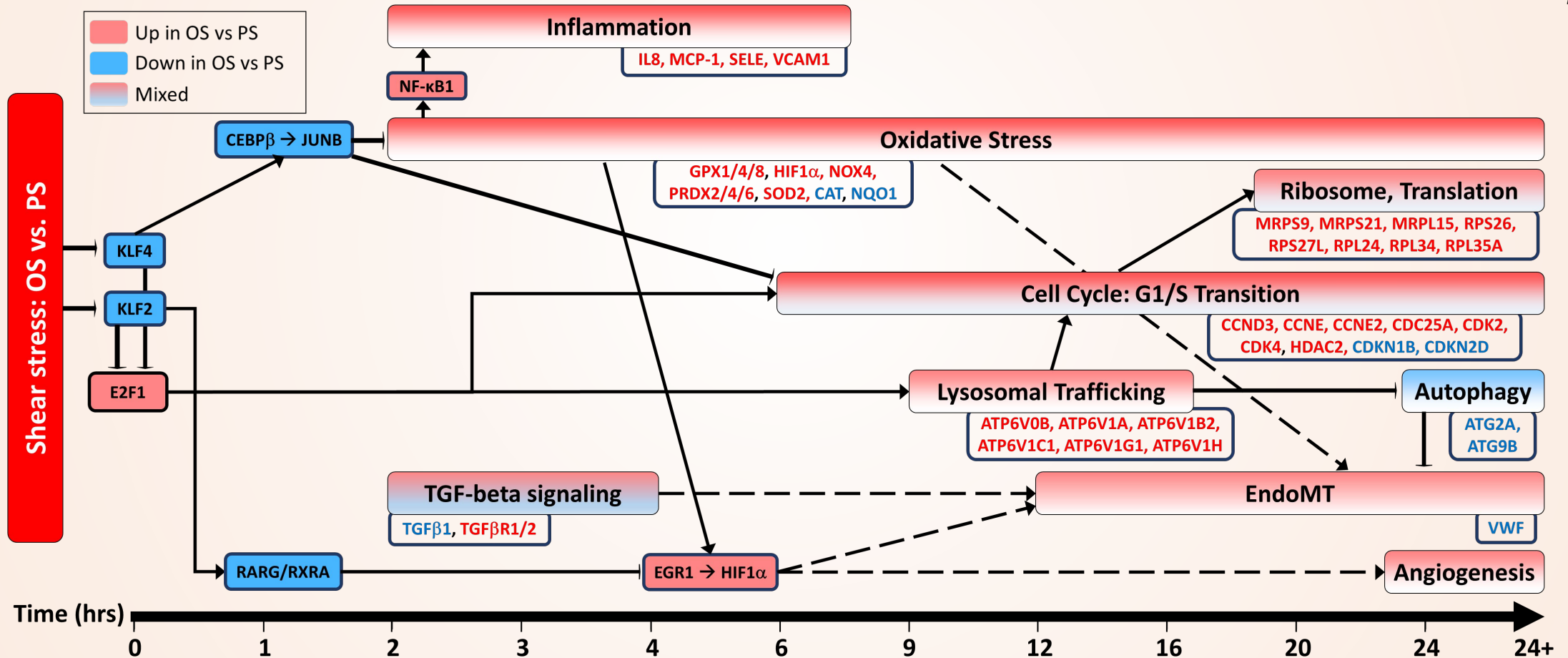
Studying ECs *in vitro*



Integrating TF Information and Pathway Enrichment



Nassim Ajami



Gene Analysis Through F.C. Comparisons Recovers Several Key EC genes

OS-Distinctive Genes	PS-Distinctive Genes
C9orf89, CCZ1, CD69, CXCR4, EIF2AK1, ENC1, ETV6, GLIPR1, GMFG, IDI1, KLHDC3, LIMS3, LYPLA2, MAGEF1, MEX3A, NFIL3, PAIP1, PCSK1, PDGFC, RNF145, SIRPA, STX6, TMEM155, TNFRSF21, WDR45L	ABCG2, ABLIM3, ACVRL1, ADAM15, ADAMTS4, ADARB1, AGXT2L2, ALS2CL, AMMECR1L, APOLD1, ARHGEF15, ARRDC2, ASAP2, ATG9B, C14orf34, C14orf49, C1orf21, C1QTNF6, C20orf160, CALML4, CARD14, CASKIN2, CCDC69, CLCF1, CRTAC1, CXCR7, DAG1, DENND4B, DGKA, DHH, DLL1, DNASE1L1, DOCK6, DUSP4, EFN1, EHB1, ENDOD1, ESAM, FAM124B, FAM65A, FGF2, FOXP1, GCH1, GCKR, GPD2, GPER, GRK5, HEG1, HR, HSPA12B, HSPA1A, HYAL1, HYAL2, IL3RA, INPP5K, ITGB4, ITGB5, ITPR3, ITS2, JOSD1, KCNJ12, KIAA1161, KLF13, KLF2 , KLF4 , LPCAT4, LPHN2, MAP4K2, MBOAT1, MN1, MOB2, MYO1C, NAGA, NDRG4, NDST2, NOS3 , NPEPPS, PLCD3, PLXND1, PMP22, PRUNE2, RAB11A, RBPM5, RECK, RNF213, RUSC1, S100A10, SEMA4B, SEPT8, SIGIRR, SLCO2A1, SORBS2, SPINK5, SPTBN1, SPTBN5, ST3GAL1, ST8SIA6, STARD8, STMN3, STOM, STXB1, SULF1, TBC1D1, TBC1D2, TECPR1, TENC1, THBD, TINAGL1, TNFAIP1, TOB2, TRAK1, TRIM56, TSC22D3, UBE3B, VANG1, VEGFA, XKR8, ZNF467

KLF2: Critical transcription factor for EC response to PS

Dekker RJ et al. Blood. 2002 Sep 1;100(5):1689-98.

KLF4: Similar to KLF2 in function, also important for PS-induced phenotype

Villarreal G et al. Biochem Biophys Res Commun. 2010 Jan 1;391(1):984-9.

NOS3: “Endothelial NOS” – produces nitric oxide and is crucial in regulating vascular tone

Förstermann U et al. Circulation. 2006 Apr 4;113(13):1708-14.



