

SUPPLEMENTARY MATERIAL**Final NONMEM code**

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$SUBROUTINE ADVAN5 TRANS1
$MODEL  COMP=(PARENT,DEFDOSE,DEFOBS) COMP=(MET1) COMP=(PERIP)
        COMP=(TRANSIT1)
$PK
;;; VCPSEX-DEFINITION START
IF(SEX.EQ.0.0000E+00) VCPSEX = 1 ; Most common
IF(SEX.EQ.1.0000E+00) VCPSEX = ( 1 + THETA(22))
;;; VCPSEX-DEFINITION END

;;; VCPMFG-DEFINITION START
IF(MFG.EQ.1.0000E+00) VCPMFG = 1 ; Most common
IF(MFG.EQ.0.0000E+00) VCPMFG = ( 1 + THETA(21))
;;; VCPMFG-DEFINITION END

;;; VCPBSA-DEFINITION START
VCPBSA = ((BSA/1.71)**THETA(20))
;;; VCPBSA-DEFINITION END

;;; VCP-RELATION START
VCPCOV=VCPBSA*VCPMFG*VCPSEX
;;; VCP-RELATION END

;;; FR2MFG-DEFINITION START
IF(MFG.EQ.1.0000E+00) FR2MFG = 1 ; Most common
IF(MFG.EQ.0.0000E+00) FR2MFG = ( 1 + THETA(19))
;;; FR2MFG-DEFINITION END

;;; FR2-RELATION START
FR2COV=FR2MFG
;;; FR2-RELATION END

;;; CLPTRTOXA-DEFINITION START
IF(TRTOXA.EQ.0.0000E+00) CLPTRTOXA = 1 ; Most common
IF(TRTOXA.EQ.1.0000E+00) CLPTRTOXA = ( 1 + THETA(18))
;;; CLPTRTOXA-DEFINITION END

;;; CLPSEX-DEFINITION START
IF(SEX.EQ.0.0000E+00) CLPSEX = 1 ; Most common
IF(SEX.EQ.1.0000E+00) CLPSEX = ( 1 + THETA(17))
;;; CLPSEX-DEFINITION END

;;; CLPMFG-DEFINITION START

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IF(MFG.EQ.1.0000E+00) CLPMFG = 1 ; Most common
IF(MFG.EQ.0.0000E+00) CLPMFG = ( 1 + THETA(16))
;;; CLPMFG-DEFINITION END

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;;; CLPASIAN-DEFINITION START
IF(ASIAN.EQ.0.0000E+00) CLPASIAN = 1 ; Most common
IF(ASIAN.EQ.1.0000E+00) CLPASIAN = ( 1 + THETA(15))
;;; CLPASIAN-DEFINITION END

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;;; CLP-RELATION START
CLPCOV=CLPASIAN*CLPMFG*CLPSEX*CLPTRTOXA
;;; CLP-RELATION END

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;;; CLMTRTOXA-DEFINITION START
IF(TRTOXA.EQ.0.0000E+00) CLMTRTOXA = 1 ; Most common
IF(TRTOXA.EQ.1.0000E+00) CLMTRTOXA = ( 1 + THETA(14))
;;; CLMTRTOXA-DEFINITION END

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;;; CLMSEX-DEFINITION START
IF(SEX.EQ.0.0000E+00) CLMSEX = 1 ; Most common
IF(SEX.EQ.1.0000E+00) CLMSEX = ( 1 + THETA(13))
;;; CLMSEX-DEFINITION END

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;;; CLMCRCL-DEFINITION START
IF(CRCL.EQ.-99) THEN
  CLMCRCL = 1
ELSE
  CLMCRCL = ((CRCL/85.04)**THETA(12))
ENDIF
;;; CLMCRCL-DEFINITION END

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;;; CLMBIL-DEFINITION START
IF(BIL.EQ.-99) THEN
  CLMBIL = 1
ELSE
  CLMBIL = ((BIL/0.41)**THETA(11))
ENDIF
;;; CLMBIL-DEFINITION END

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;;; CLM-RELATION START
CLMCOV=CLMBIL*CLMCRCL*CLMSEX*CLMTRTOXA
;;; CLM-RELATION END

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; PARENT CENTRAL

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TVCLP = THETA(1)

TVCLP = CLPCOV*TVCLP

CLP = TVCLP * EXP(ETA(4)) ; total CL for irinotecan

TVVCP = THETA(2)

TVVCP = VCPCOV*TVVCP

VCP = TVVCP * EXP(ETA(6)) ; central volume for irinotecan

,*****

KT = CLP/VCP ; total elimination rate for irinotecan

; PARENT PERIPHERAL

TVQP = THETA(3)

QP = TVQP

TVV3P = THETA(4)

V3P = TVV3P

,*****

K13 = QP/VCP ; rate from central to peripheral for irinotecan

K31 = QP/V3P ; rate from peripheral to central for irinotecan

; METABOLITE

TVFR1 = THETA(5)

TVFR2 = THETA(6)

TVFR2 = FR2COV*TVFR2

FR1 = TVFR1 * EXP(ETA(5))

FR2 = TVFR2 * EXP(ETA(3))

FM1 = FR1 / (1+FR1+FR2) ; fraction of parent metabolized via 1st order process

FM2 = FR2 / (1+FR1+FR2) ; fraction of parent metabolized via transit

,*****

K12 = FM1*KT ; fraction of total CL to SN-38 (1st order)

K14 = FM2*KT ; fraction of total CL to SN-38 (transit)

K10 = (1-FM1-FM2)*KT ; fraction of total CL not transformed to SN-38

TVKFM = THETA(7)

KFM = TVKFM * EXP(ETA(2)) ; rate of transformation out of transit

,*****

K42 = KFM

TVCLM = THETA(8)

TVCLM = CLMCOV*TVCLM

CLM = TVCLM * EXP(ETA(1)) ; SN-38 clearance

VCM = VCP ; SN-38 central compartment volume

,*****

K20 = CLM/VCM ; rate of elimination of SN-38

;Scaling parameters

S1 = VCP

S2 = VCP/1000

S3 = V3P

S4 = 1

,

\$ERROR

IPRDP = A(1)/S1

IPRDM = A(2)/S2

DEL = 0.0000001

RHO = THETA(23)

WP = THETA(9)*IPRDP

WM = THETA(10)*IPRDM

IF(CMT.EQ.1) THEN

 ;Parent

 IPRED = IPRDP

 IRES = DV-IPRED

 ;W = SQRT((THETA(9)*IPRED)**2 + THETA(10)**2)

 IWRES = IRES/(WP + DEL)

 Y = IPRED + WP*EPS(1)

ELSE

 ;Metabolite

 IPRED = IPRDM

 IRES = DV-IPRED

 ;W = SQRT((THETA(11)*IPRED)**2 + THETA(12)**2)

 IWRES = IRES/(WM + DEL)

 Y = IPRED + WM*EPS(1)*RHO + WM*EPS(2)*SQRT(1-RHO**2)

ENDIF

Population PK model development, base model

Inter-individual variability was modeled assuming a log-normal distribution for patient-level random effects:

$$\theta_{in} = \theta_{TV_n} \cdot \exp(\eta_{in})$$

$$\eta_1 \cdots \eta_m \sim MVN(0, \Omega)$$

where θ_{TV_n} is the population typical value for the nth pharmacokinetic (PK) parameter (e.g. elimination clearance) and η_{in} is the random inter-individual effect on the nth parameter for patient i. Random effects ($\eta_1 \cdots \eta_m$) were assumed to be normally distributed with zero mean and estimated variance ω^2 included in the OMEGA (Ω) matrix.

Residual unexplained variability was tested as additive, proportional, or combined (additive + proportional) on the dependent variable; the equation below describes the combination of additive and proportional residual variability:

$$Cp_{ij} = \hat{Cp}_{ij} \cdot (1 + \varepsilon_{1,ij}) + \varepsilon_{2,ij}$$

where ε_1 and ε_2 are normally distributed with zero mean and variance σ_1^2 and σ_2^2 , respectively, included in the SIGMA (Σ) matrix. In this expression, Cp_{ij} is the observation in individual i at sampling time j, \hat{Cp}_{ij} is the typical individual prediction at sampling time j, $\varepsilon_{1,ij}$ is a proportional residual error term, and $\varepsilon_{2,ij}$ is an additive residual error term.

Population PK model development, inclusion of covariates

Continuous covariates were included in the population PK model as power functions, whereas categorical covariates were implemented as factors:

$$\theta_{TV,i} = \theta_{TV,Pop} \cdot \left(\frac{x_{Cont,i}}{\text{median}(x_{Cont,i})} \right)^{\theta_1} \cdot (1 + x_{Cat,i} \cdot \theta_2)$$

where $\theta_{TV,i}$ is the typical parameter for patient i, defined as a function of the population typical value ($\theta_{TV,Pop}$) and the individual contributions from continuous (x_{Cont}) and categorical (x_{Cat} , with values 0 and 1) covariates. θ_1 and θ_2 represent the respective covariate coefficients.

Population PK model development, model evaluation

Statistical shrinkage of the Empirical Bayes Estimates (EBEs) for all variability components of the model was evaluated, as described previously.¹ The shrinkage magnitude for a structural parameter P (h-shrinkage) was calculated as follows:

