

**Supplementary Table S4. Prediction of lipids levels from the Generalized Linear Mixed-effects Model (GLMM).**

Hypercholesterolemia model	p value (correlation sign)
<b>Treatment, clinics, demographics (Null model)</b>	
After menarche	0,0079 (-)
HAART exposure before current scheme	0,0287
Time on current scheme	0,0287 (-)
Use of RTV (full-dose)	<0,0001 (+)
Use of RTV-boosted PI treatment	<0,0001 (+)
Use of D4T	0,0335 (+)
Use of NFV	<0,0001 (+)
Use of any NNRTI	0,0141 (+)
Time on RTV (full-dose) last scheme	0,0717
Time on RTV boosted PI last scheme	0,0001 (+)
Time on D4T last scheme	0,2575
Time on NFV last scheme	0,1744
Time on NNRTI last scheme	0,9131
<b>Genotype basal effect</b>	<b>0,1177<sup>1</sup></b>
UTR 3238 (SsTI) CG vs CC	0,0092 (+)
UTR 3238 (SsTI) GG vs CC	0,2964
IRE -455 (FokI) CT vs TT	0,8904
IRE -455 (FokI) CC vs TT	0,9959
IRE -482 (MspI) TC vs CC	0,5887
IRE -482 (MspI) TT vs CC	0,9971
<b>Genotype treatment-associated effect</b>	<b>0,0003<sup>2</sup></b>
<i>Effect under RTV boosted PI shemes</i>	
UTR 3238 (SsTI) CG vs CC	0,0001 (-)
UTR 3238(SsTI) GG vs CC	0,8641
IRE -482 (MspI) TC vs CC	0,4314
IRE -482 (MspI) TT vs CC	0,0063 (+)
<i>Effect under D4T including shemes</i>	
UTR 3238 (SsTI) CG vs CC	0,1243
UTR 3238(SsTI) GG vs CC	0,9566
IRE -455 (FokI) CT vs TT effect	0,7073
IRE -455 (FokI) CC vs TT effect	0,9948
IRE -482 (MspI) TC vs CC effect	0,2237
IRE -482 (MspI) TT vs CC effect	0,9910
<b>Genotype effect associated to time of exposure</b>	<b>0,0959<sup>3</sup></b>
<i>Interaction with accumulated HAART time</i>	
IRE -455 (FokI) CT vs TT	0,4283
IRE -455 (FokI) CC vs TT	0,1542
<i>Interaction with time on current scheme</i>	
IRE -482 (MspI) TC vs CC	0,1132
IRE -482 (MspI) TT vs CC	0,5043

The contribution of each factor was evaluated with Wald test, p-values are depicted. The correlation sign is depicted between brackets. Test results for hierarchical model comparison are shown in bold (LRT).

<sup>1</sup> vs Null hypothesis model

<sup>2</sup> vs Genotype basal effect model

<sup>3</sup> vs Genotype treatment-associated effect model