**Li
Zhao**



**Marcy
Martin**



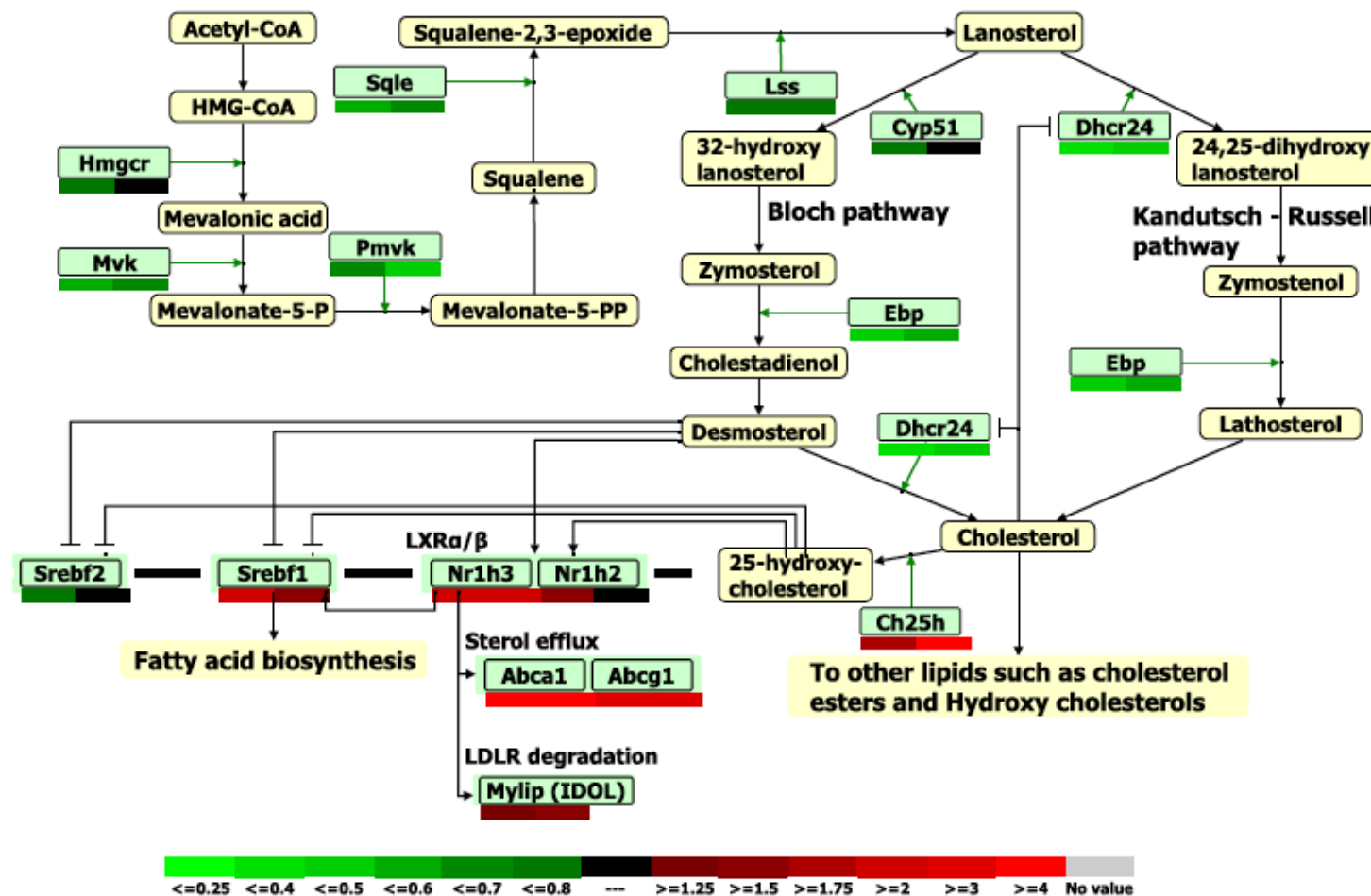
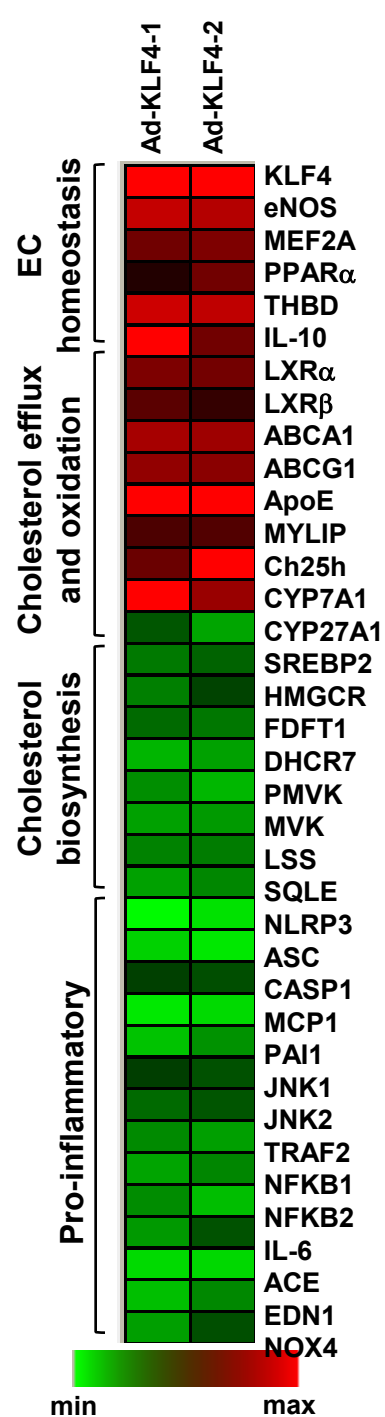
**Mano
Maurya**

KLF4 regulates cholesterol-25-hydroxylase and liver x receptor mitigating atherosclerosis susceptibility

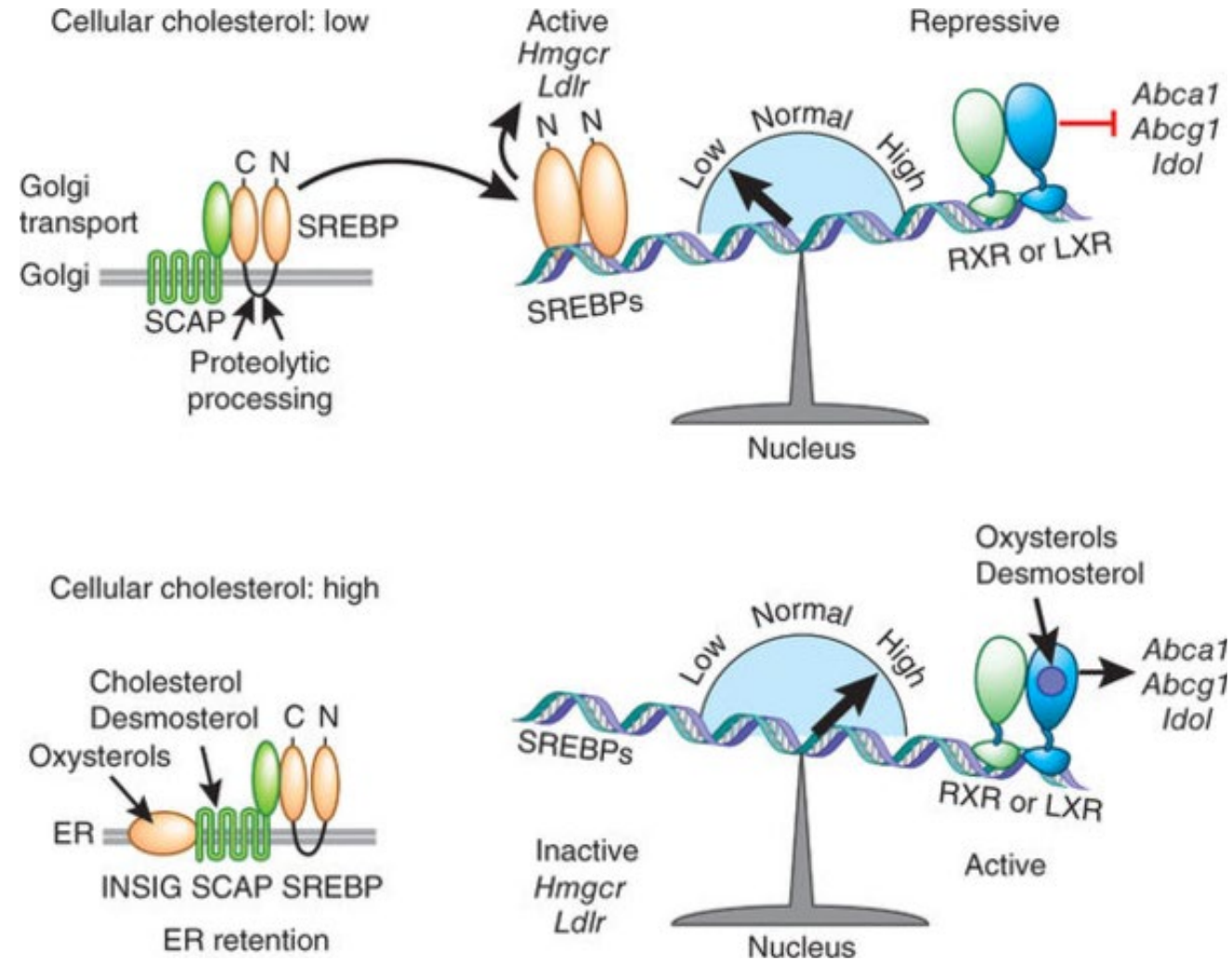
Zhao, Martin, et al. Circulation, 2017

Vasoprotective stimuli increased the expression of Ch25h and LXR via KLF4. The KLF4-Ch25h/LXR homeostatic axis functions through suppressing inflammation, evidenced by the reduction of inflammasome activity in ECs and the promotion of M1 to M2 phenotypic transition in macrophages. The increased atherosclerosis in apolipoprotein E^{-/-}/Ch25h^{-/-} mice further demonstrates the beneficial role of the KLF4-Ch25h/LXR axis in vascular function and disease.

