

**Physiologically-based pharmacokinetic modelling (PBPK) with dynamic PET data to study the *in vivo* effects of transporter inhibition on hepatobiliary clearance in mice**

## **Supplementary Figures 1 – 4**

### **Supplementary Table 1**

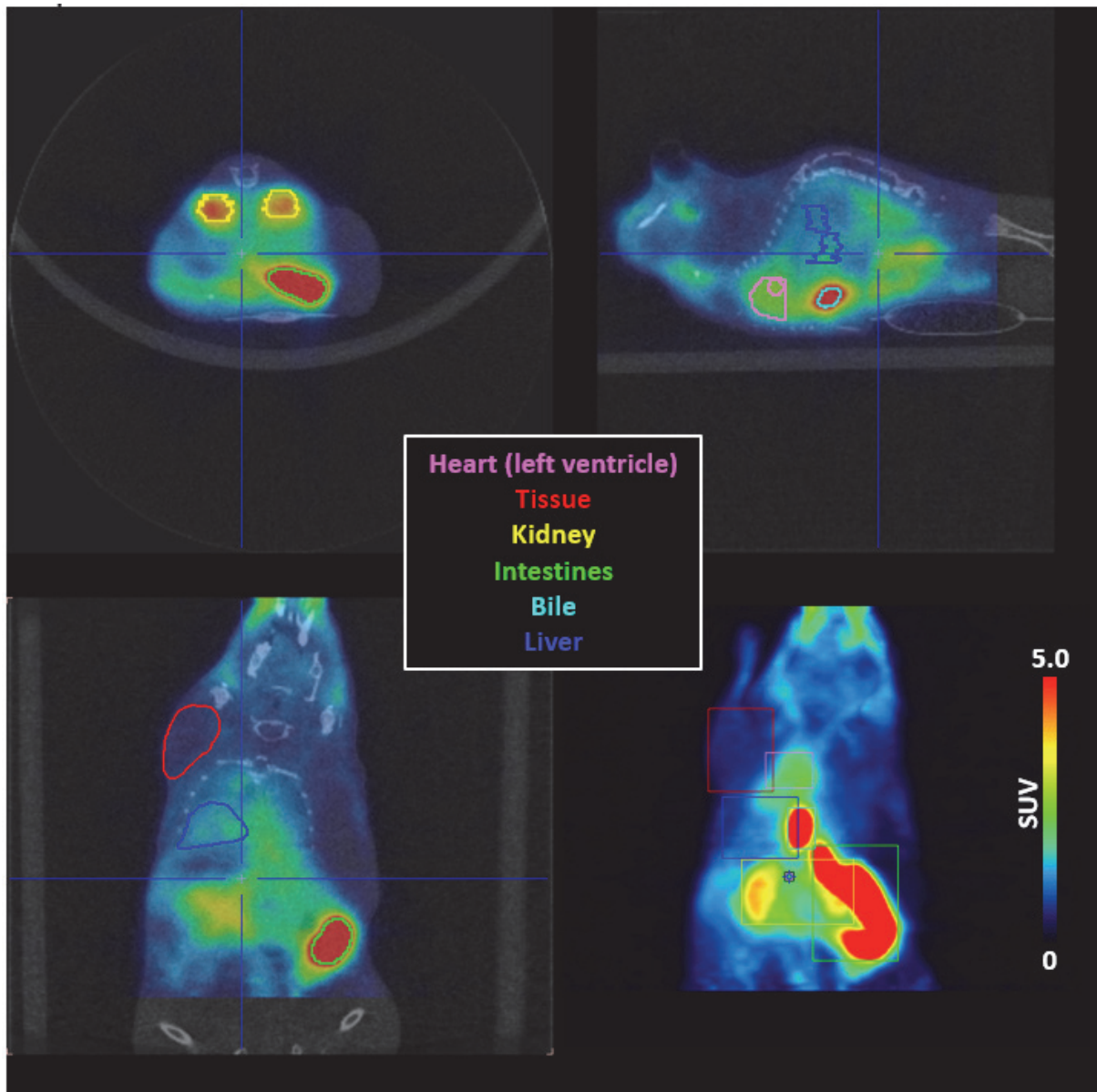
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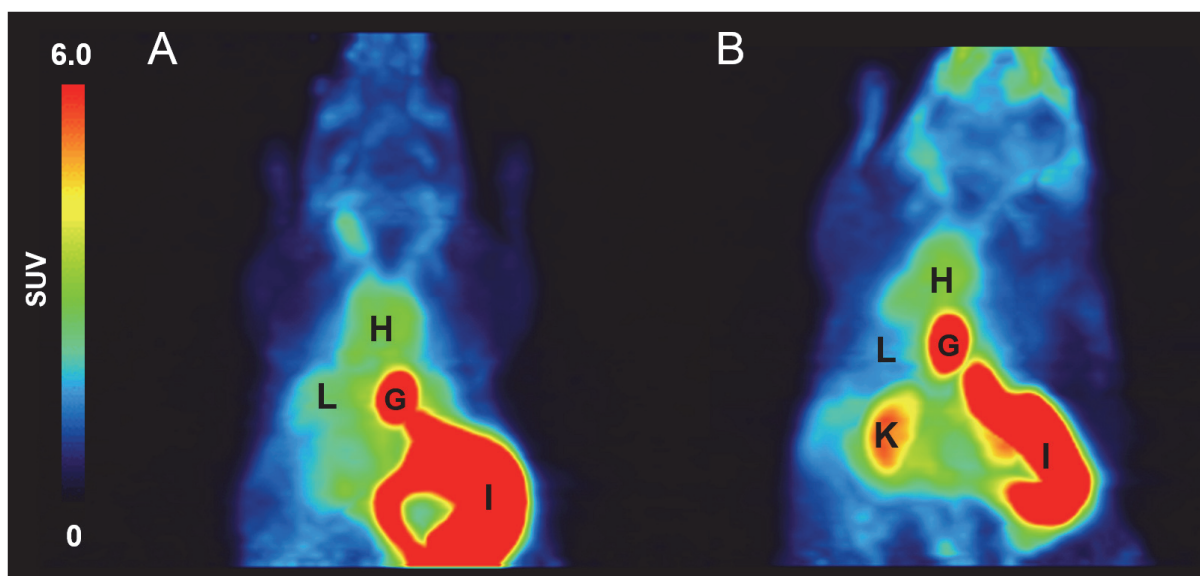
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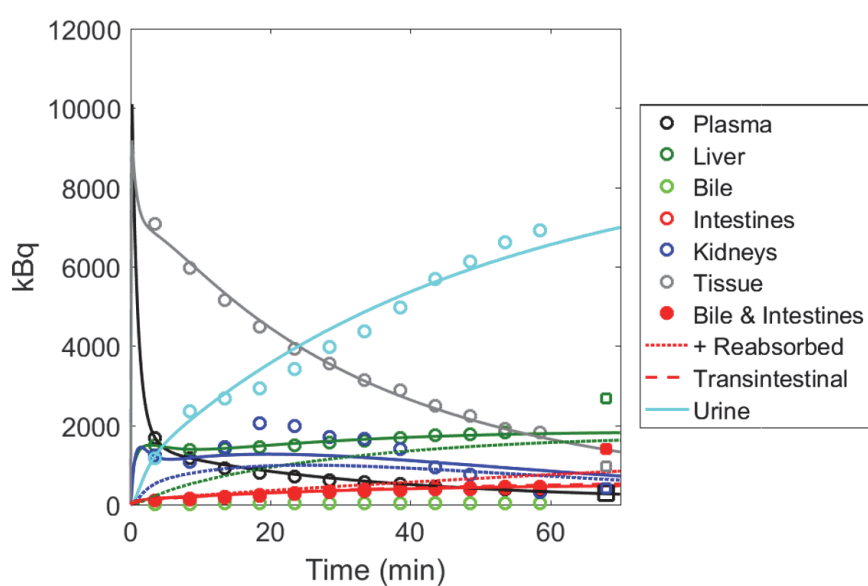
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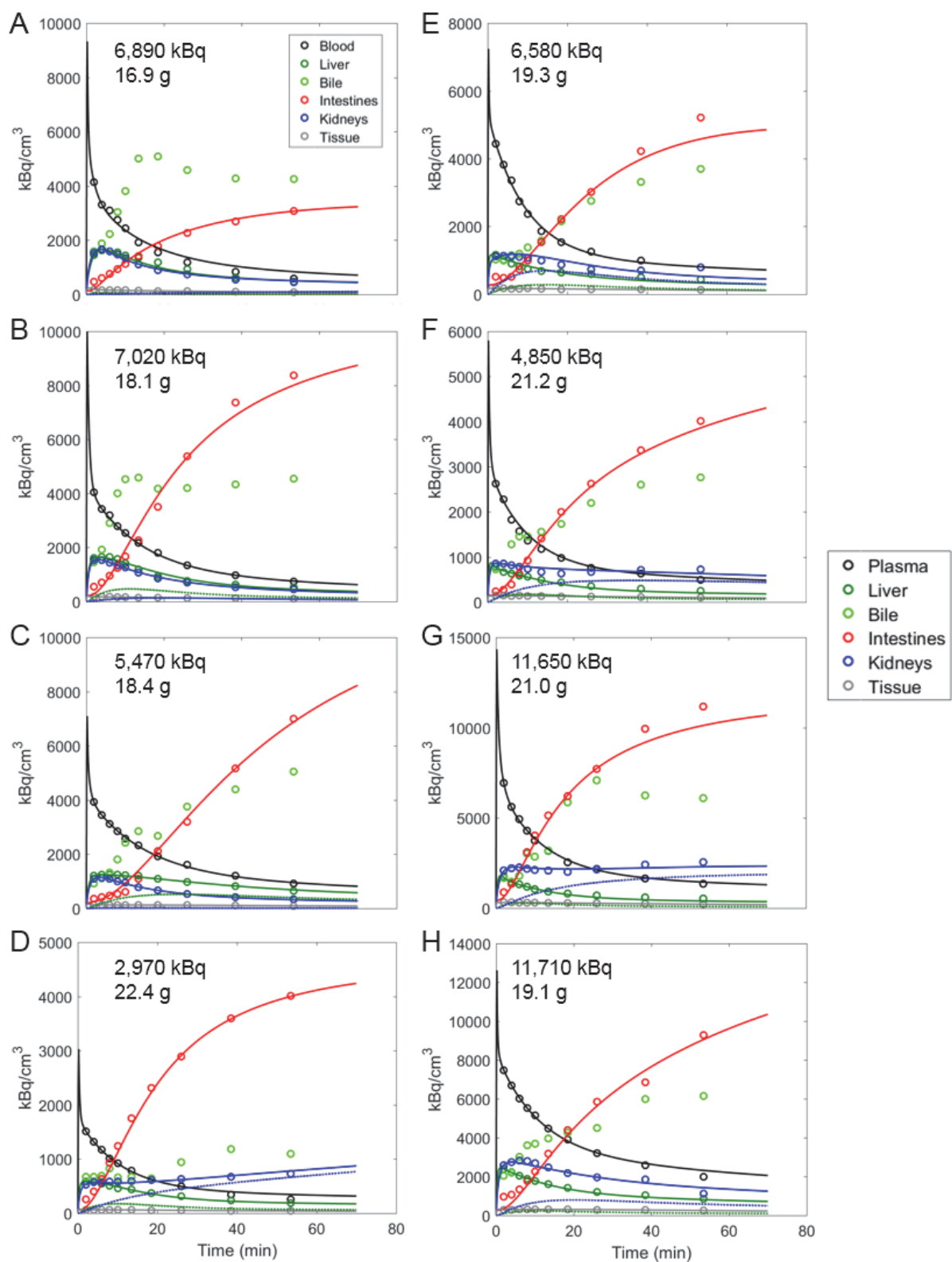
**Supplementary Figure 1.** Volumes of interest for the kinetic modelling. The heart left ventricle volume was generated with the PSEG module of the software PMOD as described in the section “Time activity curves”. All other volumes of interest were generated with the VOI tools of PMOD.



**Supplementary Figure 2.** PET images (maximal intensity projections) of mice with **A)**  $[^{11}\text{C}]\text{MT107}$ , **B)**  $[^{11}\text{C}]\text{MT107}$  after cyclosporine administration (50 mg/kg i.v.). Same data as in **Figure 4** but averaged for the complete scan duration. G, gallbladder; H, heart; I, intestines; K, kidney; L, liver; U, urinary bladder.



**Supplementary Figure 3.**  $A(t)$  experimental data and fits of the  $[^{11}\text{C}]\text{AM7}$  scan after cyclosporine treatment in **Figure 3B**. Note that the experimental  $A_{\text{kidney}}(t)$  was not well defined resulting in unreliable fitting results. The fitted parameters are shown in **Supplementary Table 1**. CD1 nu/nu mouse.



**Supplementary Figure 4.**  $C(t)$  of the scans and fits in Figure 7. Note that the fits were optimized for minimal squared residues in  $A(t)$ .

Supplementary Table 1. Fit parameters

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