

Description of Additional supplementary files:

Supplementary Data 1. Differential gene expression analysis of endothelial cells (ECs) of aortic wall of *iLpl^{-/-} Ldlr^{-/-}* mice compared to *Lpl^{fl/fl}/Ldlr^{-/-}*. Genes are listed with log₂ fold change, adjusted p-value (padj), and statistical metrics derived from pseudo-bulk scRNA-seq analysis. This table highlights genes significantly upregulated or downregulated in ECs, reflecting the transcriptional consequences of endothelial LpL deficiency in an atherosclerosis-prone background. Differential gene expression analysis was performed using a pseudo-bulk strategy on scRNA-seq data. Gene counts were aggregated by cell type and condition, followed by modeling with a negative binomial generalized linear model implemented in DESeq2. Statistical significance was assessed using the Wald test, and p-values were adjusted for multiple comparisons using the Benjamini–Hochberg false discovery rate (FDR) method.

Supplementary Data 2. Differential gene expression analysis of macrophages from the aortic wall of *iLpl^{-/-} Ldlr^{-/-}* mice compared to *Lpl^{fl/fl}/Ldlr^{-/-}* control. The table contains fold-change, padj values, and normalized expression levels. This dataset reveals macrophage-specific transcriptional changes associated with loss of LpL, highlighting potential effects on lipid uptake, inflammatory pathways, and foam cell formation. Differential gene expression analysis was performed using a pseudo-bulk strategy on scRNA-seq data. Gene counts were aggregated by cell type and condition, followed by modeling with a negative binomial generalized linear model implemented in DESeq2. Statistical significance was assessed using the Wald test, and p-values were adjusted for multiple comparisons using the Benjamini–Hochberg false discovery rate (FDR) method.

Supplementary Data 3. Differential gene expression analysis of smooth muscle cells (SMCs) from the aortic wall of *iLpl^{-/-} Ldlr^{-/-}* mice compared to *Lpl^{fl/fl}/Ldlr^{-/-}* control. Columns include log₂ fold change, padj, and gene expression values. The analysis identifies SMC transcriptional alterations in extracellular matrix regulation, contractile function, and phenotypic modulation during atherosclerosis progression under conditions of LpL deficiency. Differential gene expression analysis was performed using a pseudo-bulk strategy on scRNA-seq data. Gene counts were aggregated by cell type and condition, followed by modeling with a negative binomial generalized linear model implemented in DESeq2. Statistical significance was assessed using the Wald test, and p-values were adjusted for multiple comparisons using the Benjamini–Hochberg false discovery rate (FDR) method.

Supplementary Data 4. Pathway enrichment analysis of upregulated genes in endothelial cells (ECs) from *iLpl^{-/-} Ldlr^{-/-}* vs *Lpl^{fl/fl}/Ldlr^{-/-}* control aortic tissues. Enrichment was performed using curated KEGG databases. Significantly enriched pathways are ranked by adjusted p-values. Pathway enrichment analysis was conducted on sets of significantly upregulated genes using curated KEGG pathway databases. Enrichment was evaluated with a Fisher's exact (hypergeometric) test to assess over-representation of pathway members. Resulting p-values were corrected for multiple testing using the Benjamini–Hochberg FDR procedure.

Supplementary Data 5. Pathway enrichment analysis of upregulated genes in macrophages from *iLpl^{-/-} Ldlr^{-/-}* vs *Lpl^{fl/fl}/Ldlr^{-/-}* control aortic tissues. Enrichment was performed using curated KEGG databases. Significantly enriched pathways are ranked by adjusted p-values. Pathway enrichment analysis was conducted on sets of significantly upregulated genes using curated KEGG pathway databases. Enrichment was evaluated with a Fisher's exact (hypergeometric) test to assess over-representation of pathway members. Resulting p-values were corrected for multiple testing using the Benjamini–Hochberg FDR procedure.

Supplementary Data 6. Pathway enrichment analysis of upregulated genes in smooth muscle cells (SMCs) from *iLpl*^{-/-} *Ldlr*^{-/-} vs *Lpl*^{fl/fl}/*Ldlr*^{-/-} control aortic tissues. Enrichment was performed using curated KEGG databases. Data columns include pathway name, source database, enrichment score, and padj. Pathway enrichment analysis was conducted on sets of significantly upregulated genes using curated KEGG pathway databases. Enrichment was evaluated with a Fisher's exact (hypergeometric) test to assess over-representation of pathway members. Resulting p-values were corrected for multiple testing using the Benjamini–Hochberg FDR procedure.