Supporting information – Text S9: Flux FPLC profiles

*A computational model for the analysis of lipoprotein distributions in the mouse: Translating FPLC profiles to lipoprotein metabolism*

In this supplemental text, we provide illustration of the relations between the processes in the various phenotypes. As the interpretation of the grid itself is difficult due to the non-linearity, we have chosen to illustrate the distribution of fluxes over the FPLC profile.

The calculation of such a flux FPLC is explained in Text S3.

![Figure 1: Distribution of fluxes over the FPLC profile in wild-type *in silico* HDL metabolism. Left: parameter set X1, Right: parameter set X2](image)
Figure 2: Distribution of fluxes over the FPLC profile in wild-type *in silico* VLDL metabolism. Left: parameter set X1, Right: parameter set X2

From comparison of the wild-type VLDL production curves in Figure 2, the difference in nascent VLDL diameter is apparent.

The SR-B1 profiles show a clear absence of selective uptake (Figure 3, left). The reduction of PLTP deficient mouse cholesterol accumulation is less apparent, however a comparison of the relative scale of the figures reveals that cholesterol accumulation is much lower than in the wild-type mouse (Figure 3). In the LDLr knock-out mouse, the reduction of catabolism (and subsequent accumulation of LDL) is clearly visible.

In Figures 4-6, the acceptable parameter sets at t=14 days of LXR activation are plotted for E1 (Figure 4), E2 (Figure 5) and E3 (Figure 6).
Figure 3: Distribution of fluxes in the knock-out phenotypes. Left: HDL metabolism in the *in silico* SR-B1 knock-out mouse. The figure was generated with parameter set X1, and a value of $10^{-10}$ times the original parameter $c_{cell}$. Middle: HDL metabolism in the *in silico* PLTP knock-out mouse. The figure was generated with parameter set X1 and a value for $c_{chol}$ of 30% of the original value. Right: VLDL metabolism in the *in silico* LDLr-KO mouse. The figure was generated with X1 and a value of 40% of the original value of both Apo B uptake parameters.
The following figures depict the distribution of fluxes over the FPLC profile in the LXR-activated case – in particular, here we only depict the 14 days’ time point.
Figure 4: Distribution of fluxes in the HDL sub-model in the *in silico* 14 days LXR activated case, assuming E1. All acceptable parameter sets are included. HDL Flux FPLCs are scaled to total HDL production, in # of particles.
Figure 5: Distribution of fluxes in HDL sub-model the *in silico* 14 days LXR activated case, assuming E2. All acceptable parameter sets are included. HDL Flux FPLCs are scaled to total HDL production, in # of particles.
Figure 6: Distribution of fluxes in HDL sub-model the *in silico* 14 days LXR activated case, assuming E3. All acceptable parameter sets are included. HDL Flux FPLCs are scaled to total HDL production, in # of particles.