KLF4 Mediates Cholesterol Homeostasis

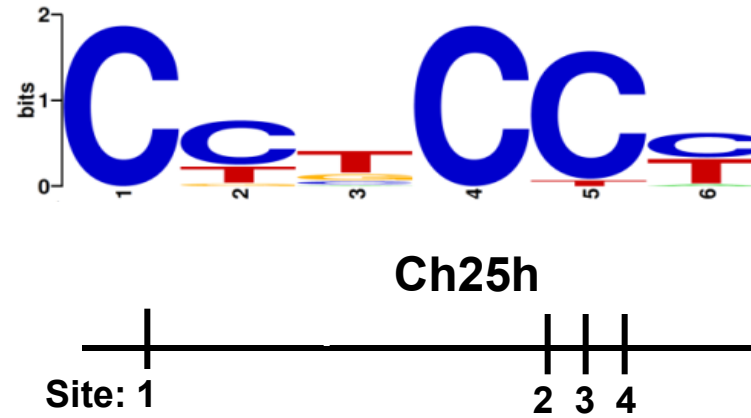


The Balance of Cholesterol Homeostasis

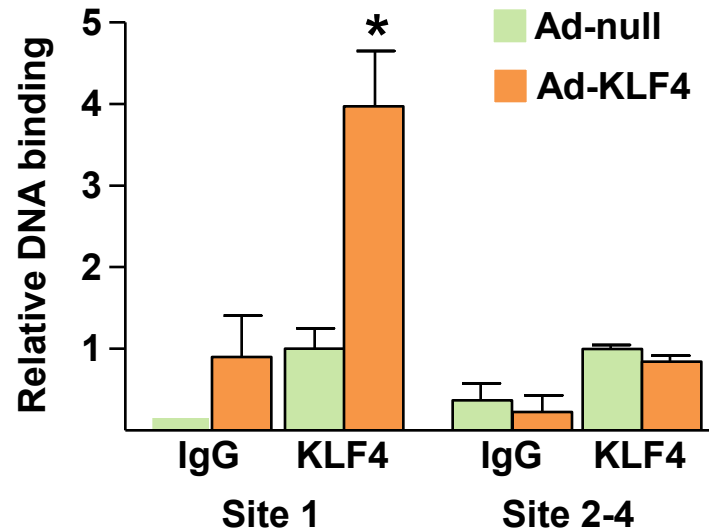


KLF4 Transactivates Ch25h

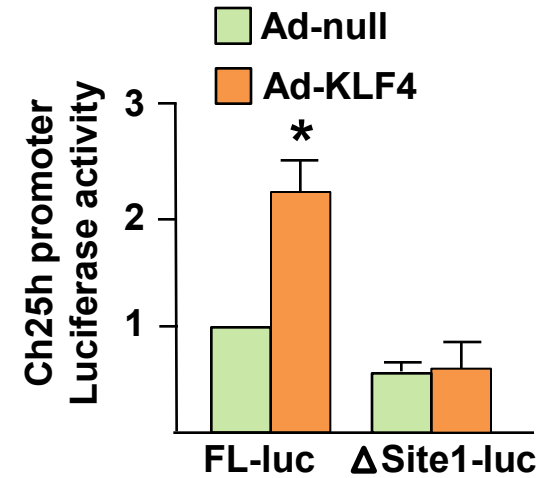
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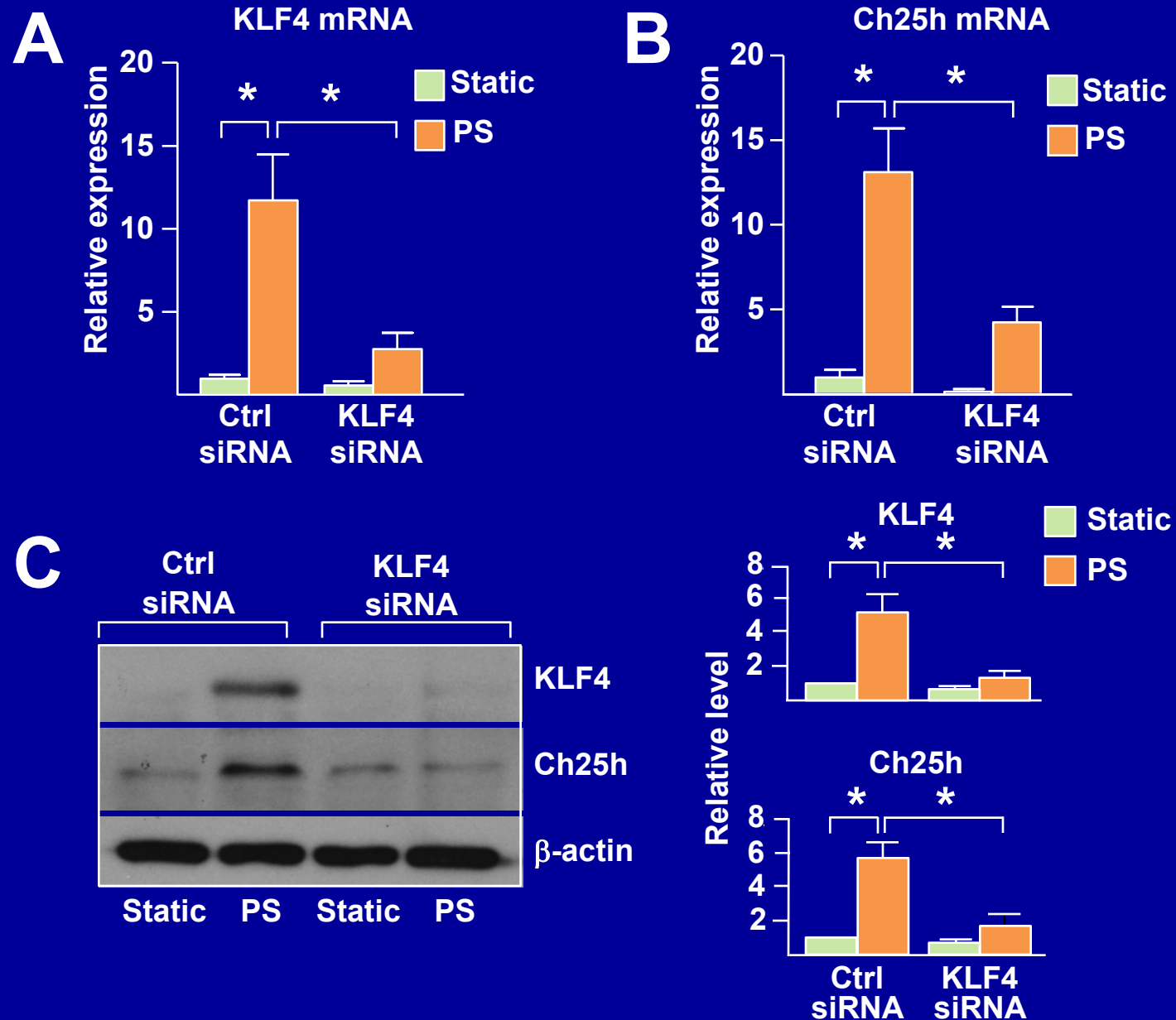
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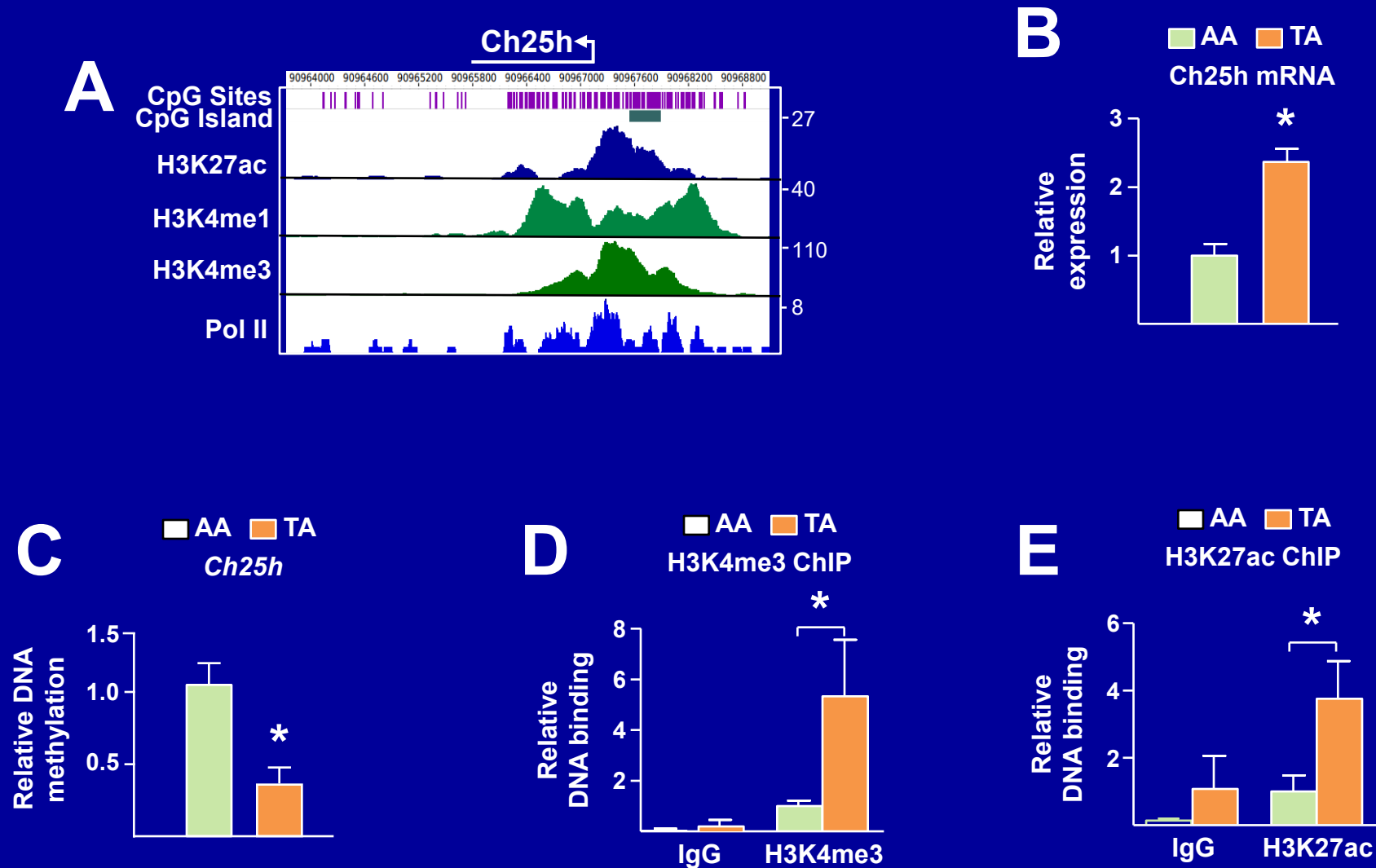
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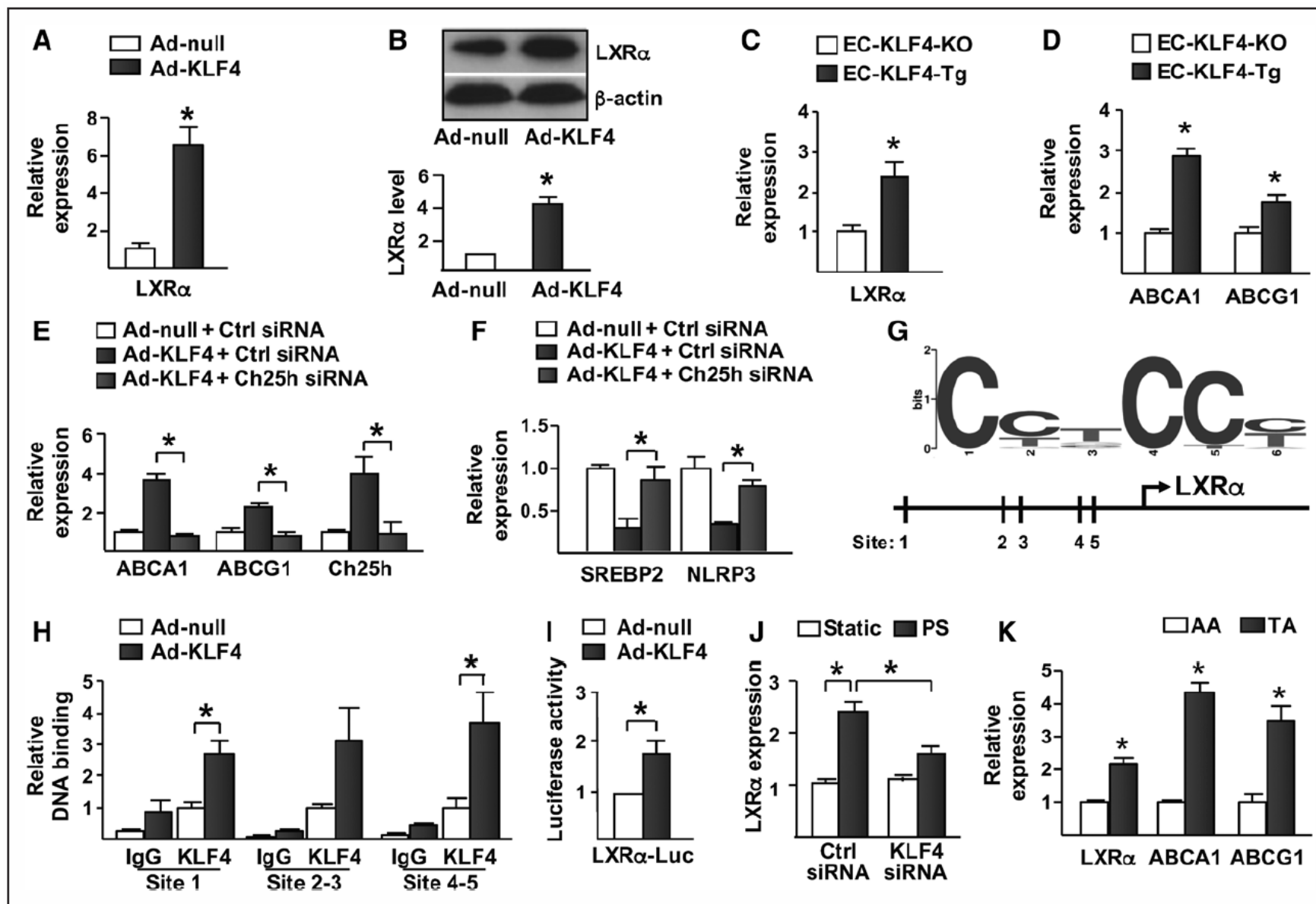
PS Regulation of Ch25h is Dependent on KLF4



