



## The WWARN Malaria Data Inventory - Data Dictionary

This is freely available to use as a reference guide for understanding the data variables listed in data files stored in the WWARN Malaria Data Inventory. This file is subject to change, to access the latest version of this file, please visit the WWARN website page here: <https://www.wwarn.org/accessing-data>. To ask questions relating to the dictionary, please email: info@wwarn.org

### Please note these important considerations when reviewing the WWARN Data Dictionary:

Not every study contributed to WWARN collected all the variables listed in the Data Dictionary

In a publication, Data Contributors may have reported collecting data listed in the Data Dictionary, but may not have shared those variables with WWARN

Occasionally some studies contain data listed in the Data Dictionary that will require curation before release. The vast majority of data is already fully curated and this only happens for very old data sets or data that may have been shared incrementally. We will let you know after receiving your request if the data requires curation and the time this is expected to take.

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
<strong>SUBJECT TABLE</strong>						
Subject	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Subject	site	This is the name of the study site for the subject.				
Subject	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Subject	mepid	This is for multiple-episode subject identification. For longitudinal studies (which are split up into episodes, each having its own <b>pid</b> ) this identifier signals the individual subjects having those multiple episodes. For example, subject 001 has three episodes of malaria during a study. This subject will have <b>pid</b> values of 001_1, 001_2, and 001_3 - all of these episodes will have a value of 001 in the <b>mepid</b> column, indicating the episodes all happened to the same individual.				
Subject	obsdate	For this table this is the information of the Time and Date of Inclusion (see <b>dateinc</b> and <b>timeinc</b> ). It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD).		YYYY-MM-DD HH:MM:SS		
Subject	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the visit. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> . <b>Note:</b> This will always be "0 days" as <b>obsdate</b> in this table = <b>dateinc timeinc</b> .		days (cumulative)		
Subject	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the visit. It is based on the <b>timeofobs</b> in this table in relation to <b>timeinc</b> in the <b>Subject Table</b> being hour 0. The unit is <u>cumulative number of hours since Day0Hour0</u> . Note: This will always be "0 hours" as <b>obsdate</b> in this table = <b>dateinc timeinc</b> .		hours (cumulative)		
Subject	ageyears	This is the age of the subject at enrollment. Ages under one year will be provided as a decimal (e.g., 7 months = 0.58 years). The default unit for the repository is years.		years	100	0
Subject	gender	This is the sex of the subject.	M=Male   F=Female			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Subject	height	This is the height of the subject at enrollment. The default unit for the repository is centimetres.		cm	250	30
Subject	weight	This is the weight of the subject at enrollment. The default unit for the repository is kilograms.		kg	120	1
Subject	muac	This is the Mid-Upper Arm Circumference (MUAC) of the subject at enrollment. The default unit for the repository is millimetres.		mm	500	80
Subject	lastdayfup	This is the day number of the last day the subject was followed-up.		days	120	0
Subject	dateinc	This is the date the subject was included in the trial. This corresponds with the date of the first dose of antimalarial treatment. Note: This is a required variable in our system. If no inclusion date is provided in the raw data, a "dummy" inclusion date will be gleaned from publications or protocols, generally coinciding with the reported start of the trial. Dummy dates are easily identified as they are the same for every subject in that study. Note: If only a few subjects within the group are missing a date of inclusion they will be dropped from the repository.		YYYY-MM-DD		
Subject	dateenrollment	This is the date the subject was enrolled in the trial (if it differs from the date of first treatment). For longitudinal studies, this records the date of the enrollment for the first malaria episode and will be the same date for the subject across all subsequent malaria episodes.		YYYY-MM-DD		
Subject	datelfu	This is the date of the last day the subject was followed-up.		YYYY-MM-DD		
Subject	timeinc	This is the time the subject was included in the trial. This corresponds with the time of the first dose of antimalarial treatment.		HH:MM:SS		
