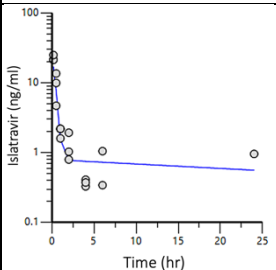
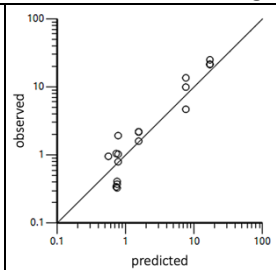
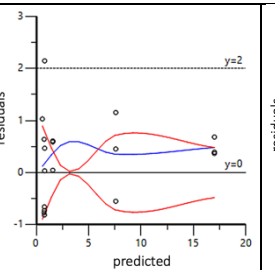
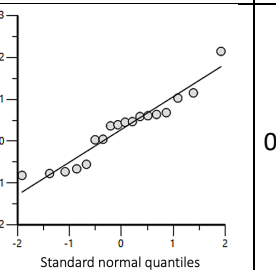
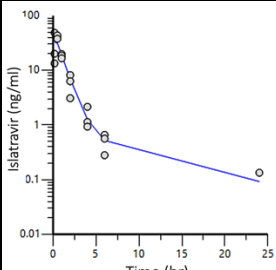
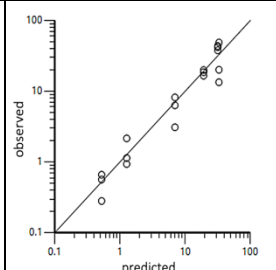
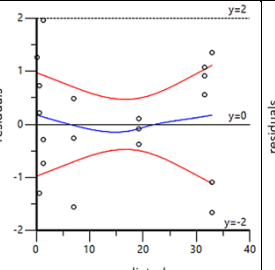
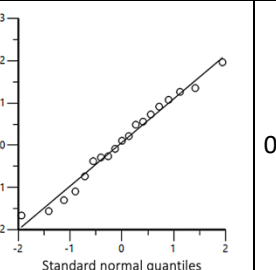
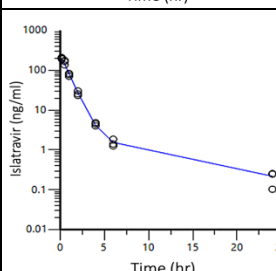
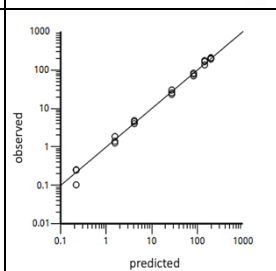
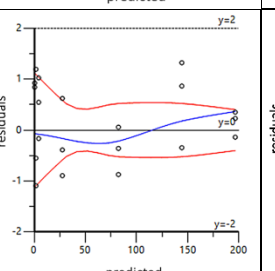
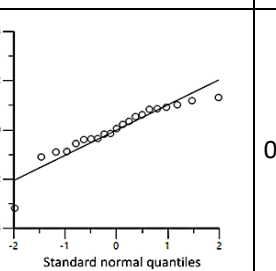


Pharmaceutics

Supplementary Material

No.		Model	Param	-2LL	AIC	BIC	Diagnostics				RSE
1	Independent Dose Models	0.1 mg/kg 2CMT NPD Multi	6	70.7	82.7	88.1					0.69
2		0.2 mg/kg 2CMT NPD Multi	6	81.1	93.8	98.8					0.36
3		1.0 mg/kg 2CMT NPD Multi	6	94.1	106.1	112.4					0.17

No.		Model	Param	-2LL	AIC	BIC	Diagnostics				RSE
4	Simultaneous Dose Model Development	1CMT NPD Multi	4	559.1	567.1	575.9					1.14
5		2CMT NPD Multi [Base Model]	6	414.8	426.4	438.7					0.90
6		Final Model	Base Model no Outlier	6	423.7	435.7	448.9				
Base Model vs. Final Model Theta Parameters											
		Final	Base	Final		Final	Base	Final		Final	Base
		Ka (1/h)		A (ng/ml)		alpha (1/h)		B (ng/ml)		beta (1/h)	
Estimate		12.23	12.79	141.60	125.66	1.21	1.18	1.39	0.83	0.103	0.037
Std error		2.06	2.12	36.34	35.83	0.06	0.05	0.33	0.30	0.007	0.023
CV%		16.83	16.59	25.7	28.5	4.6	4.1	24.1	36.4	6.6	64.0
2.5% CI		8.11	8.53	68.92	53.76	1.10	1.08	0.72	0.22	0.089	-0.010
97.5% CI		16.34	17.05	214.28	197.57	1.32	1.28	2.06	1.43	0.117	0.083

Circles are observed data; blue lines are predicted curves; red lines are distribution of residuals. CMT- compartment; NPD- naïve pooled; RSE- relative standard error; Ka- absorption rate constant; A- 1st CMT macroconstant; B- 2nd CMT macro-constant; alpha/beta- elimination rate constant; CI- confidence interval.

Table 1: Population pharmacokinetic (PopPK) model development and comparison in Phoenix NLME™.

The population pharmacokinetic (PopPK) analyses were performed using Phoenix NLME modeling software. The model building process was a stepwise approach: independent modeling of islatravir plasma concentration for the three subcutaneous bolus doses (0.1, 0.3 and 1mg/kg), identification of the most appropriate structural base model followed by developing a simultaneous base model of the collapsed dose range. The base structural model was tested for 1, 2 and 3 compartments, describing first-order absorption and linear elimination. The structural model was developed with a fit-for-purpose approach to deconvolution leveraging macro-parameterization to estimate; first-order absorption rate constant (K_a), macro-constants (A and B), elimination rate constants (α and β). A 2-compartment structural models provided a better fit for the collapsed simultaneous model of 0.1, 0.3 and 1.0mg/kg dosing levels. Residual diagnostic plots of the 2-comp Final model show some bias in the fit but do not indicate misspecification as with the 1-comp comparator. A 3 Finally, while AIC increases with addition of a second compartment the -2Loglikelihood decreases (-113). Overall, the fits and criteria indicate an improvement with a 2-compartment structure. Final overall model error decreases from 113% to 76% from a 1 to 2-compartment model when no other factors were changed.

<pre>proc model data=work.RatKinetic; by Ind; parms K0=42576; Mt= K0*t; fit Mt; run;</pre>	Zero order
<pre>proc model data=work.RatKinetic; by Ind; parms Kf=.01; LnMr=Kf*t; fit LnMr; run;</pre>	First order
<pre>proc model data=work.RatKinetic; by Ind; parms Kh=1000; Mt=Kh*(t**.5); fit Mt; run;</pre>	Higuchi
<pre>proc model data=work.RatKinetic; by Ind; parms Krp=0.001 n=0.45; Ft = Krp*(t**n); fit Ft; run;</pre>	Ritgers-Peppas

Figure 1: Model code for regression analysis of 4 kinetic models of drug distribution in SAS™ 9.4.

Top down shows each model formula and initial estimate used to fit a regression using the ordinary least squared function. Where Mt is the rate constant of each respective model, Ft is the ratio of $Mt/Minf$ (the mass loaded in the implant), n is the power exponent of release, and