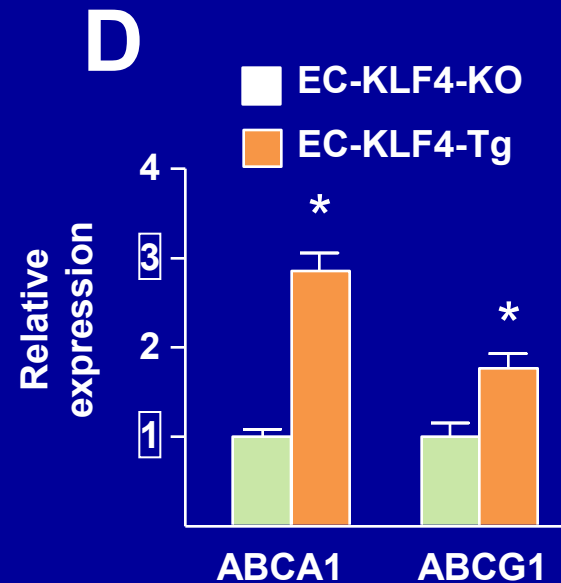
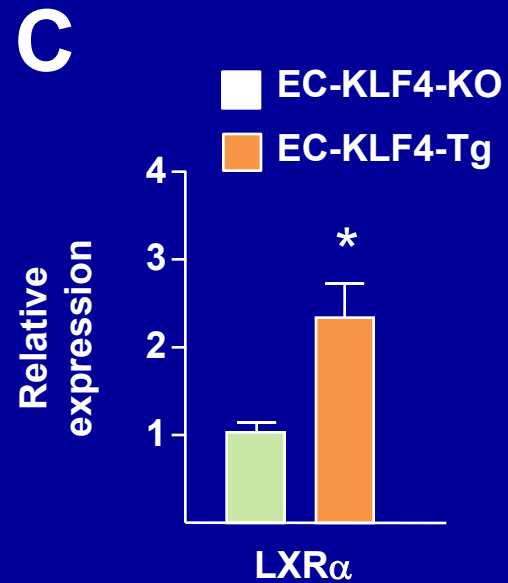
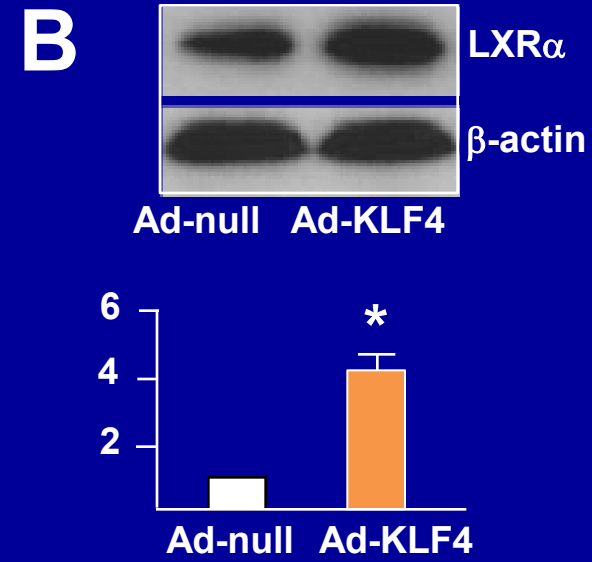
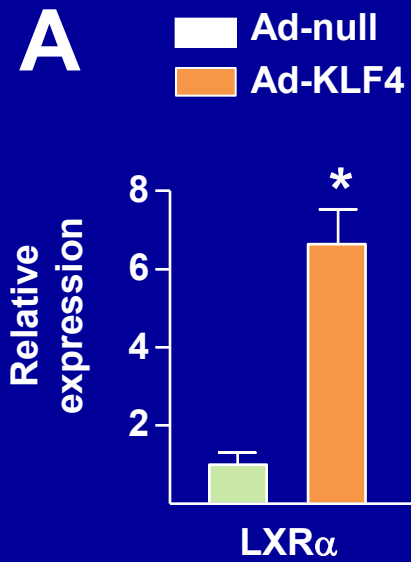
Epigenetic Regulation of the *Ch25h* promoter