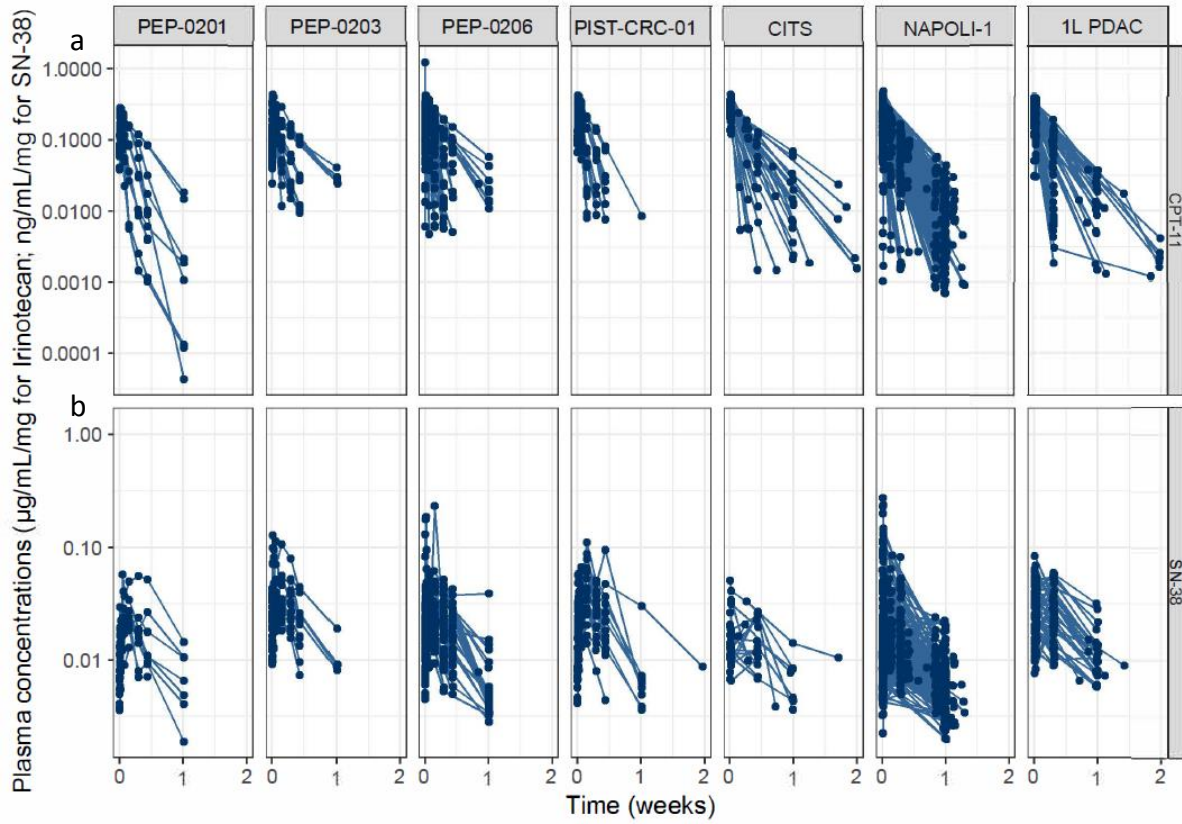
$$shp = 1 - \frac{SD(\eta_{EBE,P})}{\omega p}$$

where $SD(\eta_{EBE,P})$ is the standard deviation of the individual EBEs for parameter P and ω_p is the model estimate of the standard deviation associated with parameter P. If no shrinkage is present in parameter P, the ratio between $SD(\eta_{EBE,P})$ and ω_p is unity and shp becomes zero. Shrinkage values of $\leq 30\%$ are considered to indicate good individual estimates of a parameter of interest, while larger shrinkage values indicate that the individual Bayesian estimates "shrunk" towards the population mean values.

Reference

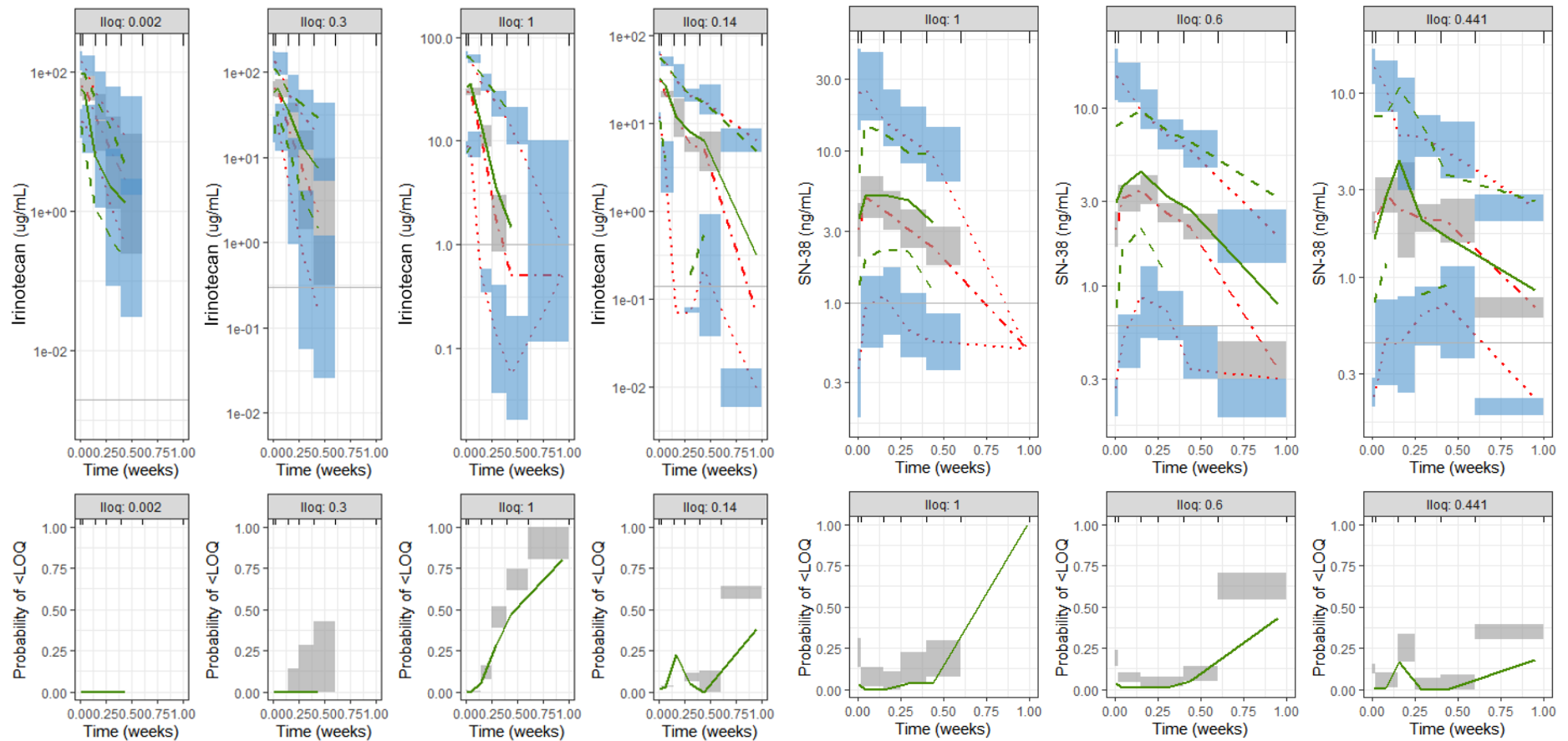
1. Karlsson, M.O. & Savic, R.M. Diagnosing model diagnostics. *Clin Pharmacol Ther* **82**, 17–20 (2007).

Figure S1 Dose-normalized total irinotecan (a) and SN-38 (b) plasma concentration–time profiles by study. Data are presented on a semi-log scale. Clinicaltrials.gov identifiers for the studies shown are: PEP0203, NCT02884128; PEP0206, NCT00813072; PIST-CRC-01, NCT00940758; CITS, NCT01770353; NAPOLI-1, NCT01494506; 1L PDAC, NCT02551991. CPT-11, irinotecan



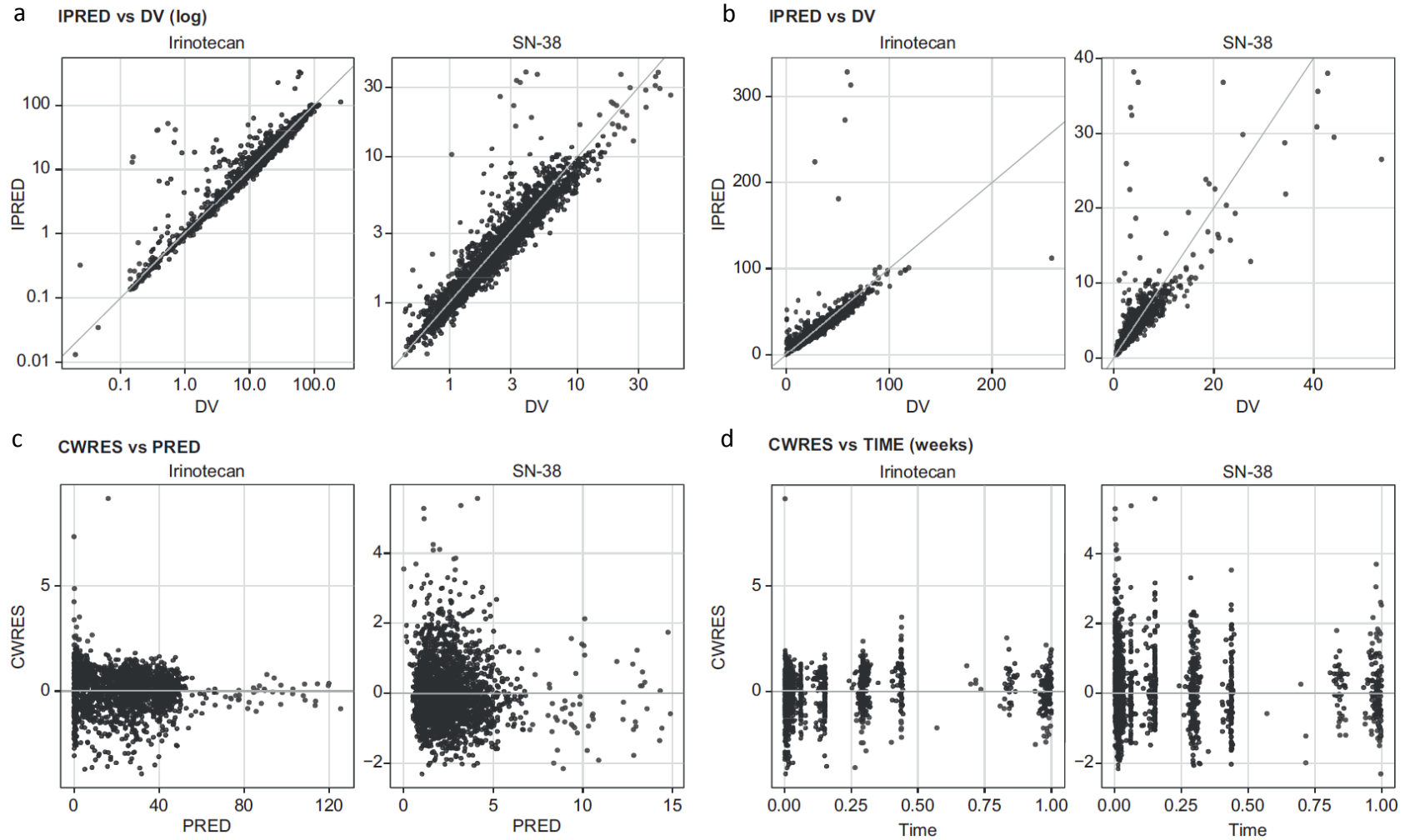
PopPK modeling of liposomal irinotecan

Figure S2 VPCs for total irinotecan and SN-38 concentrations over time. Raw data are presented on a semi-log scale, split by LLOQ values in the first row and the probability of LOQ in the second row. The observed median (green bold line) and 2.5th and 97.5th observed percentiles (green dashed lines) are compared with the 95% confidence intervals (shaded area) for the median (gray area) and the 2.5th and 97.5th percentiles of the simulated ($n = 1000$) data (blue area) and with the simulated median (red semi-dashed line) and 2.5th and 97.5th simulated percentiles (red dotted line). LLOQ, lower limit of quantification; LOQ, limit of quantification; VPC, visual predictive check



