Table 4. Population disease progression parameter estimates for albumin dynamics in TB and TB-HIV patients (base model).

parameter		HIV only		TB-HIV		Description
		mean	RSE (%)	mean	RSE (%)	
Q_0	(g/dl/hr)	0.0055	5	0.0037	2	Baseline albumin secretion rate
Q_{ss}	(g/dl/hr)	0.0061	17	0.0055	17	Maximum albumin secretion rate
R	(1/hr)	0.0003	69	0.0004	61	Rate of change from Q_0 to Q_{ss}
K	(1/hr)	0.0014	FIX	0.0014	FIX	Elimination rate constant for albumin
Random effects parameters for both HIV only and TB-HIV						
IIV_Q_0		0.0269	12			Inter-individual variability in baseline albumin secretion rate
Residual error(proportional)		0.0335	5			Variability in the residual error

Table 5. Correlation matrix of the parameter estimates from the NONMEM covariance step.

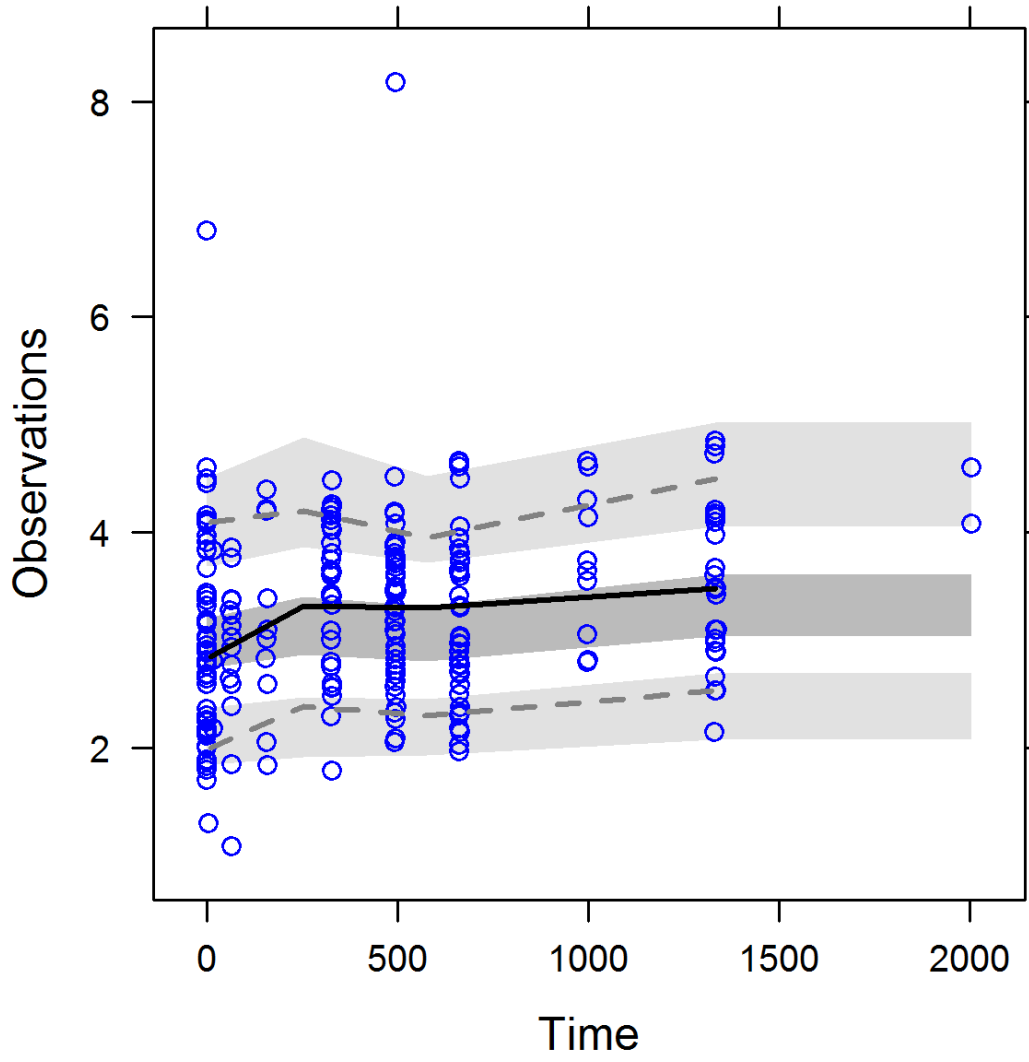|	Q_0	Q_{ss}	R	OM11	RESIDUAL
Q_0	1.13E-4				
Q_{ss}	-2.72E-1	5.66E-4			
R	1.26E-1	-6.89E-1	1.45E-4		
IIV_Q_0	2.25E-1	-4.71E-1	5.26E-1	1.03E-3	
RESIDUAL	7.21E-2	-4.54E-2	-1.05E-2	2.7E-1	3.77E-3