KLF4 transactivates LXR α



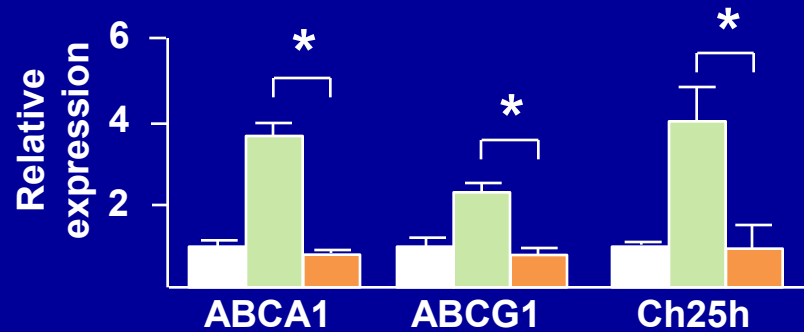
KLF4 Promotes LXR α Expression



LXR α Expression is Dependent on Ch25h

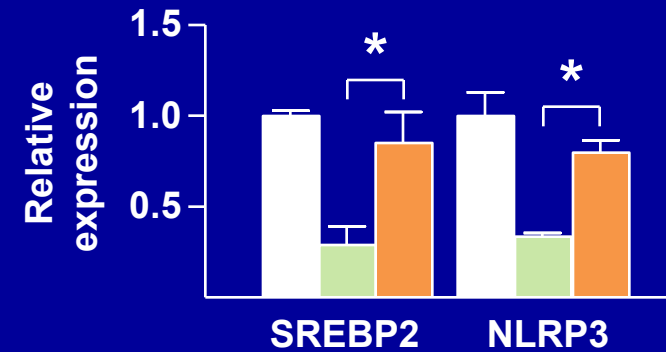
A

- Ad-null + Ctrl siRNA
- Ad-KLF4 + Ctrl siRNA
- Ad-KLF4 + Ch25h siRNA

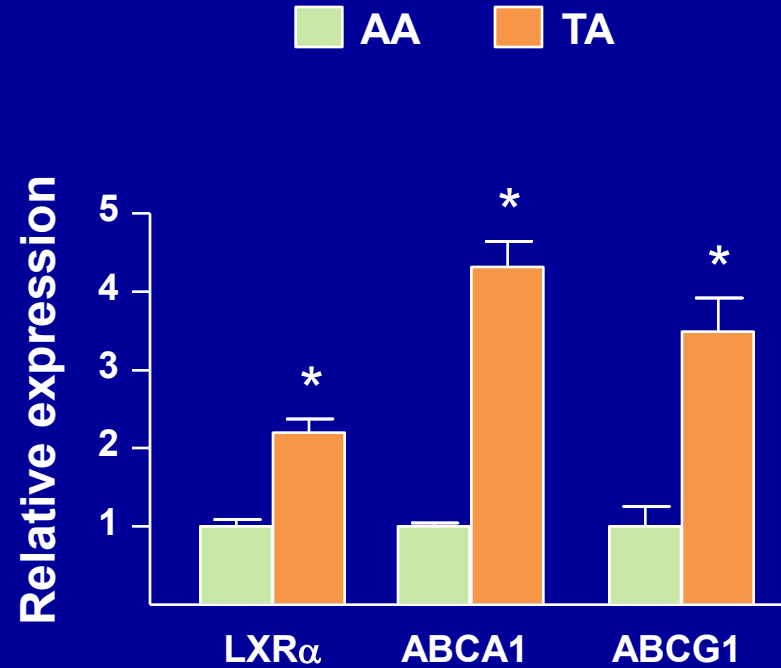
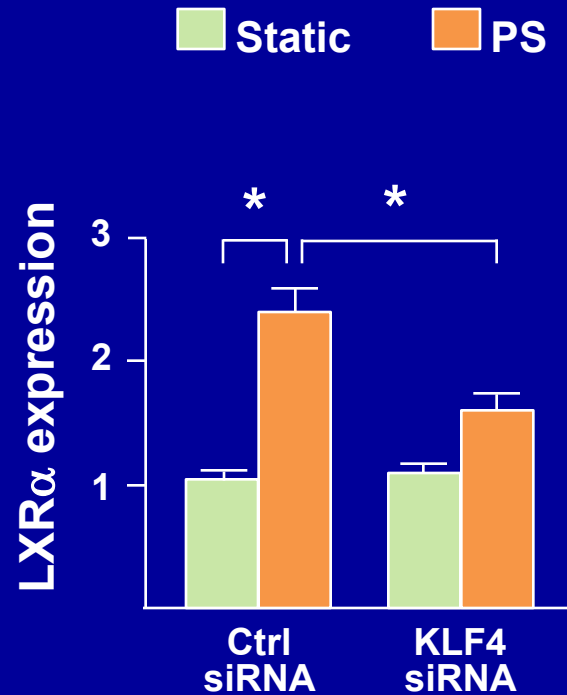