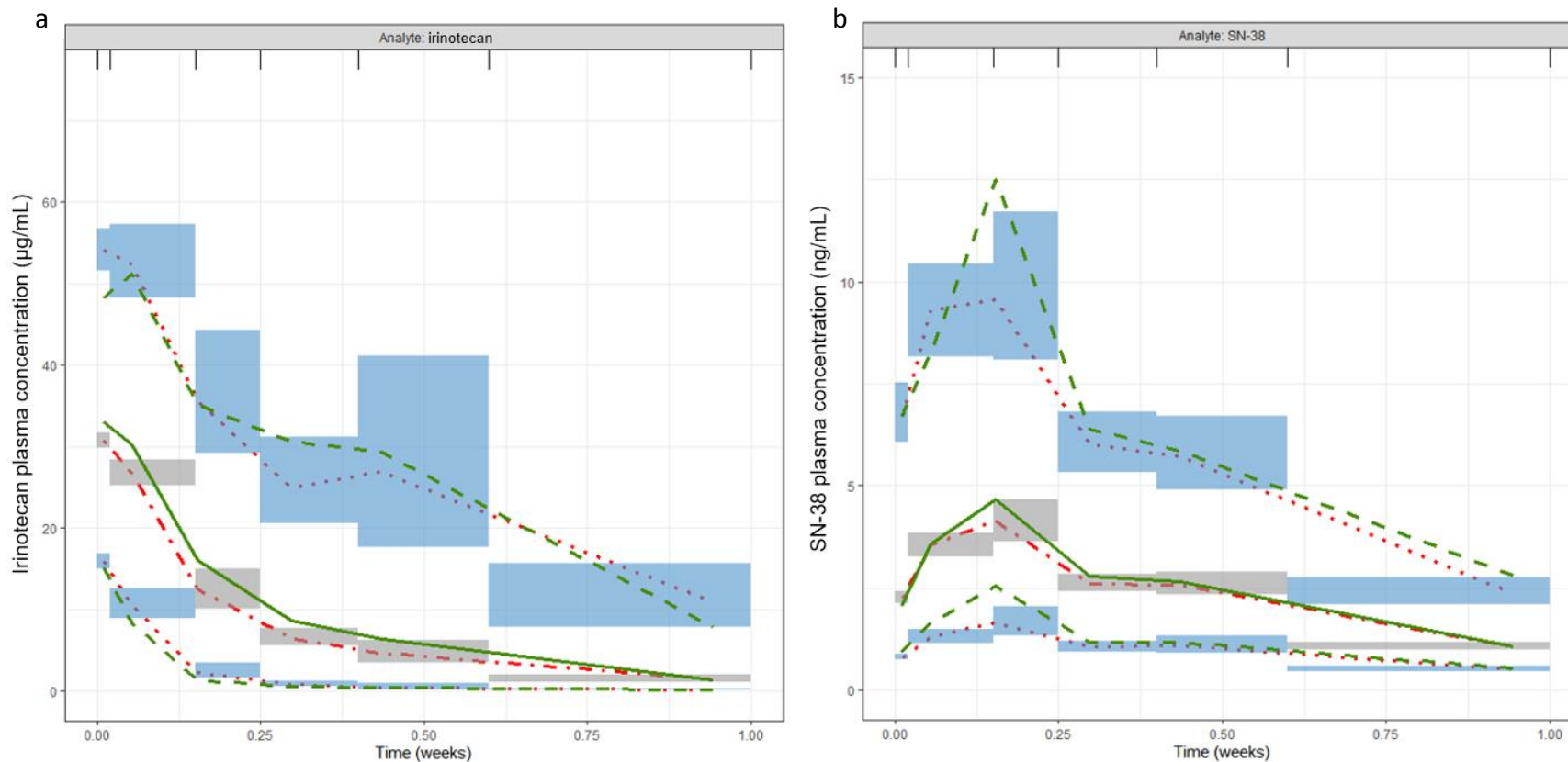
PopPK modeling of liposomal irinotecan

Figure S3 Goodness-of-fit plots for irinotecan and SN-38, including individual model-predicted concentration versus observed concentration in log scale (a), as raw data (b), conditional weighted residuals versus population model predictions (c), and conditional weighted residuals versus time (d), CWRES, conditional weighted residuals; DV, dependent variable; IPRED, individual predicted; PRED, predicted



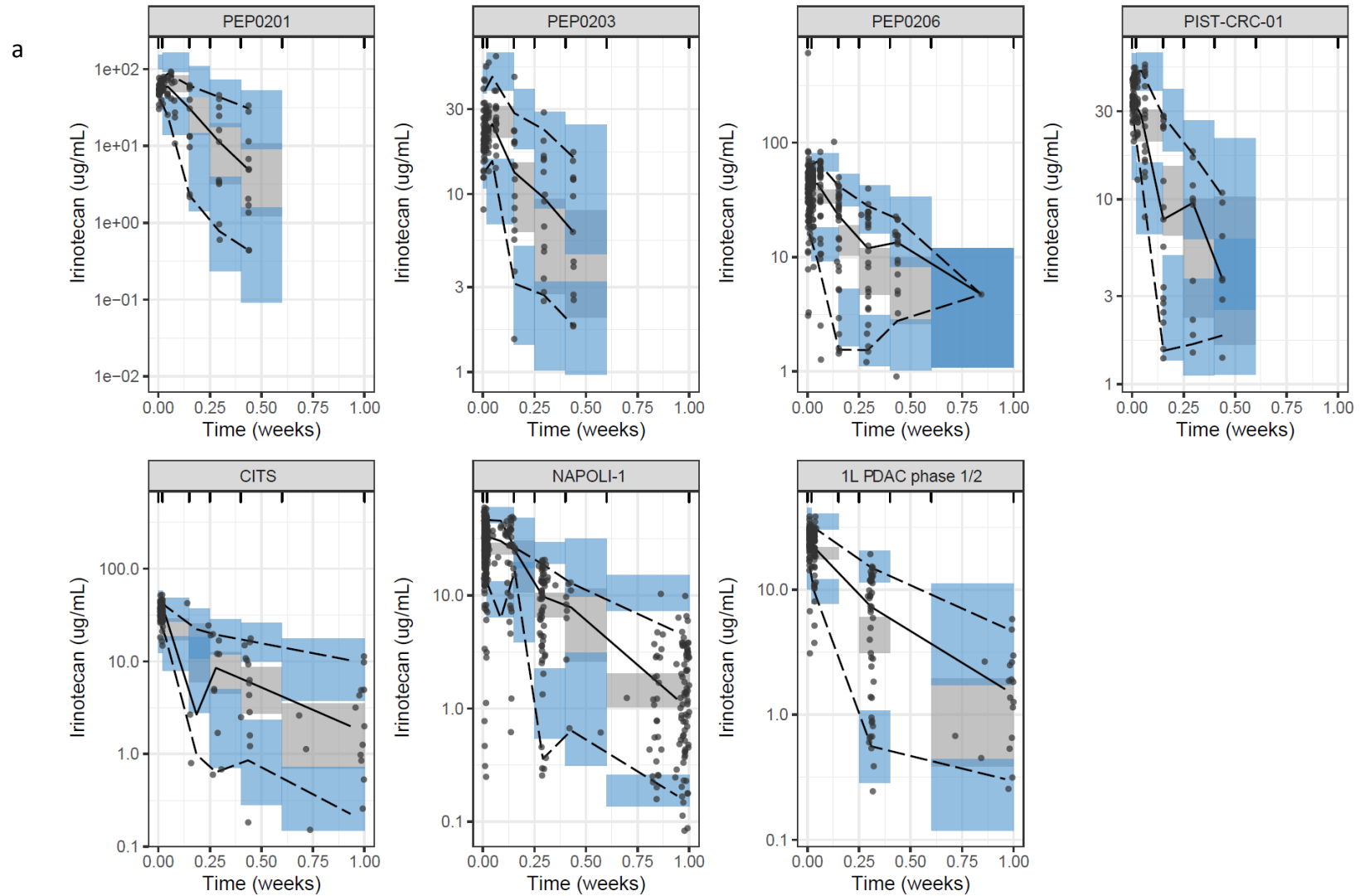
PopPK modeling of liposomal irinotecan

Figure S4 pcVPCs for total irinotecan (**a**) and SN-38 (**b**) concentrations over time. Raw data are presented. The observed median (green bold line) and 2.5th and 97.5th observed percentiles (green dashed lines) are compared with the 95% confidence intervals (shaded area) for the median (gray area) and the 2.5th and 97.5th percentiles of the simulated ($n = 1000$) data (blue area). Simulated median (red semi-dashed line) and 2.5th and 97.5th simulated percentiles (red dotted line) are overlaid.