Subject	bmi	This is the body mass index (BMI) of the subject at enrollment. The default unit for the repository is kilograms/metre <sup>2</sup> .		kg/m <sup>2</sup>	100	1
Subject	pregnancy	This is the pregnancy status of the subject at enrollment.	1=Pregnant   0=Not Pregnant			
Subject	ega	This is the estimated gestational age (EGA) for the pregnancy for pregnant subjects. The default unit for the repository is weeks.		weeks	45	5
Subject	sympmal	This indicates whether the subject presented with any malaria symptoms ("malaria symptoms" as defined by the data contributor) on the day of enrollment.	1=Yes   0=No			
Subject	healthy	This indicates whether the subject was a healthy volunteer (i.e., does not have a malaria infection).	1=Yes   0=No			
Subject	DateConsent	This is the date the subject signed informed consent.		YYYY-MM-DD		
Subject	hadmlrbfore	This indicates whether the subject had any previous instances of malaria in the last 28 days.	1=Yes   0=No			
Subject	amrlrbfore	This indicates whether the subject took any anti-malarial medications (as reported by the contributor) in the last 28 days.	1=Yes   0=No			
Subject	g6pd	This indicates the G6PD status of the subject.	Normal   Deficient   Borderline   Don't know			
Subject	g6pd_sample_type	This indicates the sample type used for the G6PD test given.	Filter paper spot   Whole blood			
Subject	g6pd_test_type	This is a description of the G6PD test given.	Quantitative   Qualitative   Both			
Subject	hiv_serology	This is the result of an HIV serology test for the subject.	Positive   Negative   No tested   Not known			
Subject	marital_status	This is the marital status of the subject. This variable is only mapped for studies involving pregnant women (Malaria In Pregnancy studies).	Single   Married/Cohabiting   Widowed   Separated/Divorced   Not known			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Subject	literacy	This is the literacy status of the subject. This variable is only mapped for studies involving pregnant women (Malaria In Pregnancy studies).	Literate   Illiterate   Not known			
Subject	highest_education	This is the educational status of the subject. This variable is only mapped for studies involving pregnant women (Malaria In Pregnancy studies).	No Schooling   Primary   Secondary   Professional   University   Not known			
Subject	est_delivery_date	This indicates the estimated date of delivery for the subject. This variable is only mapped for studies involving pregnant women (Malaria In Pregnancy studies).		YYYY-MM-DD		
Subject	period_date	This indicates the date of the last menstrual period of the subject. This variable is only mapped for studies involving pregnant women (Malaria In Pregnancy studies).		YYYY-MM-DD		
Subject	bed_net_use	This indicates whether the subject slept under a bed net in the previous week. This variable is only mapped for studies involving pregnant women (Malaria In Pregnancy studies).	Yes   No   Provided use unknown   Not known			
<b>CLINICAL TABLE</b>						
Clinical	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Clinical	site	This is the name of the study site for the subject.				
Clinical	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Clinical	obsdate	For this table this is the timing information of the clinical visit. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		
Clinical	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the clinical visit. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
Clinical	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the clinical visit. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
Clinical	feverhist	This indicates whether the subject reported a fever in the last 24 hours.	1=Yes   0=No			
Clinical	fever	This indicates whether the subject presented with a fever on the day of the visit.	1=Yes   0=No			
Clinical	diarrhea	This indicates whether the subject presented with diarrhea on the day of the visit.	1=Yes   0=No			
Clinical	spleen	This indicates whether the subject presented with splenomegaly on the day of the visit.	1=Yes   0=No			
Clinical	liver	This indicates whether the subject presented with hepatomegaly on the day of the visit.	1=Yes   0=No			
Clinical	vomit	This indicates whether the subject presented with vomiting on the day of the visit.	1=Yes   0=No			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Clinical	sympmal2	This indicates whether the subject presented with any malaria symptoms ("malaria symptoms" as defined by the data contributor) on the day of the visit. This is where multiple visits having symptomatic malaria can be recorded - the presence of symptomatic malaria at baseline is captured in the Subject Table in the variable <b>sympmal</b> . Any additional measurements of malaria symptoms are recorded here in the <b>Clinical Table</b> , with one row per measurement.	1=Yes   0=No			