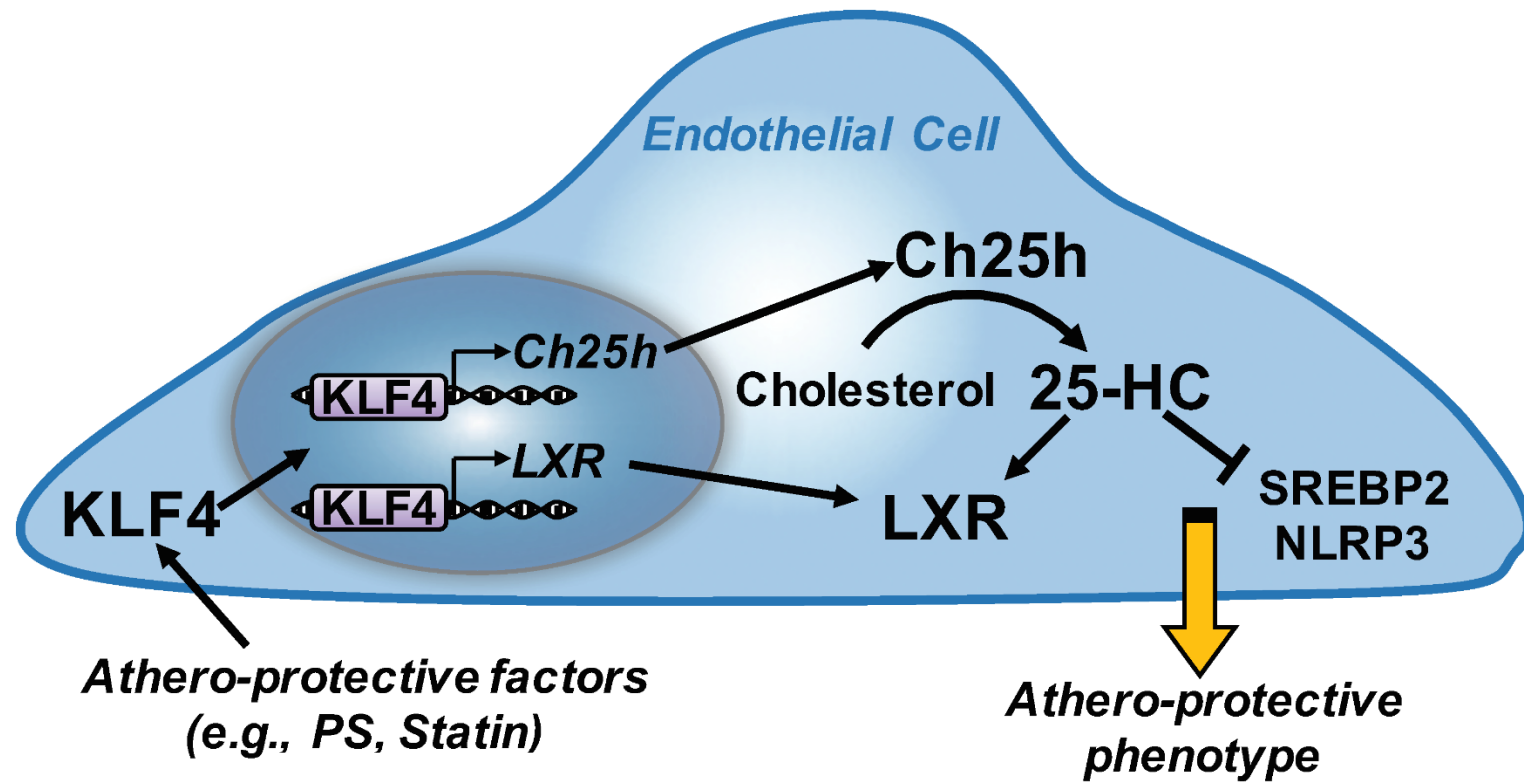
B

- Ad-null + ctrl siRNA
- Ad-KLF4 + ctrl siRNA
- Ad-KLF4 + Ch25h siRNA

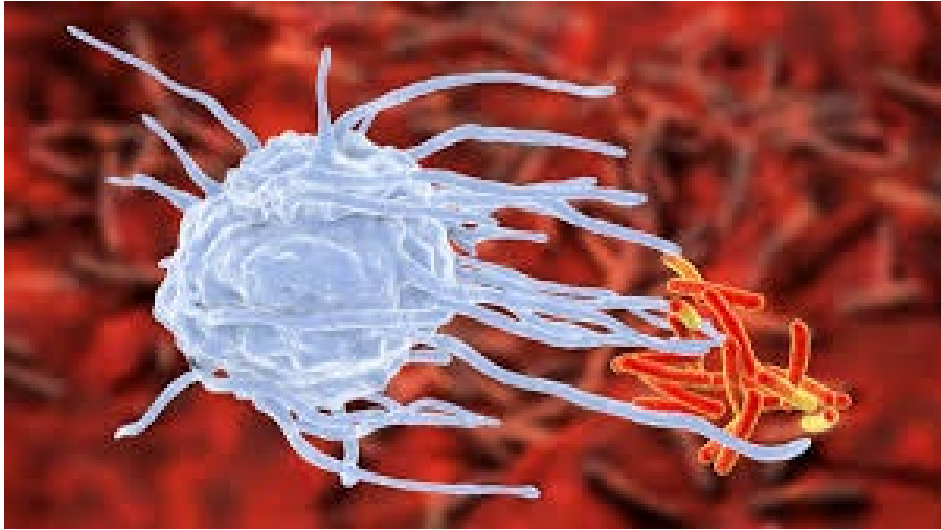


PS Regulation of LXR α in ECs Is KLF4-Dependent





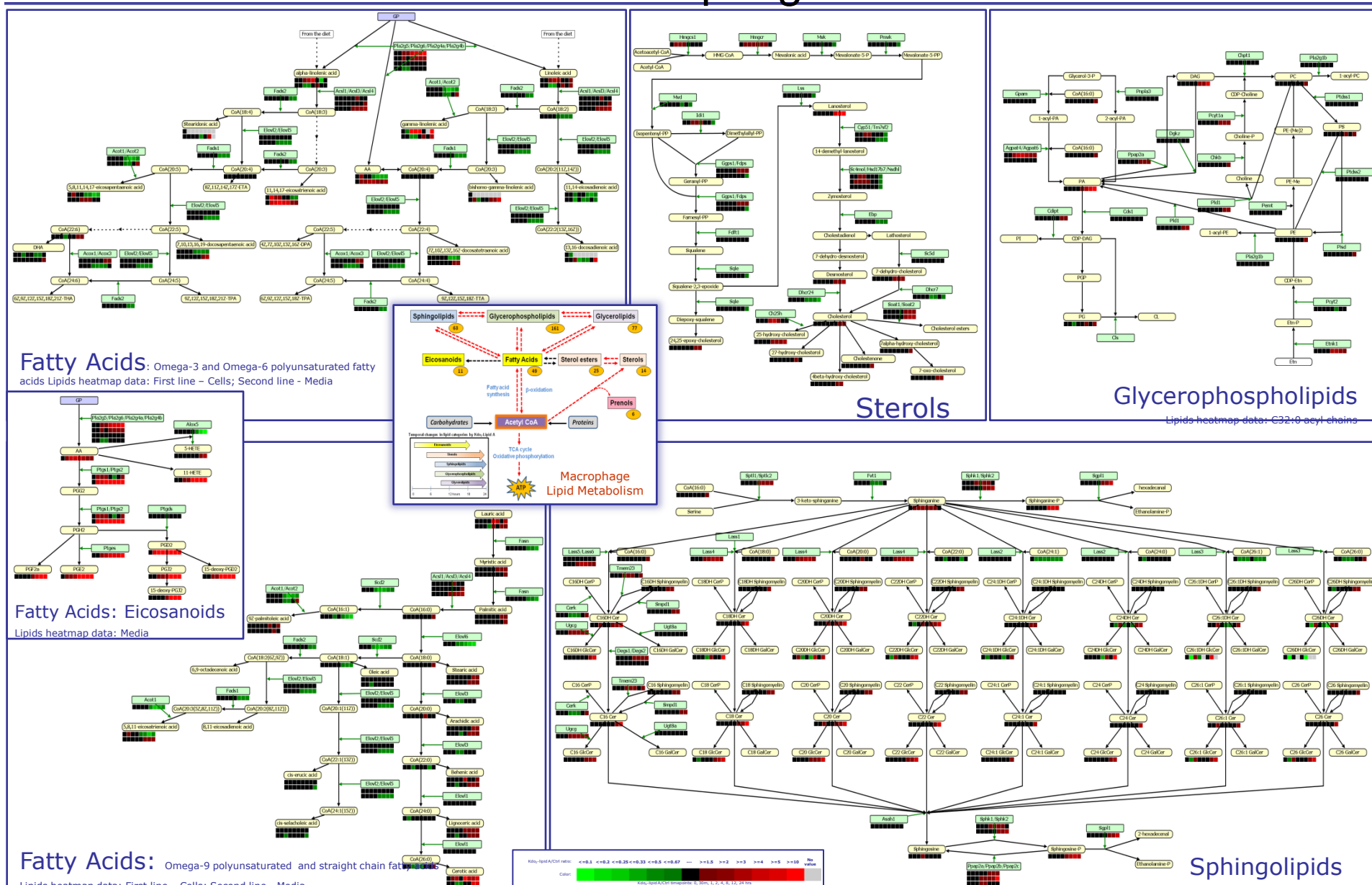
Inflammed Macrophage Cell



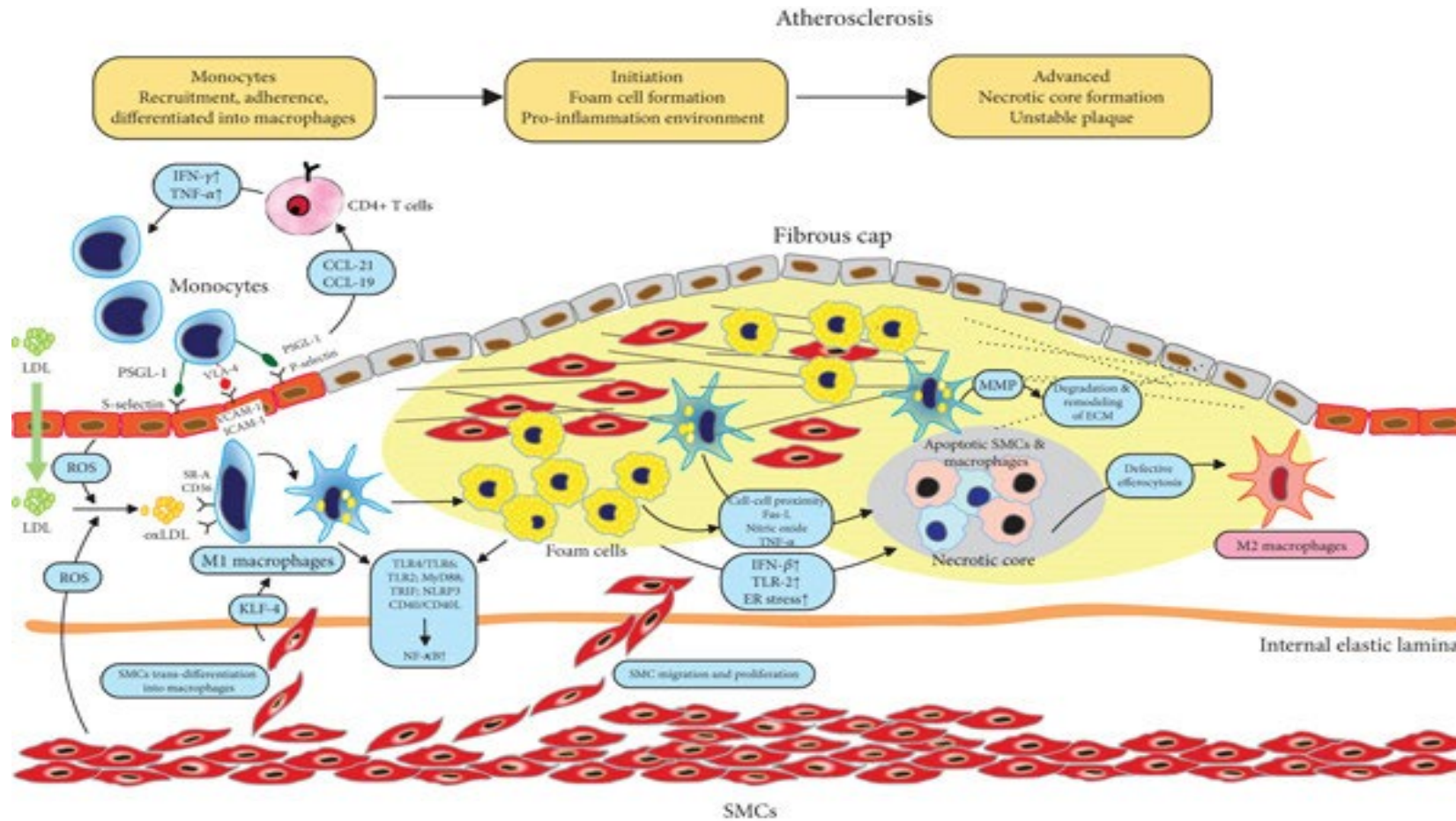
Defining Macrophage Inflammation The LIPIDMAPS project