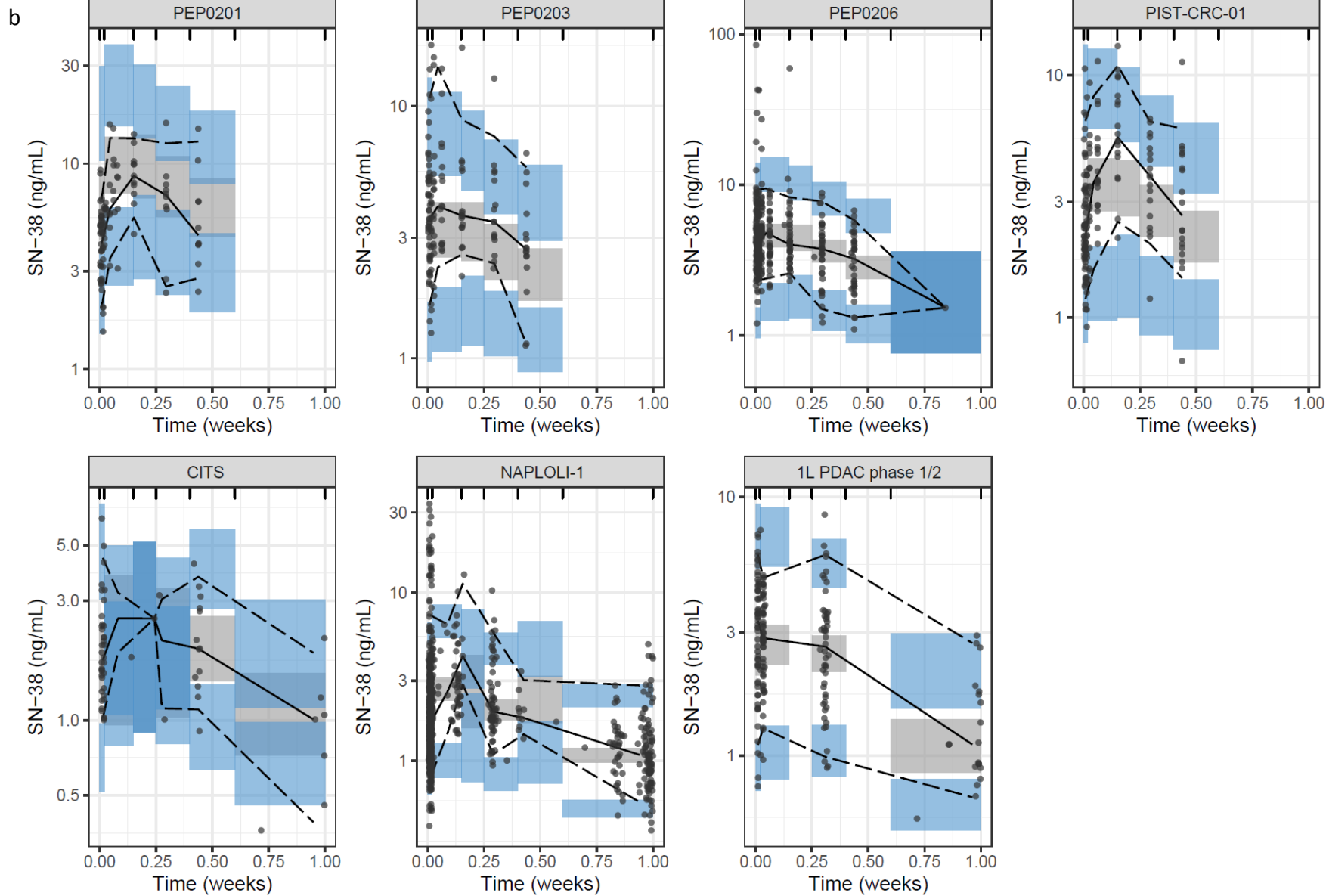


PopPK modeling of liposomal irinotecan

Figure S5 pcVPCs for total irinotecan (a) and SN-38 (b) concentrations over time. Raw data are presented by study. The median (bold line) and 2.5th and 97.5th percentiles (dashed lines) are compared with the 95% confidence intervals (shaded area) for the median (gray area) and the 2.5th and 97.5th percentiles of the simulated ($n = 1000$) data (blue area).

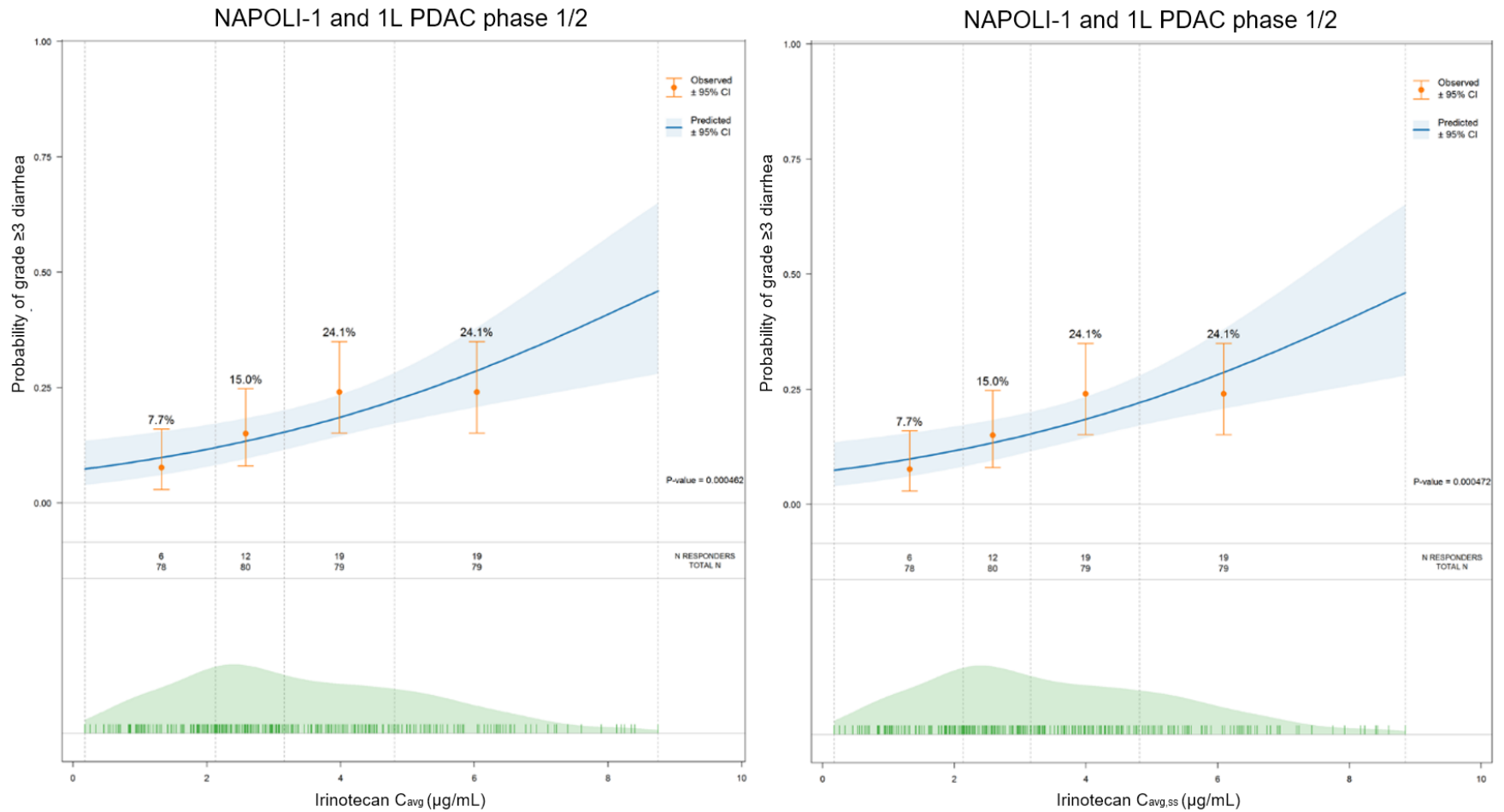


PopPK modeling of liposomal irinotecan



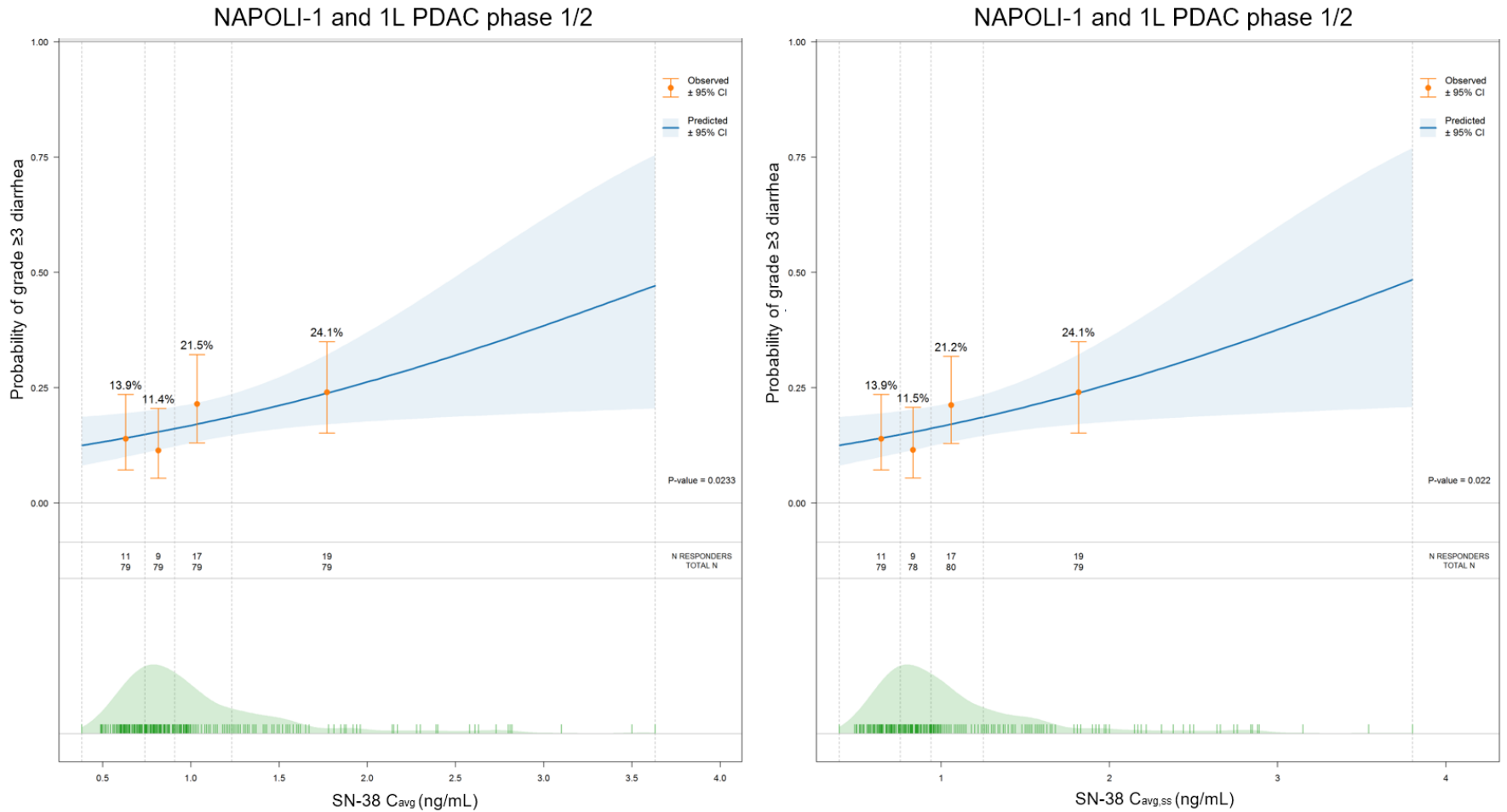
PopPK modeling of liposomal irinotecan

Figure S6 Probability of developing grade ≥ 3 diarrhea as a function of C_{avg} at first event (**left panel**) and $C_{avg,ss}$ for total irinotecan (**right panel**) after administration of liposomal irinotecan. C_{avg} , average plasma concentration; $C_{avg,ss}$, average plasma concentration at steady state; CI, confidence interval