Clinical	thermo	This notes the location of the body temperature measurement recorded in <b>temp</b> .	OR=Oral   TY=Tympanic   RE=Rectal   AX=Axial			
Clinical	temp	This is the subject's recorded body temperature at the visit. The default unit for the repository is degrees Celsius.		celsius	42	34
Clinical	pulse_rate	This is the subject's recorded pulse rate at the visit. The default unit for the repository is beats per minute.		beats/min	250	30
Clinical	systolic_bp	This is the subject's recorded systolic blood pressure at the visit. The default unit for the repository is millimetres of mercury.		mm/Hg	200	30
Clinical	diastolic_bp	This is the subject's recorded diastolic blood pressure at the visit. The default unit for the repository is millimetres of mercury.		mm/Hg	250	30
Clinical	respiration_rate	This is the subject's recorded respiration rate at the visit. The default unit for the repository is breaths per minute.		breaths/min	90	1
Clinical	variable_weight	This is the subject's recorded weight at the visit. The default unit for the repository is kilograms. This is where multiple weight measurements can be recorded - the weight at baseline is captured in the <b>Subject Table</b> in the variable <b>weight</b> . Any additional measurements of weight are recorded here in the <b>Clinical Table</b> , with one row per measurement.		kg	120	1
Clinical	variable_height	This is the subject's recorded height at the visit. The default unit for the repository is centimetres. This is where multiple height measurements can be recorded - the height at baseline is captured in the <b>Subject Table</b> in the variable <b>height</b> . Any additional measurements of height are recorded here in the <b>Clinical Table</b> , with one row per measurement.		cm	250	30
Clinical	variable_bmi	This is the subject's recorded body mass index (BMI) at the visit. The default unit for the repository is kilograms/metre <sup>2</sup> . This is where multiple BMI measurements can be recorded - the BMI at baseline is captured in the <b>Subject Table</b> in the variable <b>bmi</b> . Any additional measurements of bmi are recorded here in the <b>Clinical Table</b> , with one row per measurement.		kg/m <sup>2</sup>	100	1
Clinical	variable_muac	This is the subject's recorded mid upper arm circumference (MUAC) at the visit. The default unit for the repository is millimetres. This is where multiple MUAC measurements can be recorded - the MUAC at baseline is captured in the <b>Subject Table</b> in the variable <b>muac</b> . Any additional measurements of muac are recorded here in the <b>Clinical Table</b> , with one row per measurement.		mm	500	80
Clinical	fetal_heart_rate1	This is the recorded fetal heart rate at the visit of a pregnant woman. The default unit for the repository is beats per minute.		beats/min	500	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
<b>MOLECULAR TABLE</b>						
Molecular	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Molecular	site	This is the name of the study site for the subject.				
Molecular	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Molecular	obsdate	For this table this is the timing information the blood sample taken for genotyping was collected. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		
Molecular	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> that the blood sample taken for genotyping was collected. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative</u> number of days since Day0Hour0.		days (cumulative)		
Molecular	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> that the blood sample taken for genotyping was collected. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative</u> number of hours since Day0Hour0.		hours (cumulative)		
Molecular	moi	This is the number of <i>Plasmodium falciparum</i> infections present, detected by PCR genotyping.				
Molecular	pfrm1cn	This is the number of copies of the pfrm1 gene.				
Molecular	pvmr1cn	This is the number of copies of the pvmr1 gene.				
Molecular	pfcrt_72	This is the genotype of the pfcrt gene at amino acid 72.	C   S   C/S   Not genotyped   Genotyping Failure			
Molecular	pfcrt_73	This is the genotype of the pfcrt gene at amino acid 73.	V   Not genotyped   Genotyping Failure			
Molecular	pfcrt_74	This is the genotype of the pfcrt gene at amino acid 74.	M   I   M/I   Not genotyped   Genotyping Failure			
Molecular	pfcrt_75	This is the genotype of the pfcrt gene at amino acid 75.	N   E   N/E   Not genotyped   Genotyping Failure			
Molecular	pfcrt_76	This is the genotype of the pfcrt gene at amino acid 76.	K   T   K/T   Not genotyped   Genotyping Failure			