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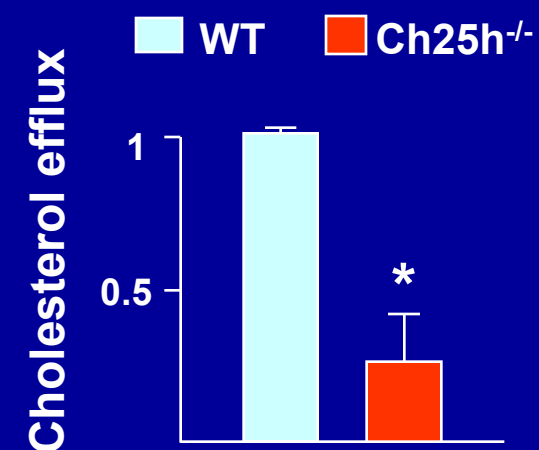
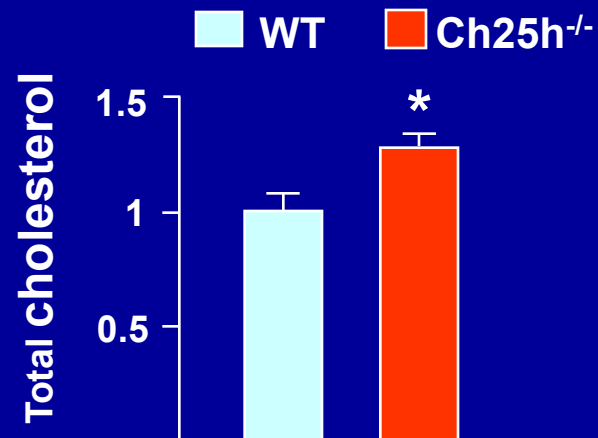
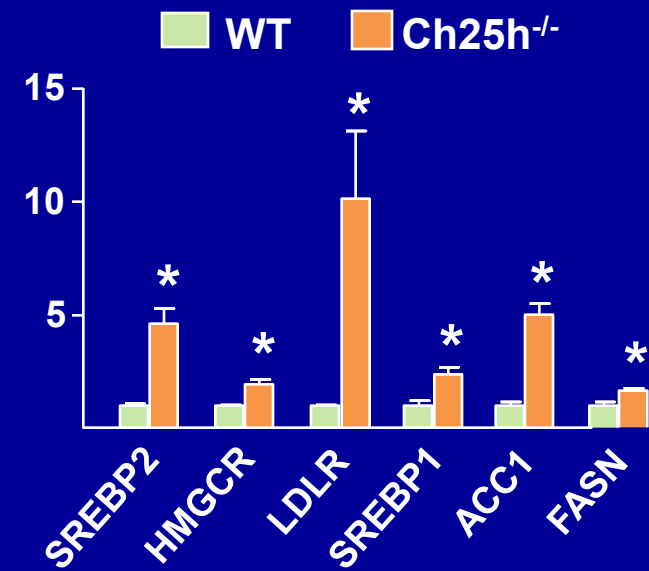
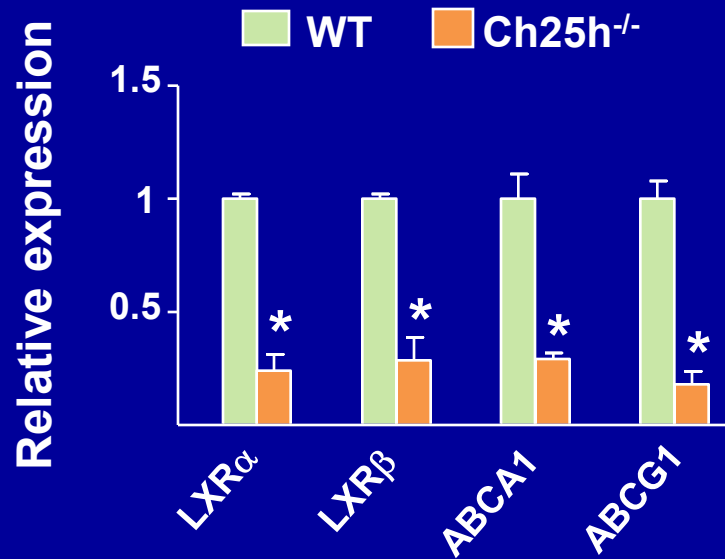
Integration of lipidomics, transcriptomics, and biological networks in macrophage inflammation



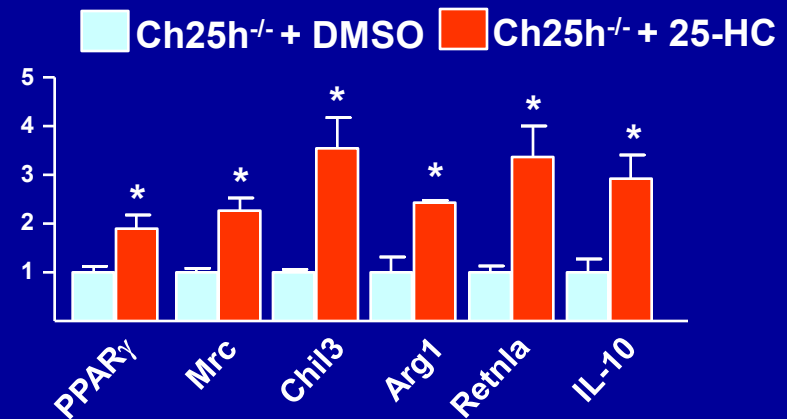
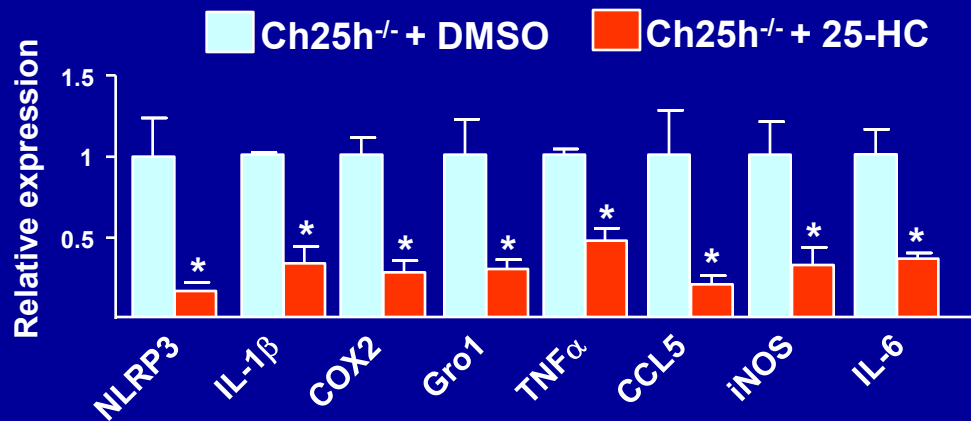
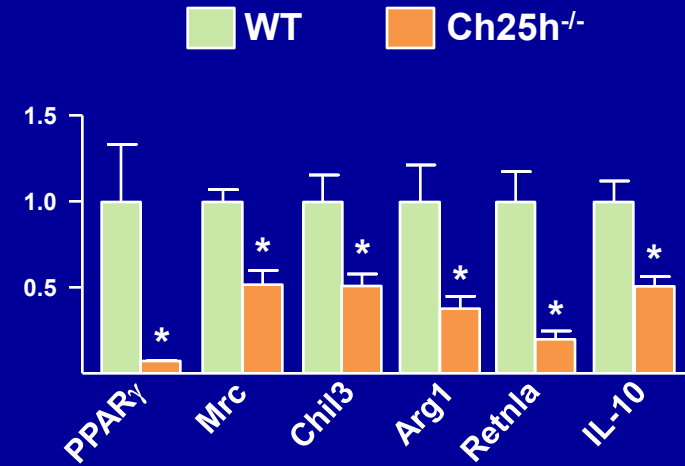
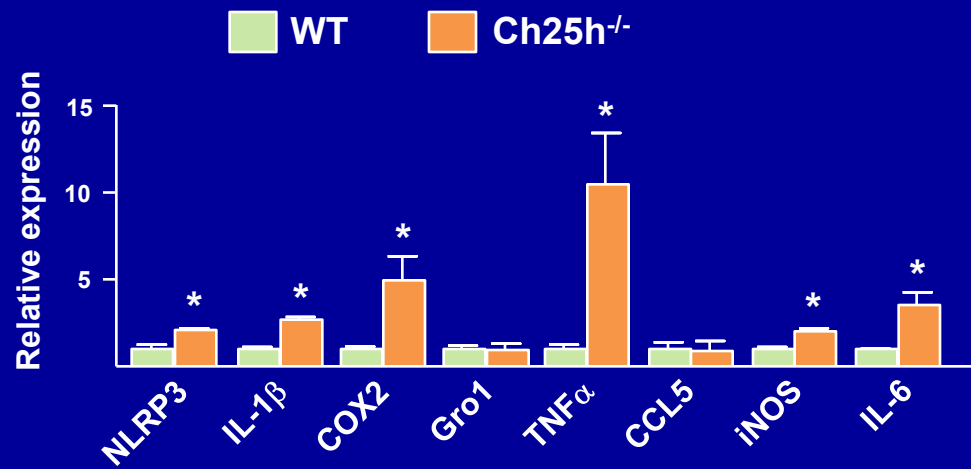
Endothelial Cell - Inflamed Macrophage Cell Crosstalk



