Supplementary Table II: HDL effect on OxPAPC co-expression modules

	Number of genes in module (in Romanoski et al)	Number of genes in module assayed in this study	Number of genes significantly affected by OxPAPC	Number of genes reversed by HDL	Fraction of genes reversed by HDL	GO terms	GO IDs
black	83	79	32	11	34%	endocytosis	GO:0006897
blue	255	236	126	48	38%	sulfur amino acid metabolic process, glutamine family amino acid metabolic process, fat cell differentiation, positive regulation of protein polymerization	GO:0000096, GO:0009064, GO:0045444, GO:0032273
brown	244	230	85	43	50%	interspecies interaction between organisms, golgi organization	GO:0044419, GO:0007030
green	174	161	65	21	32%	membrane protein ectodomain proteolysis, regulation of actin filament polymerization	GO:0006509, GO:0030833
greenyellow	33	31	10	7	70%	cell migration	GO:0016477
grey	53	46	6	2	33%	-	-
magenta	74	71	28	12	42%	negative regulation of cyclin-dependent protein kinase activity	GO:0045736
pink	76	72	33	10	30%	embryonic morphogenesis	GO:0048598
purple	45	43	25	5	20%	protein folding, response to unfolded protein	GO:0006457, GO:0006986
red	130	119	50	22	44%	elevation of cytosolic calcium ion concentration	GO:0007204
turquoise	323	292	66	37	56%	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, gene expression, ribosome biogenesis, spindle checkpoint, negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle, DNA damage checkpoint, DNA unwinding during replication, mitotic cell cycle checkpoint, DNA repair, DNA-dependent, DNA replication	GO:0006l39, GO:0010467, GO:0042254, GO:003l577, GO:005l436, GO:0000077, GO:0006268, GO:0007093, GO:0006281, GO:0006261, GO:0009262, GO:0006284, GO:0006298
yellow	245	228	64	38	59%	deoxyribonucleotide metabolic process, base-excision repair, mismatch repair	GO:0007l65, GO:0016070

The effect of HDL on genes that are part of the co-expression modules reported in Romanoski et al. Hub genes were determined as genes with k-within scaled >0.8.