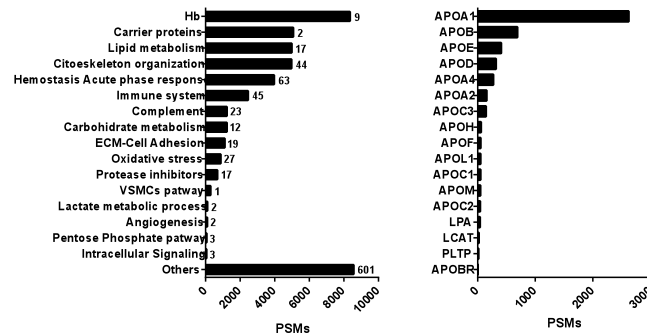


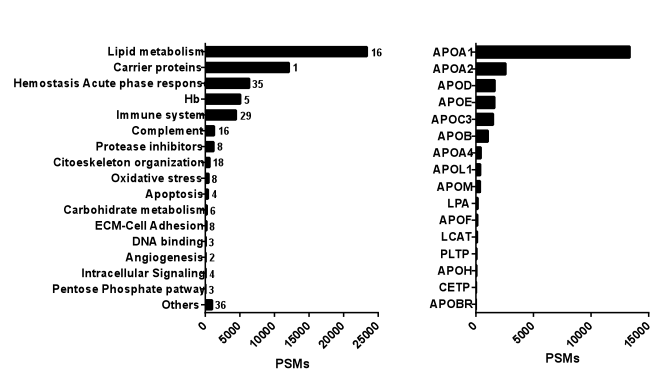
Protein	Classification	Peptide/PSMs	
		HDL-T	HDL-CM
APOA1	Oxidation	48/233	61/567
	Phospho	9/25	5/30
	Deamidation	8/24	1/1
	Methylmalonylation	10/22	6/57
	Methylation	3/4	1/1
	AGE	1/1	
	Other	27/68	17/84
APOA2	Oxidation	2/7	13/124
	Deamidation	1/1	1/29
	Methylation		4/24
	Methylmalonylation	1/4	2/18
	Phospho		1/1
	Other		6/19
APOA4	Oxidation	3/6	13/47
	Deamidation	7/12	3/16
	Other	1/1	
APOB	Deamidation	16/53	7/24
	Oxidation	5/5	19/29
	Other		2/4
APOC1	Deamidation	2/7	1/3
APOC2	Oxidation	2/3	7/64
	Deamidation	4/5	2/13
APOC3	Deamidation		6/43
	Methylmalonylation	1/2	5/33
	Oxidation	4/5	5/18
	Methylation	2/2	2/8
	Phospho		2/7
	AGE		1/2
	Other		3/10
APOD	Oxidation	5/9	23/167
	Deamidation	9/51	5/67
	Methylmalonylation	1/2	
	Other		7/8
APOE	Oxidation	7/14	27/143
	Deamidation	4/8	9/34
	Phospho		2/3
	Other	3/3	7/12
APOF	Oxidation	3/4	3/20
	Deamidation	1/2	
	Phospho		2/2
	Other	1/2	1/1
APOH	Deamidation	1/13	
	Oxidation		2/8
APOL1	Oxidation		7/16
	Deamidation	2/4	3/4
	Other		3/9
APOM	Oxidation	1/2	7/63
	Deamidation	2/2	3/16
	Other	2/2	3/9
LCAT	Oxidation	1/1	9/17
	Deamidation		1/1
LPA	Oxidation	1/1	6/19
	Deamidation	1/1	2/13
	Other		3/12
PLTP	Oxidation	1/1	2/10
	Deamidation		1/1

Supplementary Table 1.- Distribution of most abundant PTMs in proteins of the lipid metabolism category. Number of peptides/PSMs in each protein and type of PTM. Classification was made semi automatically as described in Supplementary Material and Methods. Modifications that could not be unequivocally assigned to PTMs were classified as “Other”



Supplementary Figure 1.- Proteomics characterization of HDL-like particles from tissue.

Quantitative distribution (spectral counting) of proteins from HDL-like particles. Left: distribution among functional categories. Right: distribution of proteins related to lipid metabolism.

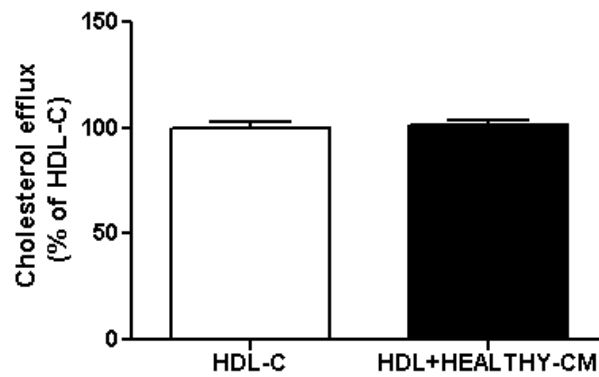


Supplementary Figure 2.- Proteomics characterization of HDL incubated with AAA ILT-CM. Quantitative distribution (spectral counting) of proteins from HDL isolated from plasma and incubated with AAA tissue-conditioned media. Left: distribution among functional categories. Right: distribution of proteins related to lipid metabolism.