Figure 4. VPC of the validation dataset.

Figure 5. Parameter versus Parameter plots showing correlation between parameter estimates from 950 bootstrap estimates.
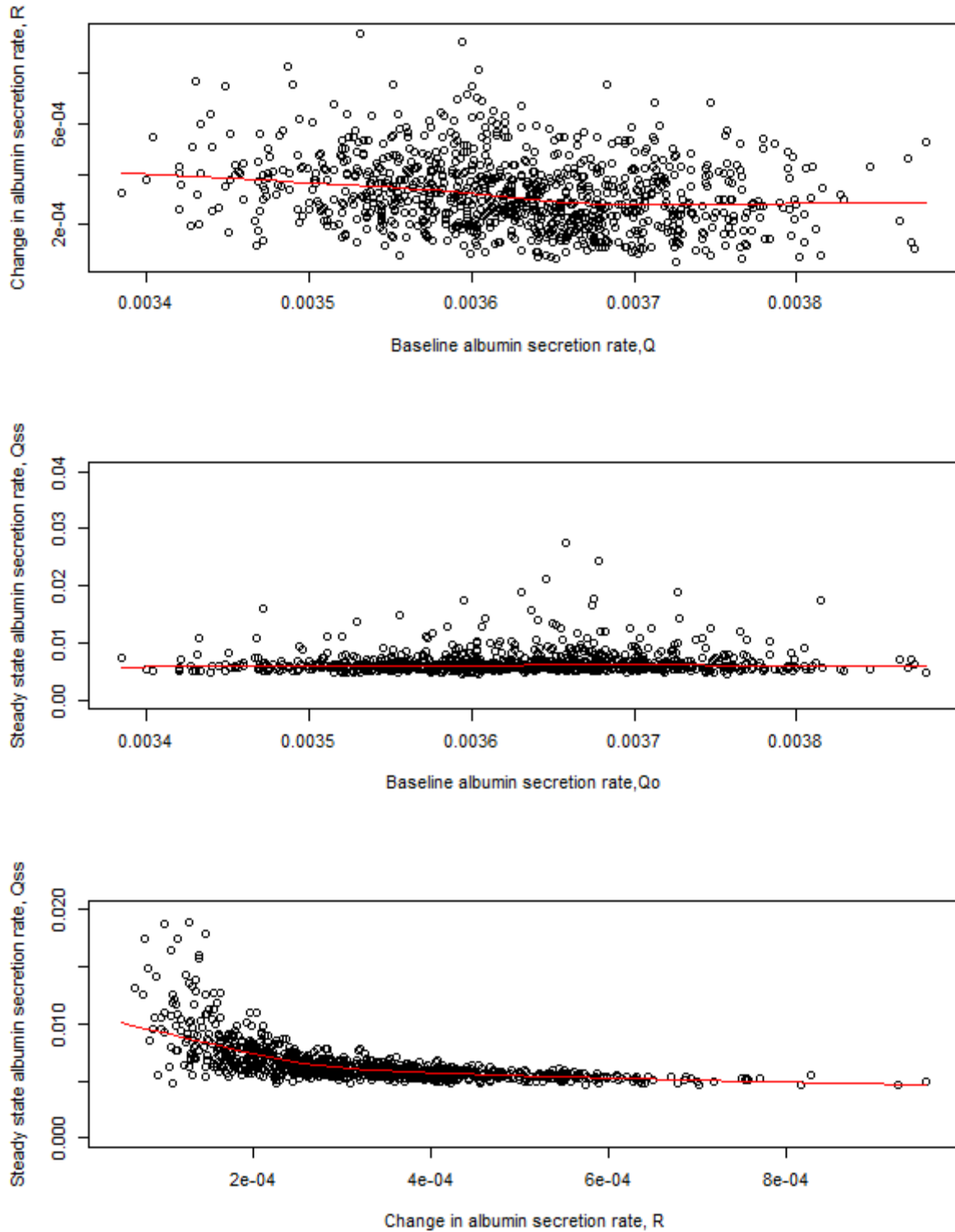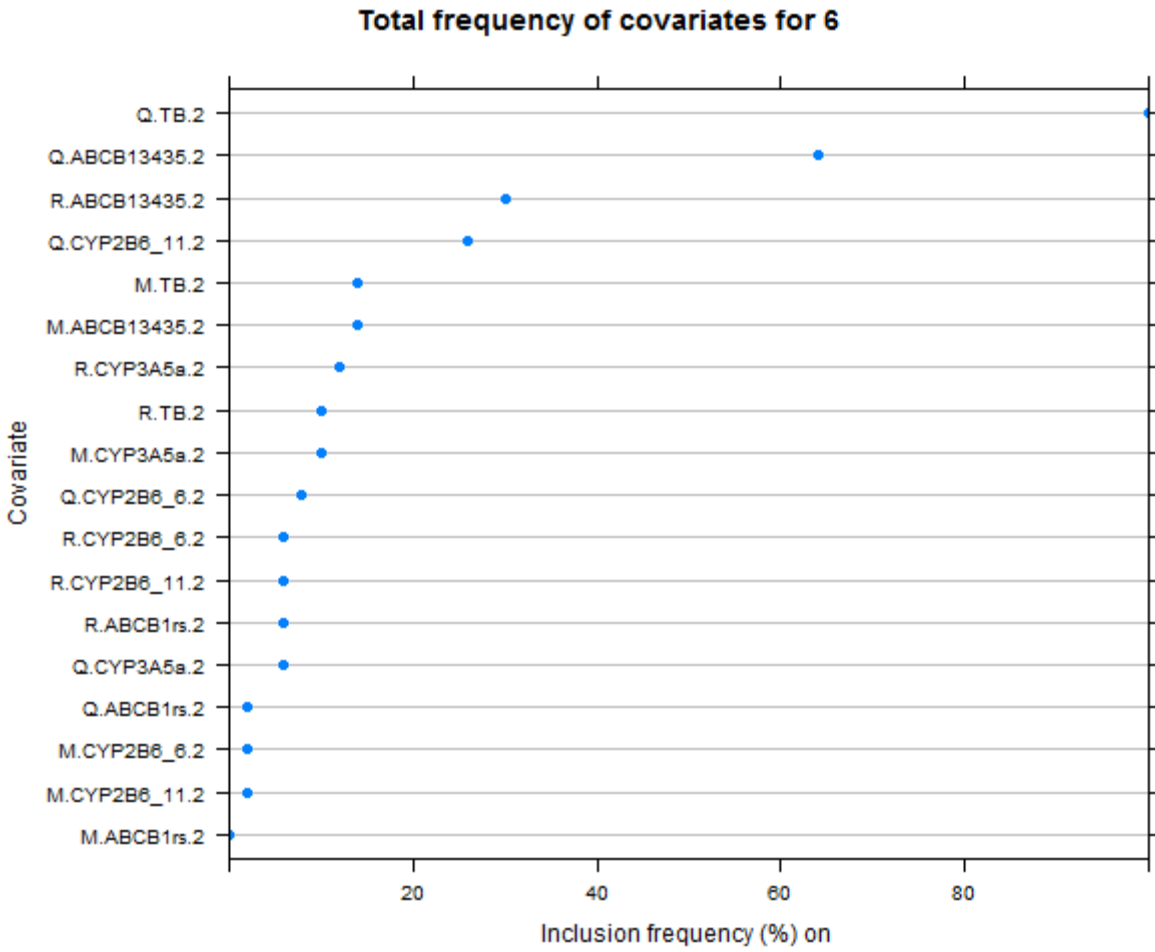
Figure 6. Inclusion frequence of covariates following 50 bootstraps of the stepwise covariate modeling.

The Y axis represents " Parameter.covariate.relationship". e.g. Q.TB.2 means TB is a covariate on parameter Q with a proportional relationship. Q stands for Q_0 M stands Q_{ss}.

Figure 7. Goodness of fit plot using a simple exponential albumin production model.