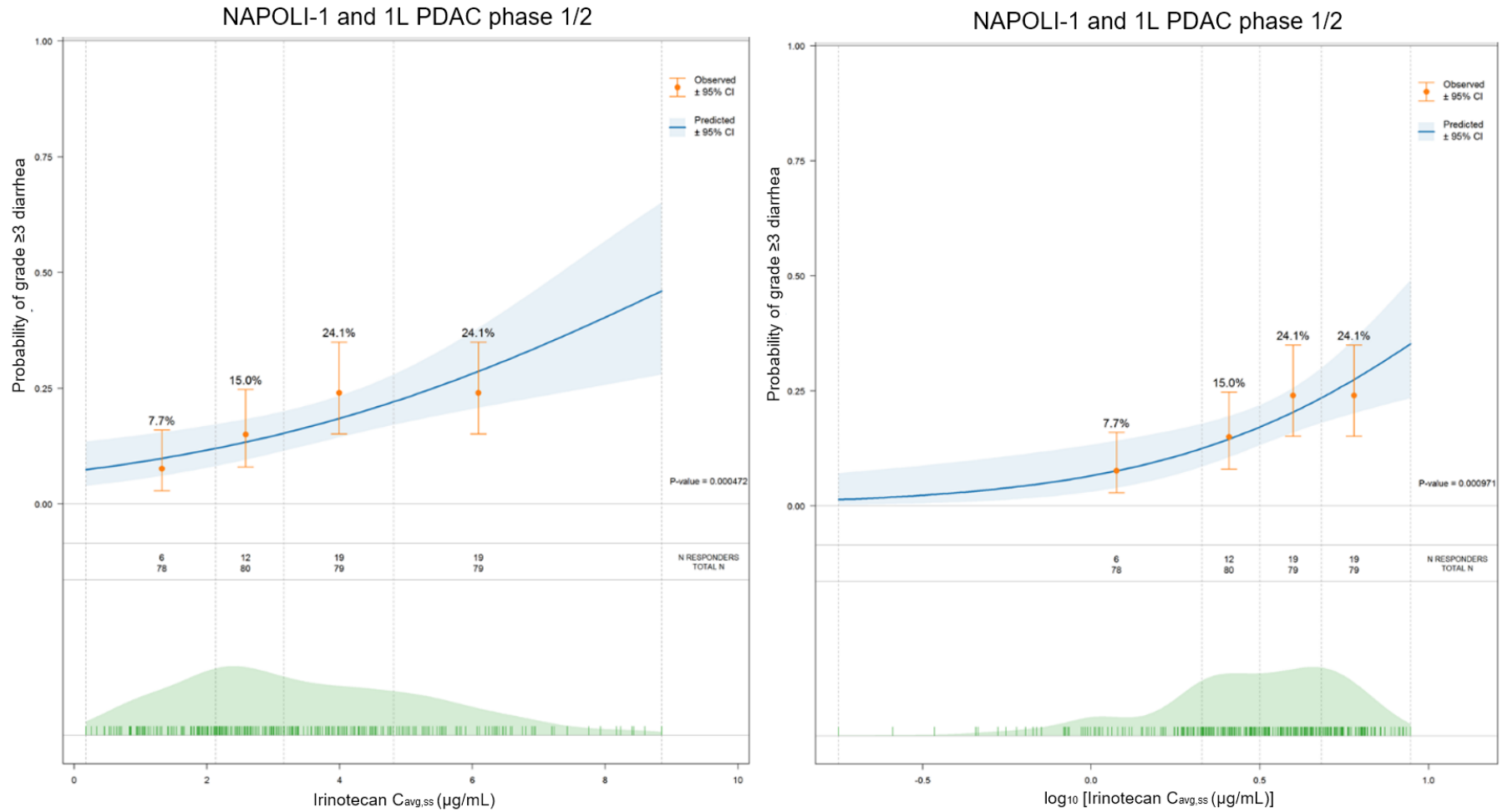
PopPK modeling of liposomal irinotecan

Figure S7 Probability of developing grade ≥ 3 diarrhea as a function of C_{avg} at first event (**left panel**) and $C_{avg,ss}$ for SN-38 (**right panel**) after administration of liposomal irinotecan. C_{avg} , average plasma concentration; $C_{avg,ss}$, average plasma concentration at steady state; CI, confidence interval



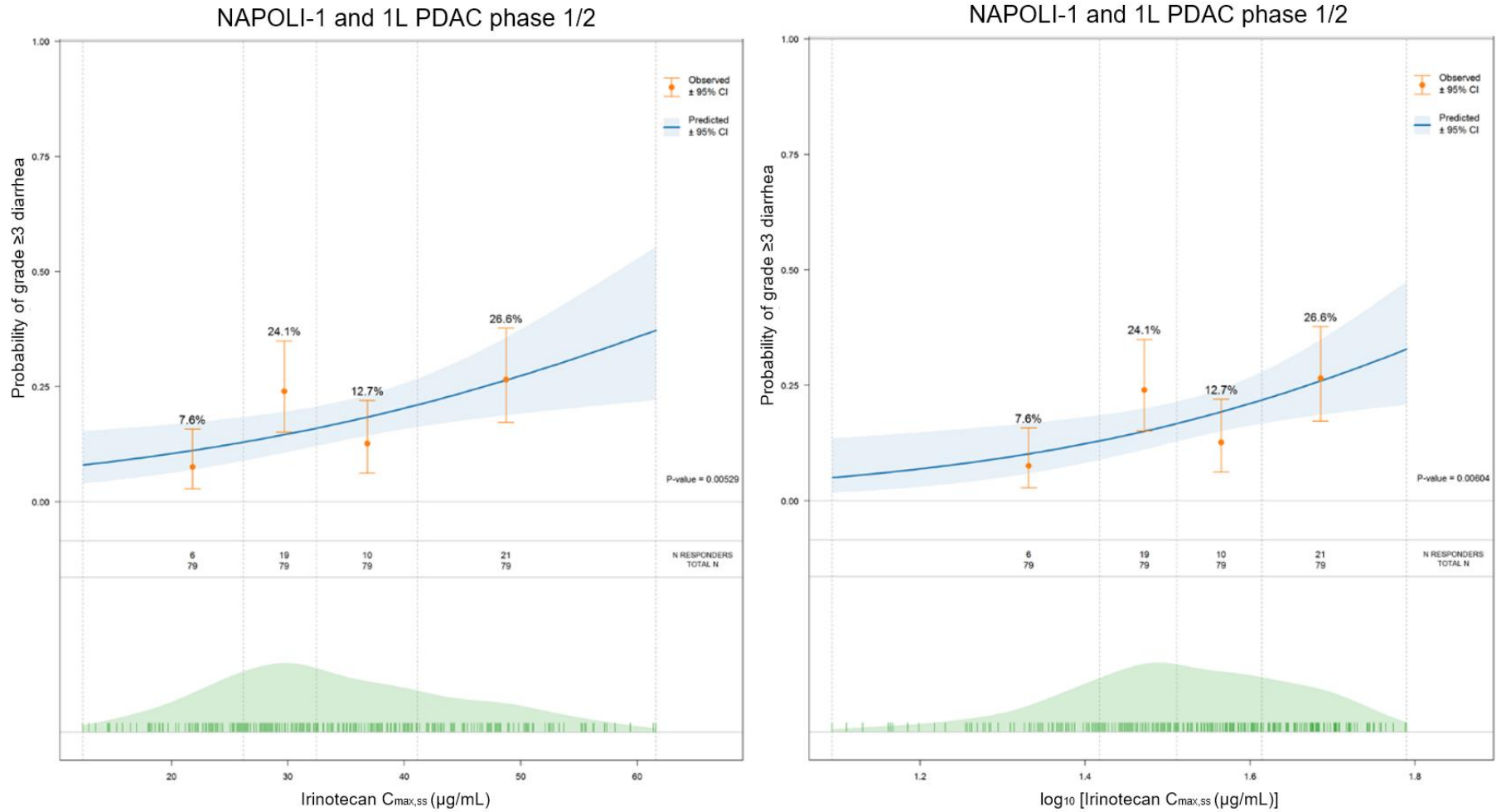
PopPK modeling of liposomal irinotecan

Figure S8 Probability of developing grade ≥ 3 diarrhea as a function of $C_{avg,ss}$ (**left panel**) and log-transformed $C_{avg,ss}$ for total irinotecan (**right panel**) after administration of liposomal irinotecan. $C_{avg,ss}$, average plasma concentration at steady state; CI, confidence interval