A

	aa	AoS	Z _{pq}	t _{test}	PTMs	Sequence
M	112		1	0.44	32	WQEE M2ox ELYR
	72		1	0.22	25	EQLGPVTQEF Wkyn DNLEK
	72		1	0.46	229	EQLGPVTQEF Wox DNLEK
	72		1	0.37	195	EQLGPVTQEF W2ox DNLEK
W	50		1	0.38	379	LLDN W2ox DSVTSTFSK
	50		1	0.42	207	LLDN Wox DSVTSTFSK
	50		0	0.61	55	LLDN Wkyn DSVTSTFSK
	108		-1	0.15	53	Wox QEEMELYR
	108		-1	0.09	72	W2ox QEEMELYR
	108		-2	0.08	26	W3ox QEEMELYR
	29		0	0.79	119	DYox VSQFEGSALGK
Y	18		0	0.84	76	DLATV Yox VDVLK
	100		0	0.86	97	VQP Yox LDDFQK
	166		-1	0.39	30	THLAP Yox SDELRL
	192		-1	0.15	9	LA EYox HAK
	115		-1	0.21	18	WQEE MELYox R
	166		-1	0.38	2	THLAP Y3ox SDELRL
H	162		1	0.36	11	THox LAPYSDELRL
	199		0	0.34	8	ATE Hox LSTLSEK
P	200		1	0.18	33	QG LLP2ox VLESFK
	99		1	0.43	35	VQ Pox YLDDFQK
	165		0	0.77	18	THLAP Pox YSDELRL
	165		0	0.46	42	THLAP P2ox YSDELRL

B



Supplementary Figure 3.- PTMs and cholesterol efflux in HDL isolated from plasma and incubated with healthy wall-CM.

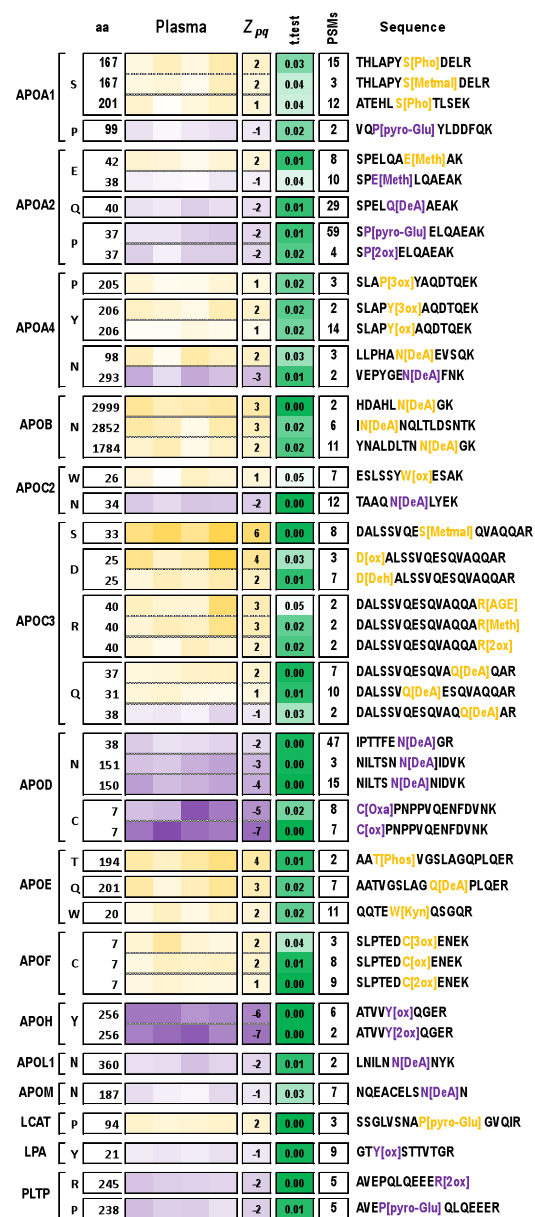
A) Abundance changes of oxidatively modified ApoA1 peptides in HDL-control (HDL-C) as compared to healthy tissue conditioned media expressed in terms of the standardized log2 ratio Z_{pq} (n=3, p=ns). Aox=Healthy-CM; Aa=aminoacid. Ox, 2ox and 3ox: addition of one, two or three oxygens, respectively.