Molecular	pfcrt_77	This is the genotype of the pfcrt gene at amino acid 77.	I   Not genotyped   Genotyping Failure			
Molecular	pfcrt_78	This is the genotype of the pfcrt gene at amino acid 78.	F   Not genotyped   Genotyping Failure			
Molecular	pfcrt_97	This is the genotype of the pfcrt gene at amino acid 97.	H   L   Q   H/L   H/Q   L/Q   Not genotyped   Genotyping Failure			
Molecular	pfcrt_144	This is the genotype of the pfcrt gene at amino acid 144.	A   F   T   Y   A/F   A/T   A/Y   F/T   F/Y   T/Y   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	pfcrt_148	This is the genotype of the pfcrt gene at amino acid 148.	L   I   L/I   Not genotyped   Genotyping Failure			
Molecular	pfcrt_152	This is the genotype of the pfcrt gene at amino acid 152.	T   A   T/A   Not genotyped   Genotyping Failure			
Molecular	pfcrt_160	This is the genotype of the pfcrt gene at amino acid 160.	L   Y   L/Y   Not genotyped   Genotyping Failure			
Molecular	pfcrt_163	This is the genotype of the pfcrt gene at amino acid 163.	S   R   S/R   Not genotyped   Genotyping Failure			
Molecular	pfcrt_194	This is the genotype of the pfcrt gene at amino acid 194.	I   T   I/T   Not genotyped   Genotyping Failure			
Molecular	pfcrt_218	This is the genotype of the pfcrt gene at amino acid 218.	I   Not genotyped   Genotyping Failure			
Molecular	pfcrt_219	This is the genotype of the pfcrt gene at amino acid 219.	S   Not genotyped   Genotyping Failure			
Molecular	pfcrt_220	This is the genotype of the pfcrt gene at amino acid 220.	A   S   A/S   Not genotyped   Genotyping Failure			
Molecular	pfcrt_271	This is the genotype of the pfcrt gene at amino acid 271.	Q   E   Q/E   Not genotyped   Genotyping Failure			
Molecular	pfcrt_326	This is the genotype of the pfcrt gene at amino acid 326.	N   D   S   N/D   N/S   D/S   Not genotyped   Genotyping Failure			
Molecular	pfcrt_333	This is the genotype of the pfcrt gene at amino acid 333.	T   S   T/S   Not genotyped   Genotyping Failure			
Molecular	pfcrt_352	This is the genotype of the pfcrt gene at amino acid 352.	Q   Not genotyped   Genotyping Failure			
Molecular	pfcrt_356	This is the genotype of the pfcrt gene at amino acid 356.	I   L   T   I/L   I/T   L/T   Not genotyped   Genotyping Failure			
Molecular	pfcrt_371	This is the genotype of the pfcrt gene at amino acid 371.	R   I   T   R/I   R/T   I/T   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_16	This is the genotype of the pfdhfr gene at amino acid 16.	A   V   A/V   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_50	This is the genotype of the pfdhfr gene at amino acid 50.	C   R   C/R   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_51	This is the genotype of the pfdhfr gene at amino acid 51.	N   I   N/I   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_59	This is the genotype of the pfdhfr gene at amino acid 59.	C   R   C/R   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_108	This is the genotype of the pfdhfr gene at amino acid 108.	S   N   T   N/T   S/T   S/N   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_140	This is the genotype of the pfdhfr gene at amino acid 140.	V   Not genotyped   Genotyping Failure			
Molecular	pfdhfr_164	This is the genotype of the pfdhfr gene at amino acid 164.	I   L   I/L   Not genotyped   Genotyping Failure			
Molecular	pfdhps_431	This is the genotype of the pfdhps gene at amino acid 431.	V   I   I/V   Not genotyped   Genotyping Failure			
Molecular	pfdhps_436	This is the genotype of the pfdhps gene at amino acid 436.	S   A   F   C   Y   H   S/A   S/F   S/C   S/Y   A/F   A/C   A/Y   C/F   F/Y   C/Y   Not genotyped   Genotyping Failure			
Molecular	pfdhps_437	This is the genotype of the pfdhps gene at amino acid 437.	A   G   A/G   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	pfdhps_540	This is the genotype of the pfdhps gene at amino acid 540.	K   E   K/E   N   K/N   E/N   Not genotyped   Genotyping Failure			
Molecular	pfdhps_581	This is the genotype of the pfdhps gene at amino acid 581.	A   G   A/G   Not genotyped   Genotyping Failure			
Molecular	pfdhps_613	This is the genotype of the pfdhps gene at amino acid 613.	A   S   T   G   A/S   A/T   S/T   Not genotyped   Genotyping Failure			
Molecular	pfmdr1_86	This is the genotype of the pfmdr1 gene at amino acid 86.	N   Y   N/Y   Not genotyped   Genotyping Failure			
Molecular	pfmdr1_184	This is the genotype of the pfmdr1 gene at amino acid 184.	Y   F   Y/F   Not genotyped   Genotyping Failure			
Molecular	pfmdr1_1034	This is the genotype of the pfmdr1 gene at amino acid 1034.	S   C   S/C   Not genotyped   Genotyping Failure			
Molecular	pfmdr1_1042	This is the genotype of the pfmdr1 gene at amino acid 1042.	N   D   N/D   Not genotyped   Genotyping Failure			