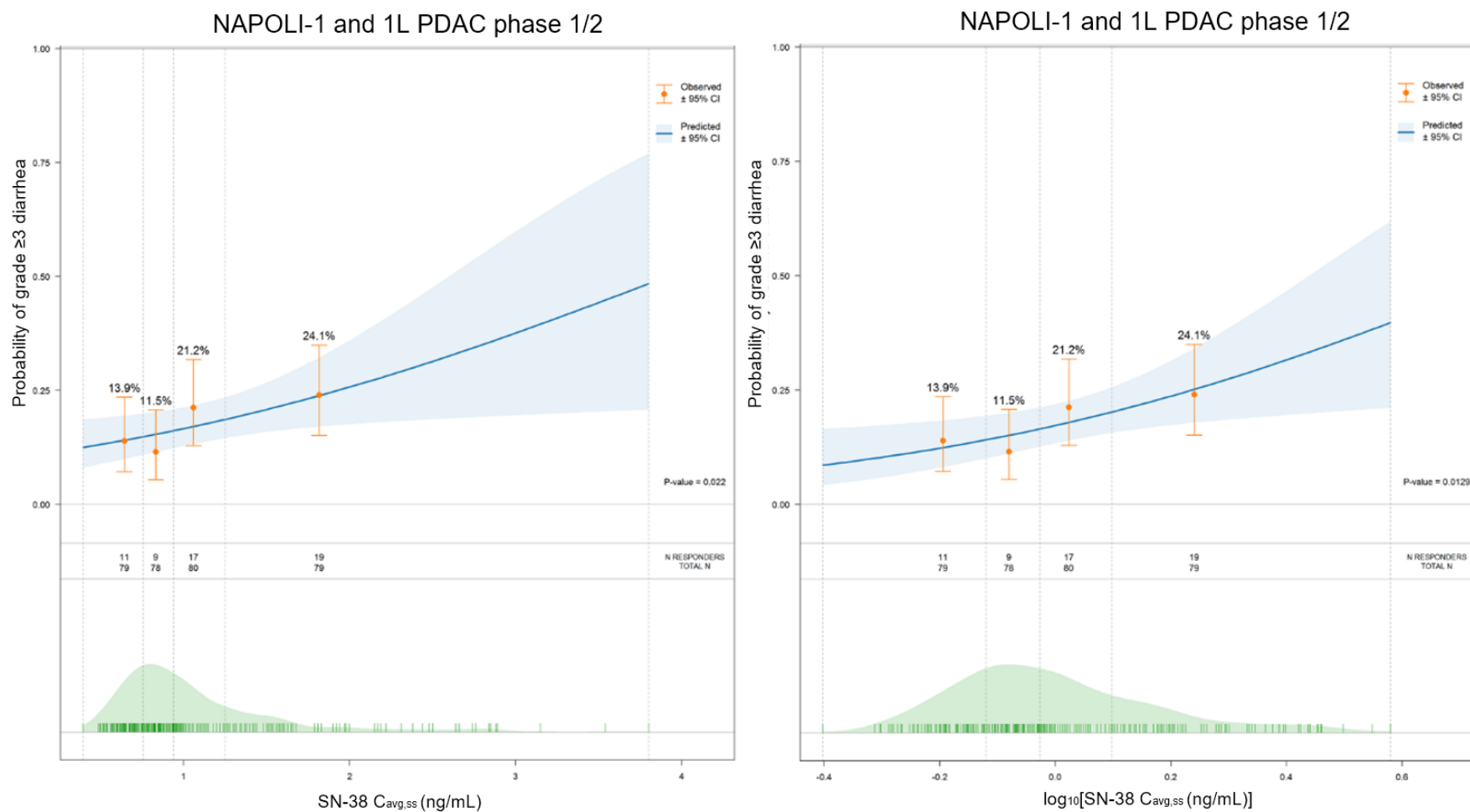
PopPK modeling of liposomal irinotecan

Figure S9 Probability of developing grade ≥ 3 diarrhea as a function of $C_{max,ss}$ (**left panel**) and log-transformed $C_{max,ss}$ for total irinotecan (**right panel**) after administration of liposomal irinotecan. $C_{max,ss}$, maximum plasma concentration at steady state; CI, confidence interval



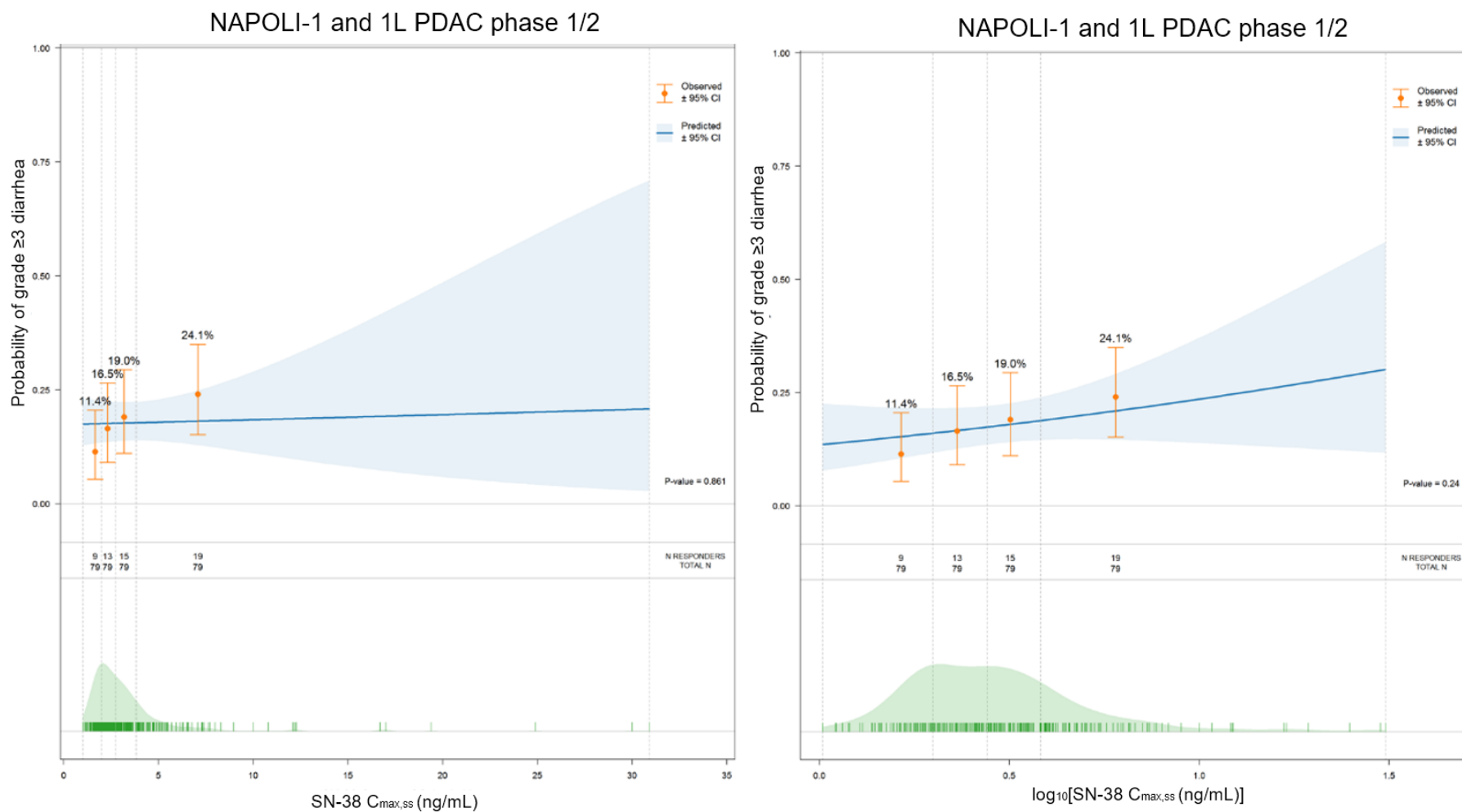
PopPK modeling of liposomal irinotecan

Figure S10 Probability of developing grade ≥ 3 diarrhea as a function of $C_{avg,ss}$ (**left panel**) and log-transformed $C_{avg,ss}$ for SN-38 (**right panel**) after administration of liposomal irinotecan. $C_{avg,ss}$, average plasma concentration at steady state; CI, confidence interval



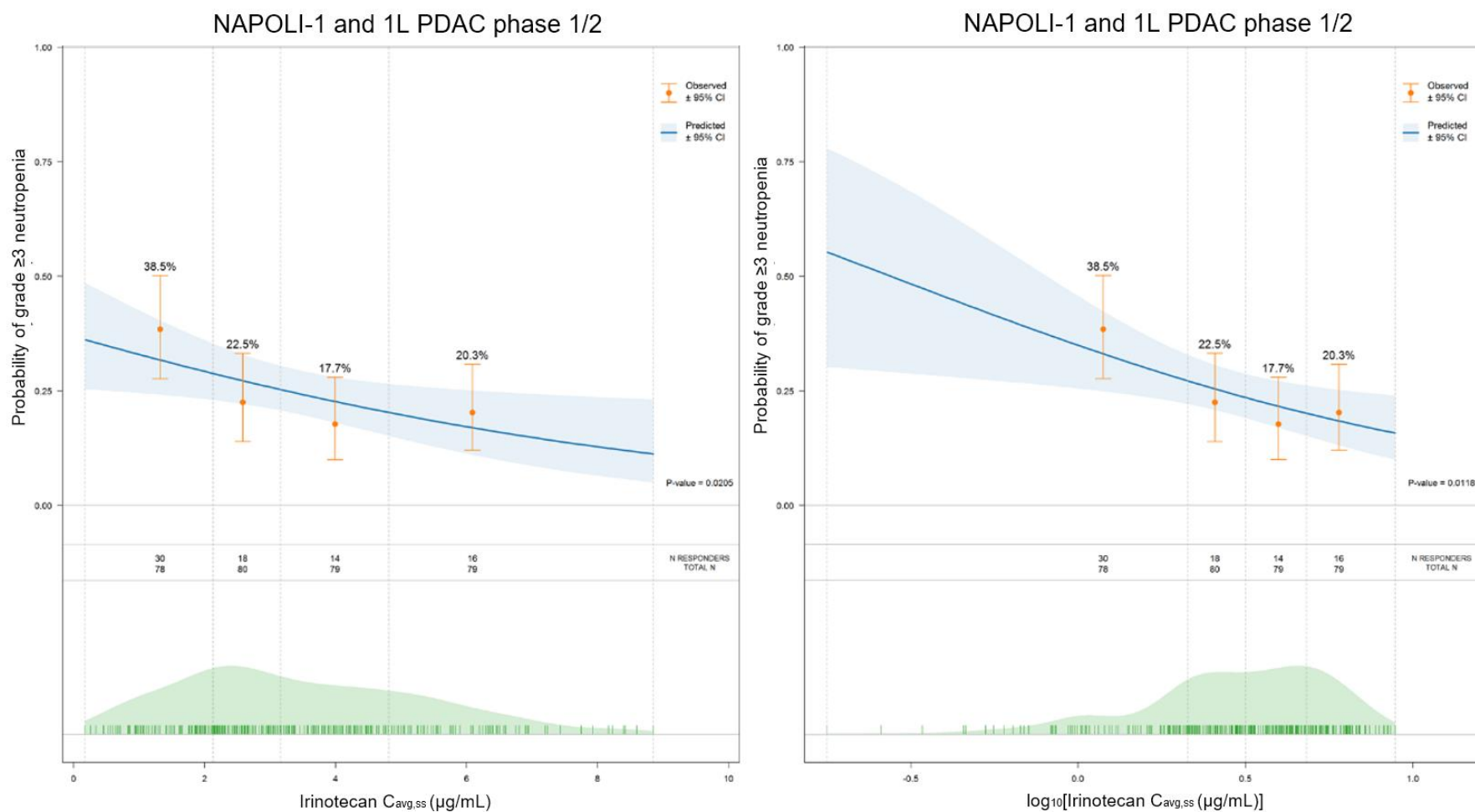
PopPK modeling of liposomal irinotecan

Figure S11 Probability of developing grade ≥ 3 diarrhea as a function of $C_{\max,ss}$ (**left panel**) and log-transformed $C_{\max,ss}$ for SN38 (**right panel**) after administration of liposomal irinotecan. $C_{\max,ss}$, maximum plasma concentration at steady state; CI, confidence interval