B) Ability of HDL healthy- CM and HDL-control for promoting cholesterol efflux from J774A.1 [3H]cholesterol-labeled mouse macrophages. After 4 h of incubation, efflux of cholesterol was determined and expressed as [3H]cholesterol medium /([3H]cholesterol cells + [3H]cholesterol medium) x 100. Values were normalized as percent of HDL-C and represent means ± SEM (n=3, p=ns).

	aa	H.wall	P.wall	Z _{pq}	ttest	Thrbs	Z _{pq}	ttest	PSMs	Sequence
APOA1	D 102			6	0.00		7	0.02	2	VQPYL D[Deh]DFQK
	N 74			3	0.09		3	0.05	3	EQLGPVTQEFWDN[DeA]LEK
	Y 29			1	0.40		3	0.03	10	DY[Iodo]VSQFEGSALGK
	Y 192			-5	0.00		-5	0.01	4	LAELY[Iodo]HAK
	S 31			4	0.04		1	0.55	3	DYVS[MethMal]QFEGSALGK
	S 31			-4	0.06		-4	0.05	3	DYVS[Phos]QFEGSALGK
	S 167			-4	0.02		-5	0.04	6	THLAPYS[MethMal]DELR
	S 142			-6	0.01		-10	0.00	2	LS[Dideh]PLGEEMR
	P 165			-3	0.04		-3	0.01	2	THLAP[pyro-Glu]YSDELRL
	Q 105			-3	0.01		-6	0.14	4	VQPYLDDF Q[DeA]K
APOA2	Q 105			-4	0.05		-6	0.12	5	VQPYLDDF Q[DeA]K
	Q 109			-4	0.01		-6	0.01	5	WQ[DeA]EEMELYL
	P 37			8	0.01		10	0.00	6	SP[pyro-Glu]ELQAEAK
APOA4	N 98			-6	0.05		-7	0.03	4	LLPHAN[DeA]EVSQK
APOB	N 3814			1	0.32		4	0.03	4	SVSDGIAALDLN[DeA]AVANK
	N 696			3	0.00		4	0.04	10	ALYWV N[DeA]GGVPDGVSK
	N 2852			4	0.03		3	0.04	3	IN[DeA]NQLTLDNNTK
	N 1811			2	0.03		3	0.42	7	YNALDLTN N[DeA]GK
	N 2844			-3	0.01		-4	0.01	4	NTLELSN[DeA]GVIVK
	N 3688			-4	0.00		-4	0.00	2	NPN[DeA]GYSFIPVK
	N 1053			0	0.82		-4	0.02	2	VN[DeA]DESTEGK
	N 2999			-7	0.01		-5	0.01	3	HDAHLN[DeA]GK
APOC1	N 16			-3	0.04		-4	0.02	6	EFGN[DeA]TLEDK
	W 41			-3	0.08		-7	0.00	2	EW[kyn]FSETFQK
APOC3	Q 37			-3	0.15		-6	0.03	2	DALSSVQESQVA Q[DeA]QAR
	S 33			-6	0.02		-10	0.00	2	DALSS[Methmal]VQESQVAQQAR
APOD	P 133			2	0.39		4	0.03	2	NPNLP[pyro-Glu]PETVDSLK
	N 170			3	0.01		4	0.16	25	NILTSN[DeA]NIDVK
APOE	S 149			-2	0.00		-4	0.00	2	NILTS[Methmal]NNIDVK
	Y 180			3	0.01		3	0.07	2	LAV Y[ox]QAGAR
	W 282			4	0.04		3	0.05	2	SW[ox]FEPLVDMQR
	W 293			2	0.07		3	0.02	2	QW[ox]AGLVEK
APOF	W 293			5	0.00		3	0.25	4	QW[2ox]AGLVEK
	C 7			-6	0.01		-10	0.00	2	SLPTDC[2ox]ENEK
APOH	N 73			2	0.01		3	0.01	13	VCPFAGILE N[DeA]GAVR
APOM	C 183			0	0.91		-5	0.02	2	NQEA C[ox]ELSNN

Supplementary Figure 4. Post-translational modifications in lipid metabolism proteins of HDL recovered from AAA tissue. Abundance changes of peptides in proteins of the lipid metabolism category in HDL from pathological wall (P. wall) and thrombus (Thrbs), as compared to HDL from healthy tissue (H wall) expressed in terms of the standardized log2 ratio Z_{pq} (n=3, p<0.05). Ox: Oxidation, DeA: Deamidation, MethylMal: Methylmalonylation, Phos: Phosphorylation, Methyl: Methylation, AGE: Advanced glycation end products, Pyro-Glu: Pyroglutamic acid, Kyn: Kynurenine.

Supplementary Figure 5.- Abundance changes of modified peptides in HDL incubated with ILT-CM.



Supplementary Figure 5.- Abundance changes of modified peptides in HDL incubated with ILT-CM.

Statistically significant changes of PTMs peptides in proteins of the lipid metabolism category in HDL isolated from plasma and incubated with ILT conditioned media as compared to control HDL expressed in terms of the standardized log2 ratio Z_{pq} (n=4, p<0.05). Ox: Oxidation, DeA: Deamidation, MethylMal: Methylmalonylation, Phos: Phosphorylation, Methyl: Methylation, Pyro-Glu: Pyroglutamic acid, Oxa: Oxoalanine, Kyn: Kynurenine, AGE: Advanced glycation end products.