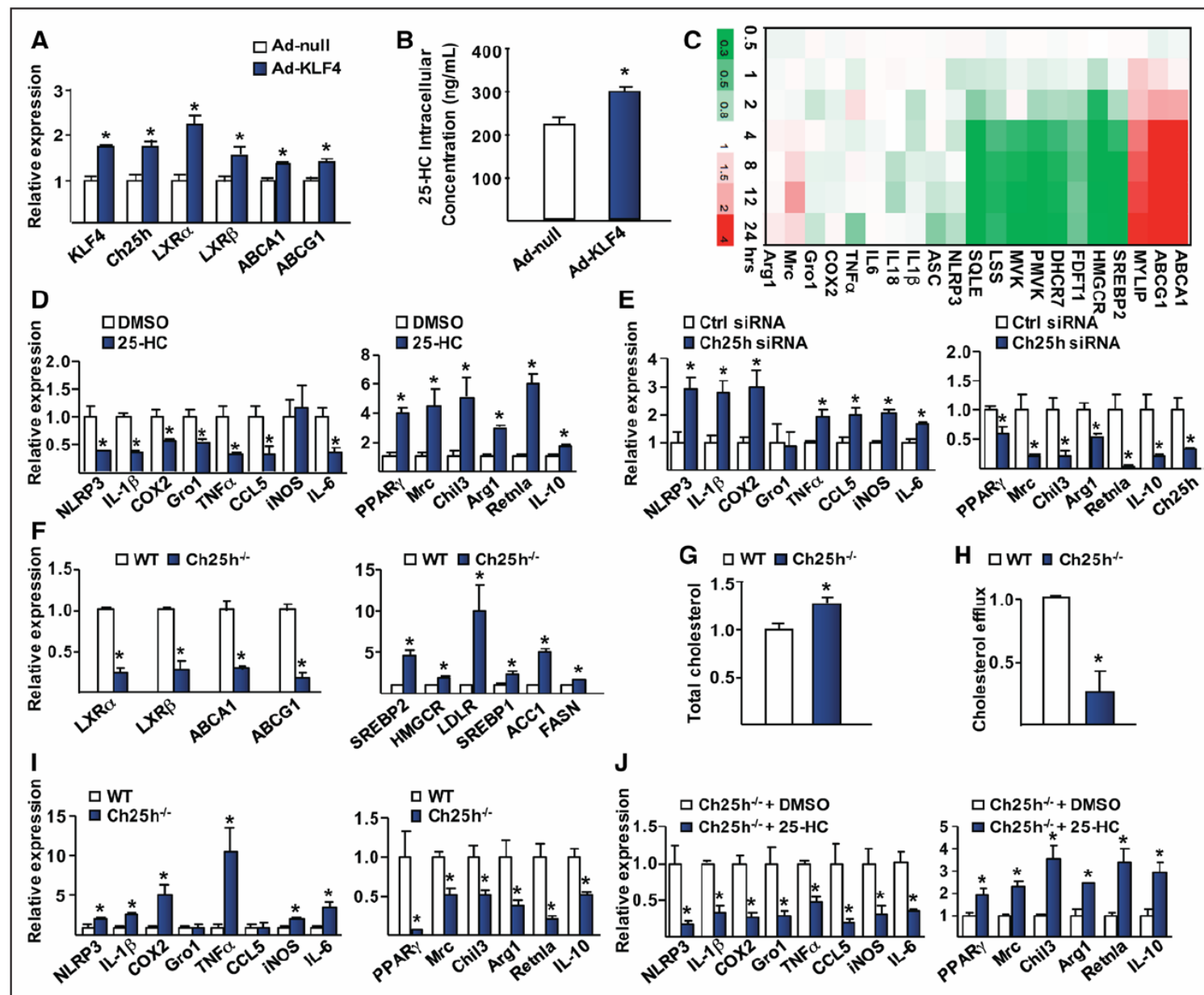
Impaired Cholesterol Homeostasis in Ch25h^{-/-} Macrophage



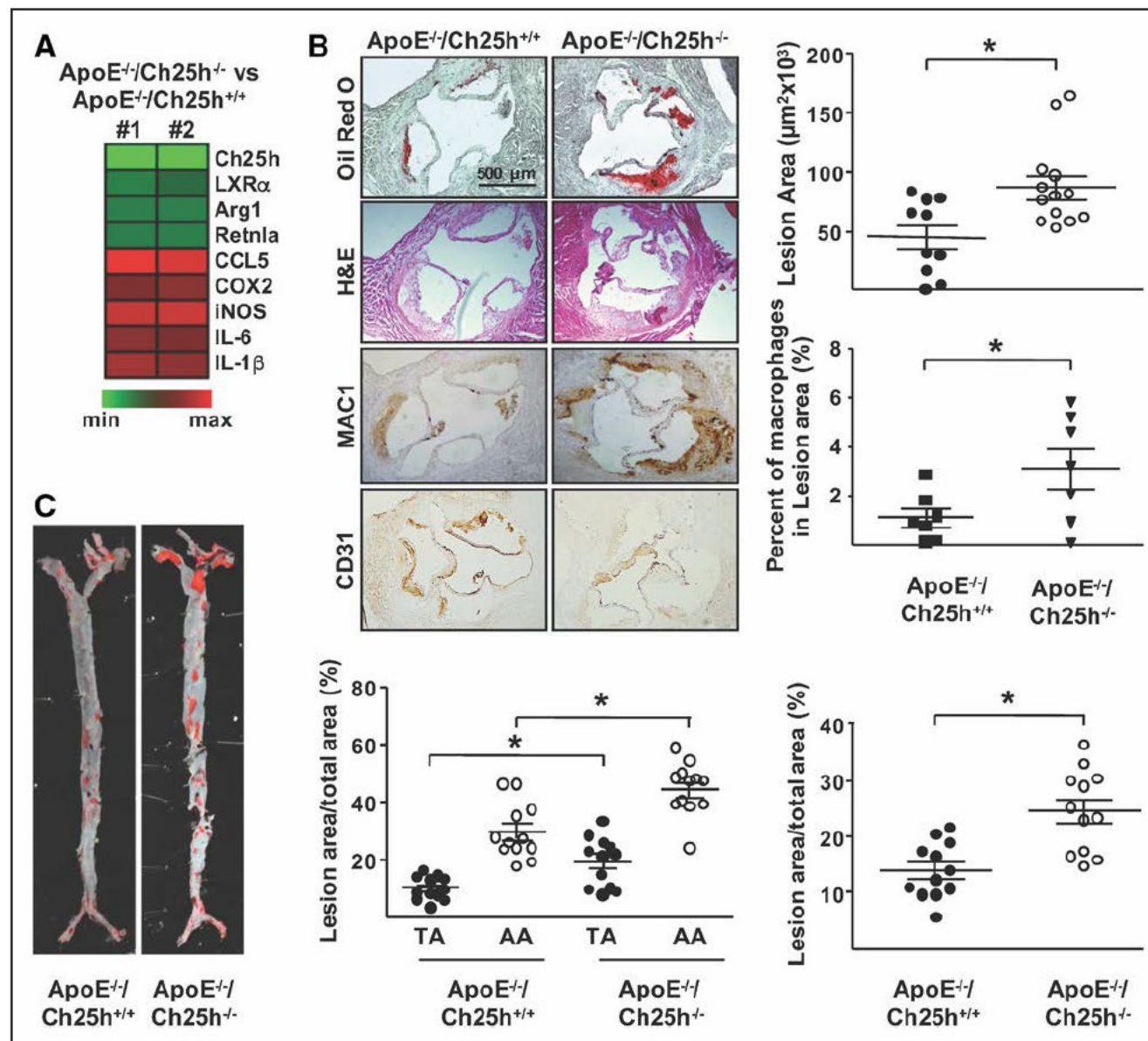
M2 Polarization in Ch25h^{-/-} Macrophages



KLF4 regulation of Ch25h/LXR in M ϕ promotes M2 polarization



Ch25h ablation increases atherosclerosis susceptibility



KLF4 mediates Ch25h and LXR in ECs and Mfs to promote atheroprotection