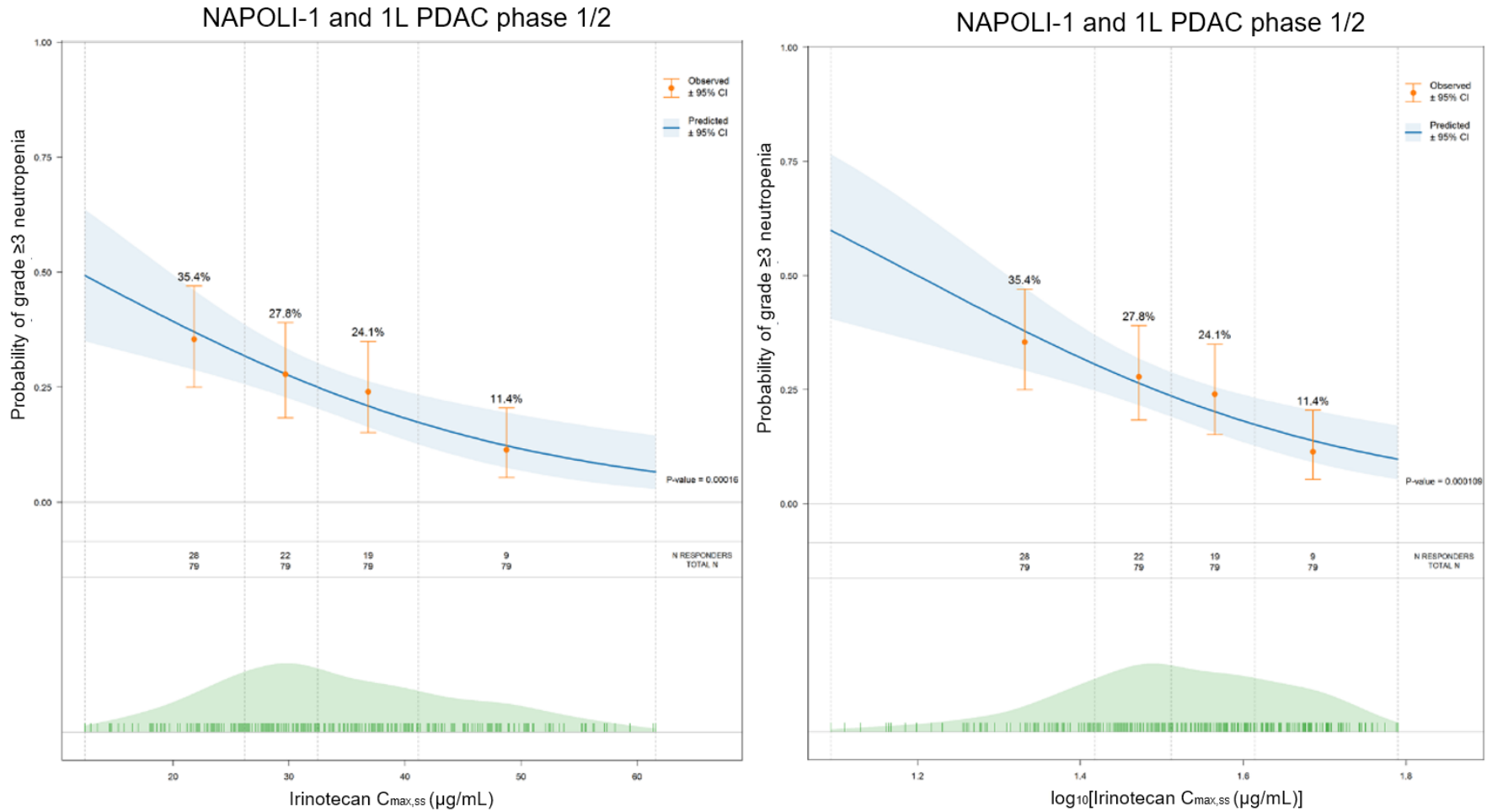
PopPK modeling of liposomal irinotecan

Figure S12 Probability of developing grade ≥ 3 neutropenia as a function of $C_{avg,ss}$ (**left panel**) and log-transformed $C_{avg,ss}$ for total irinotecan (**right panel**) after administration of liposomal irinotecan. $C_{avg,ss}$, average plasma concentration at steady state; CI, confidence interval



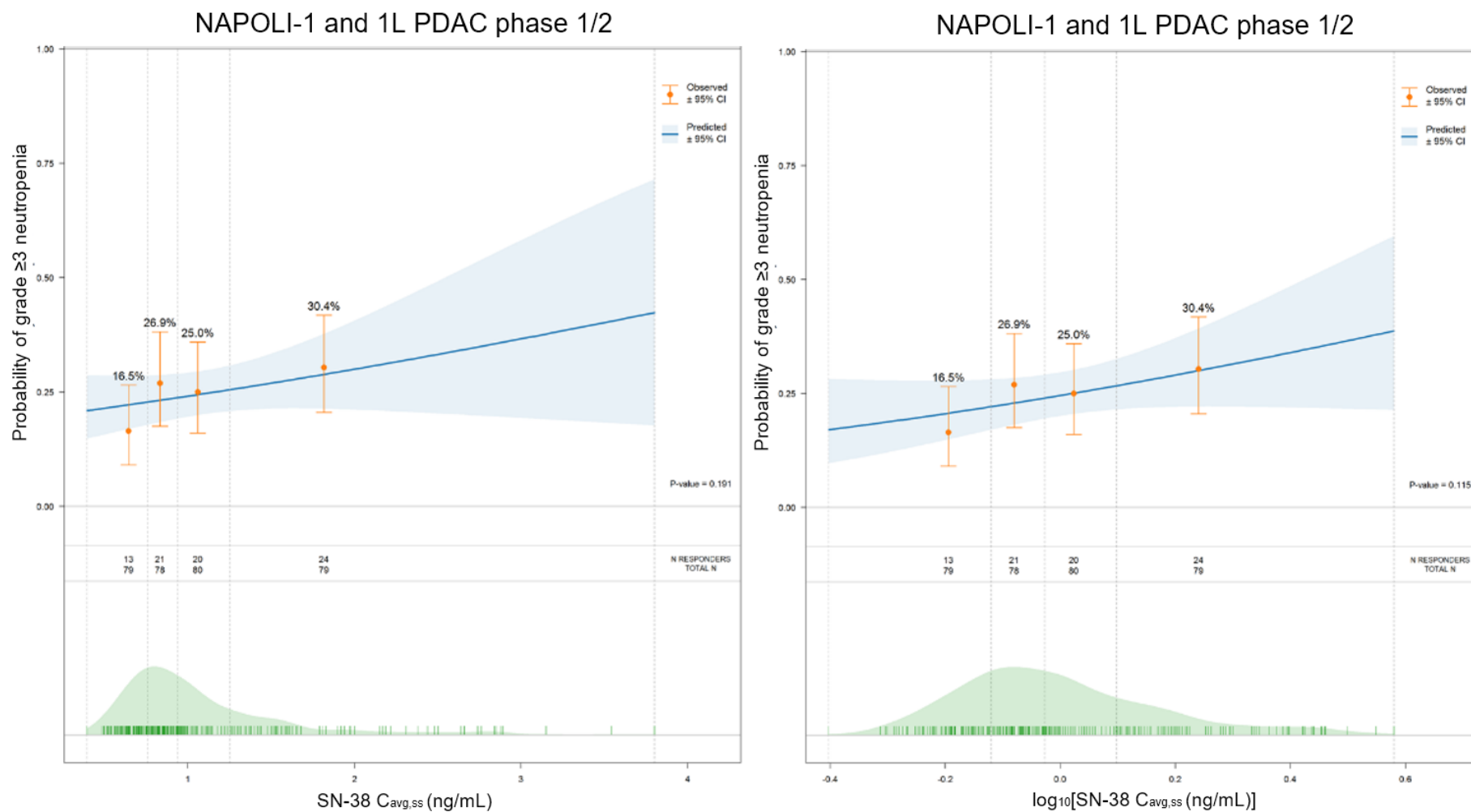
PopPK modeling of liposomal irinotecan

Figure S13 Probability of developing grade ≥ 3 neutropenia as a function of $C_{max,ss}$ (**left panel**) and log-transformed $C_{max,ss}$ for total irinotecan (**right panel**) after administration of liposomal irinotecan. $C_{max,ss}$, maximum plasma concentration at steady state; CI, confidence interval



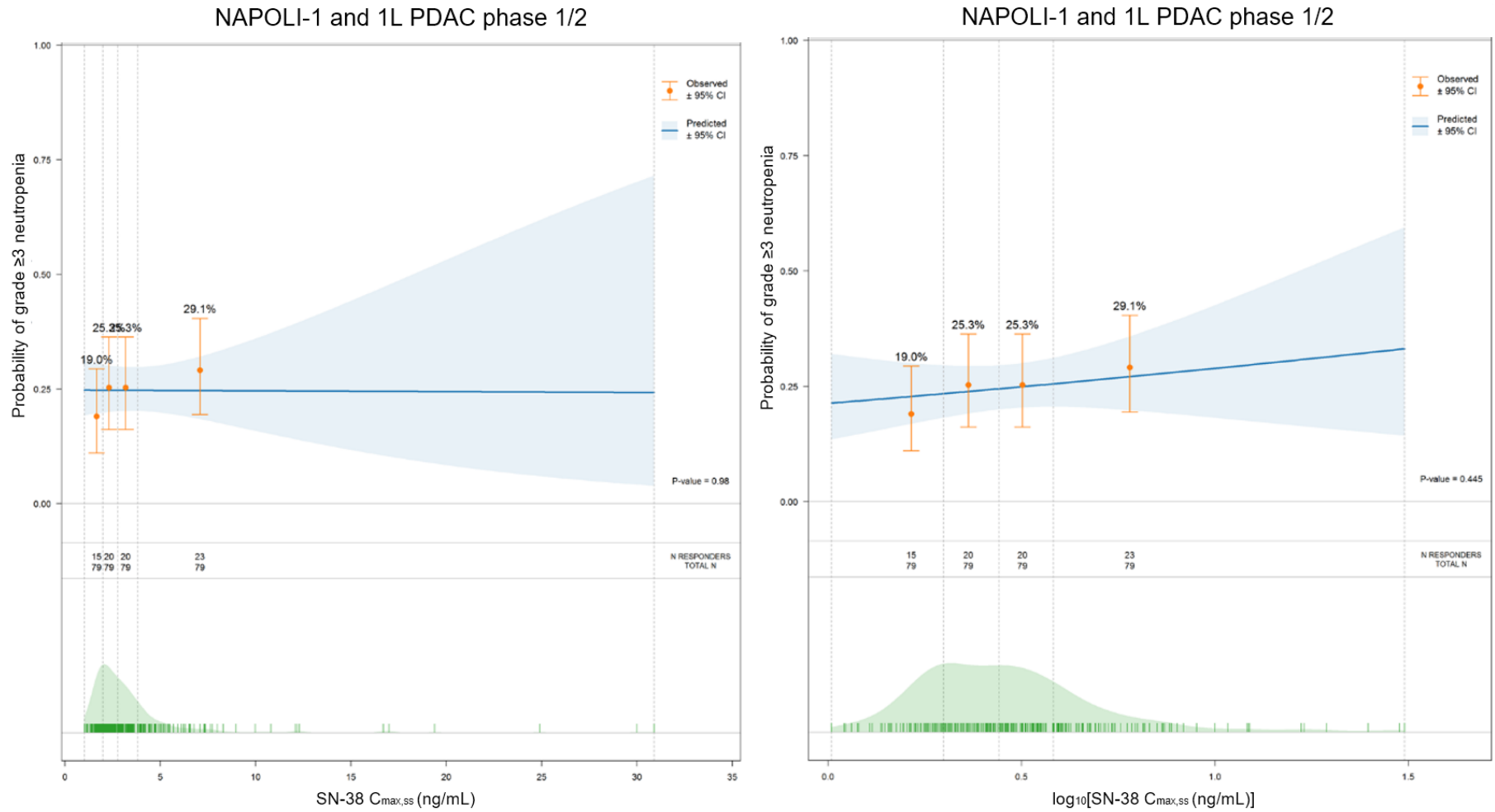
PopPK modeling of liposomal irinotecan

Figure S14 Probability of developing grade ≥ 3 neutropenia as a function of $C_{avg,ss}$ (**left panel**) and log-transformed $C_{avg,ss}$ for SN38 (**right panel**) after administration of liposomal irinotecan. $C_{avg,ss}$, average plasma concentration at steady state; CI, confidence interval



PopPK modeling of liposomal irinotecan

Figure S15 Probability of developing grade ≥ 3 neutropenia as a function of $C_{max,ss}$ (**left panel**) and log-transformed $C_{max,ss}$ for SN38 (**right panel**) after administration of liposomal irinotecan. $C_{max,ss}$, maximum plasma concentration at steady state; CI, confidence interval



PopPK modeling of liposomal irinotecan

Table S1 Continuous and categorical covariates (*N* = 440 patients)

Continuous covariate	Mean (SD)	Median (range)
Age, years	61 (11)	62 (28–87)
Albumin, g/dL	3.9 (0.47)	4 (2.1–5.1)
ALT, IU/L	31 (23)	24 (4–202)
Bilirubin, mg/dL	0.51 (0.26)	0.41 (0.12–2.11)
BSA, m ²	1.73 (0.22)	1.71 (1.29–2.48)
CrCl (mL/min)	88 (30)	85 (27–177)
Categorical covariate	Proportion of patients, %	
Asian		
Yes	35.2	
No	64.8	
Gender		
Male	51.4	
Female	48.6	
Liver metastasis		
Yes	43.2	
No	26.8	
Missing	30	
Manufacturing site		
Old	18.6	
Actual	81.4	
Co-administration with 5FU/LV		
Yes	42.7	
No	57.3	
Co-administration with oxaliplatin		
Yes	12.7	
No	87.3	
UGT1A1*28 homozygous 7/7		
Yes	6.1	
No	93.9	

5FU/LV, 5-fluorouracil/leucovorin; ALT, alanine aminotransferase; BSA, body surface area; CrCl, creatinine clearance; SD, standard deviation

PopPK modeling of liposomal irinotecan

Table S2 Comparison of the effect of the M1 and M3 methods on parameters generated using the base model

Parameter	Base model (M1 method) estimate, RSE%	Base model (M3 method) estimate, RSE%	Wald test statistics
[CLP]	18.6 (4.3)	24.1 (8)	2.63 (S)
[VCP]	3.71 (1.60)	3.57 (1216)	0.003 (NS)
[QP]	1.48 (29.4)	1.1 (2473)	0.014 (NS)
[V3P]	0.453 (21.9)	0.325 (7631)	0.005 (NS)
[FR1]	0.195 (23.7)	0.477 (51.6)	1.12 (NS)
[FR2]	0.841 (24.9)	2.8 (55)	1.26 (NS)
[KFM]	2.13 (4.70)	2.42 (16.4)	0.71 (NS)
[CLM]	18100 (11.4)	26400 (1856)	0.017 (NS)
[PR_P]	0.25 (6%)	0.269 (38.7)	–
[PR_M]	0.283 (5%)	0.304 (17.7)	–
[IIV_CLM]	0.203 (9.9)	0.212 (49.5)	–
[IIV_KFM]	0.122 (31.1)	0.115 (52.20)	–
[IIV_CLP]	0.554 (9.7)	0.77 (60.3)	–
[IIV_FR1]	0.722 (13.20)	2.47 (2.4)	–
[IIV_FR2]	0.185 (46.9)	0.957 (9)	–
[IIV_VCP]	0.0735 (26.1)	0.0668 (0.5)	–

CLM, SN-38 clearance; CLP, total irinotecan clearance; FR1, fraction of irinotecan metabolized by first-order process; FR2, fraction of irinotecan metabolized via transit; IIV, inter-individual variation; KFM, rate of transformation after delay; PR M, proportional residual error for SN-38; PR P, proportional residual error for total irinotecan; QP, inter-compartmental clearance for total irinotecan; RSE, residual standard error; V3P, irinotecan peripheral volume; VCP, irinotecan central volume of distribution

PopPK modeling of liposomal irinotecan

Table S3 Estimated population PK parameters from the final model and performance of the PK model (bootstrap results)

Parameter	Estimate	RSE, %	Bootstrap results, median (95% CI)
Irinotecan total clearance, L/week	17.9	5.14	17.8 (16.3, 19.7)
Asian race ^a	1.204	44.6	0.192 (0.0423, 0.377)
Manufacturing site ^a	1.515	27.9	0.547 (0.275, 0.82)
Gender ^a	0.799	23.5	-0.199 (-0.292, -0.106)
Oxaliplatin administration ^a	1.339	28.1	0.345 (0.166, 0.547)
Irinotecan central volume, L	4.09	2.23	4.07 (3.92, 4.26)
Body surface area ^b	$(BSA/1.71)^{0.573}$	17.9	0.587 (0.383, 0.786)
Manufacturing site ^a	0.872	29.4	-0.117 (-0.19, -0.0576)
Gender ^a	0.886	22.9	-0.116 (-0.167, -0.066)
Fraction of delayed irinotecan total rate of elimination	0.629	23.4	0.625 (0.399, 1.02)
Manufacturing site ^a	1.376	41	0.379 (0.124, 0.677)
Fraction of direct irinotecan total rate of elimination	0.152	22.4	0.15 (0.095, 0.248)
Irinotecan inter-compartmental clearance, L/week	1.35	28.6	1.28 (0.681, 2.22)
Irinotecan peripheral volume, L	0.421	22.6	0.405 (0.177, 0.628)
SN-38 total clearance, L/week	19 800	12.8	19 700 (15 000, 24 900)
Bilirubin ^b	$(BIL/0.41)^{-0.266}$	17.5	-0.234 (-0.326, -0.15)
Creatinine clearance ^b	$(CrCL/85.04)^{0.25}$	28.7	0.235 (0.0821, 0.368)
Gender ^a	0.802	20.3	-0.198 (-0.278, -0.121)
Oxaliplatin administration ^a	0.656	14.1	-0.346 (-0.432, -0.235)
Rate of transformation after delay, 1/week	2	5.1	2.01 (1.81, 2.19)
Between-patient variability			
Irinotecan total clearance	0.545 (CV, 85.2%)	11	0.532 (0.428, 0.647)
Irinotecan central volume	0.066 (CV, 26.1%)	27.5	0.0577 (0.036, 0.0938)
Fraction of delayed irinotecan total rate of elimination	0.188 (CV, 45.4%)	26.4	0.19 (0.09, 0.286)
Fraction of direct irinotecan total rate of elimination	0.928 (CV, 124%)	10.9	0.916 (0.737, 1.12)

PopPK modeling of liposomal irinotecan

Parameter	Estimate	RSE, %	Bootstrap results, median (95% CI)
SN-38 total clearance	0.126 (CV, 36.6%)	13.6	0.123 (0.0892, 0.155)
Rate of transformation after delay	0.135 (CV, 38%)	29.1	0.133 (0.0576, 0.216)
Covariance (correlation) between irinotecan total clearance and fraction of direct transformation	-0.558 (-0.785)	12	-0.55 (-0.681, -0.434)
Covariance (correlation) between irinotecan total clearance and central volume	0.117 (0.617)	17.8	0.109 (0.0758, 0.154)
Covariance (correlation) between irinotecan central volume and fraction of direct transformation	-0.103 (-0.416)	24.4	-0.0952 (-0.147, -0.052)
Residual error			
Proportional error on irinotecan	0.243 (CV, 24.3%)	6.25	0.24 (0.215, 0.27)
Proportional error on SN-38	0.291 (CV, 29.1%)	5.23	0.289 (0.26, 0.317)
Correlation between irinotecan and SN-38 errors	0.323	26.4	0.279 (0.149, 0.399)

BIL, bilirubin; BSA, body surface area; CI, confidence interval; CrCL, creatinine clearance; CV, coefficient of variation; PK, pharmacokinetic; RSE, relative standard error

^aCategorical covariates

^bContinuous covariates:

irinotecan total clearance, $i = 17.9 \times 1.204^{ASIAN} \times 1.515^{Manufacturing\ site} \times 0.799^{Gender} \times 1.339^{Oxaliplatin\ coadministration}$

irinotecan central volume, $i = 4.09 \times \left(\frac{BSA, i^{0.573}}{1.71}\right) \times 0.872^{Manufacturing\ site} \times 0.886^{Gender}$

fraction of delayed irinotecan total rate of elimination, $i = 0.629 \times 1.376^{Manufacturing\ site}$

fraction of direct irinotecan total rate of elimination, $i = 0.152$

irinotecan intercompartmental clearance, $i = 1.35$

irinotecan peripheral volume, $i = 0.421$

SN - 38 total clearance, $i = 19\ 800 \times \left(\frac{BIL, i^{-0.266}}{0.41}\right) \times \left(\frac{CrCL, i^{0.25}}{85.04}\right) \times 0.802^{Gender} \times 0.656^{Oxaliplatin\ coadministration}$