Molecular	pfmdr1_1184	This is the genotype of the pfmdr1 gene at amino acid 1184.	Y   F   Y/F   Not genotyped   Genotyping Failure			
Molecular	pfmdr1_1246	This is the genotype of the pfmdr1 gene at amino acid 1246.	D   Y   D/Y   Not genotyped   Genotyping Failure			
Molecular	pvmdr1_89	This is the genotype of the pvmdr1 gene at amino acid 89.	N   S   N/S   Not genotyped   Genotyping Failure			
Molecular	pvmdr1_500	This is the genotype of the pvmdr1 gene at amino acid 500.	N   D   N/D   Not genotyped   Genotyping Failure			
Molecular	pvmdr1_908	This is the genotype of the pvmdr1 gene at amino acid 908.	M   L   M/L   Not genotyped   Genotyping Failure			
Molecular	pvmdr1_976	This is the genotype of the pvmdr1 gene at amino acid 976.	Y   F   Y/F   Not genotyped   Genotyping Failure			
Molecular	pvmdr1_1076	This is the genotype of the pvmdr1 gene at amino acid 1076.	F   L   F/L   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_13	This is the genotype of the pvdhfr gene at amino acid 13.	I   L   I/L   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_33	This is the genotype of the pvdhfr gene at amino acid 33.	P   L   P/L   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_57	This is the genotype of the pvdhfr gene at amino acid 57.	F   L   I   L/I   F/L   F/I   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_58	This is the genotype of the pvdhfr gene at amino acid 58.	S   R   S/R   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_61	This is the genotype of the pvdhfr gene at amino acid 61.	T   M   T/M   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_117	This is the genotype of the pvdhfr gene at amino acid 117.	S   N   T   N/T   S/N   S/T   Not genotyped   Genotyping Failure			
Molecular	pvdhfr_173	This is the genotype of the pvdhfr gene at amino acid 173.	I   L   F   L/F   I/L   I/F   Not genotyped   Genotyping Failure			
Molecular	pvdhps_382	This is the genotype of the pvdhps gene at amino acid 382.	S   A   C   A/C   S/A   S/C   Not genotyped   Genotyping Failure			
Molecular	pvdhps_383	This is the genotype of the pvdhps gene at amino acid 383.	A   G   A/G   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	pvdhps_512	This is the genotype of the pvdhps gene at amino acid 512.	K   M   T   E   M/T   M/E   T/E   K/M   K/T   K/E   Not genotyped   Genotyping Failure			
Molecular	pvdhps_553	This is the genotype of the pvdhps gene at amino acid 553.	A   G   C   G/C   A/G   A/C   Not genotyped   Genotyping Failure			
Molecular	k13_WT_AnyMut	This indicates if the subject has any mutant genotypes of the k13 gene (Mutant = means at least one amino acid was a mutant; WT = means all amino acids genotyped were wild type; Not genotyped = the k13 gene was not genotyped).	WT   Mutant   Not genotyped			
Molecular	k13_87	This is the genotype of the k13 gene at amino acid 87.	N   K   N/K   Not genotyped   Genotyping Failure			
Molecular	k13_92	This is the genotype of the k13 gene at amino acid 92.	K   N   K/N   Not genotyped   Genotyping Failure			
Molecular	k13_98	This is the genotype of the k13 gene at amino acid 98.	N   T   N/T   Not genotyped   Genotyping Failure			
Molecular	k13_112	This is the genotype of the k13 gene at amino acid 112.	G   E   G/E   Not genotyped   Genotyping Failure			
Molecular	k13_119	This is the genotype of the k13 gene at amino acid 119.	L   Not genotyped   Genotyping Failure			
Molecular	k13_143	This is the genotype of the k13 gene at amino acid 143.	L   P   L/P   Not genotyped   Genotyping Failure			
Molecular	k13_149	This is the genotype of the k13 gene at amino acid 149.	T   S   T/S   Not genotyped   Genotyping Failure			
Molecular	k13_175	This is the genotype of the k13 gene at amino acid 175.	A   T   A/T   Not genotyped   Genotyping Failure			
Molecular	k13_189	This is the genotype of the k13 gene at amino acid 189.	K   T   N   K/T/N   K/T   K/N   T/N   Not genotyped   Genotyping Failure			
Molecular	k13_205	This is the genotype of the k13 gene at amino acid 205.	I   T   I/T   Not genotyped   Genotyping Failure			
Molecular	k13_217	This is the genotype of the k13 gene at amino acid 217.	N   H   N/H   Not genotyped   Genotyping Failure			
Molecular	k13_223	This is the genotype of the k13 gene at amino acid 223.	R   K   R/K   Not genotyped   Genotyping Failure			
Molecular	k13_239	This is the genotype of the k13 gene at amino acid 239.	R   Q   R/Q   Not genotyped   Genotyping Failure			
Molecular	k13_252	This is the genotype of the k13 gene at amino acid 252.	E   Q   E/Q   Not genotyped   Genotyping Failure			
Molecular	k13_255	This is the genotype of the k13 gene at amino acid 255.	R   K   R/K   Not genotyped   Genotyping Failure			
Molecular	k13_258	This is the genotype of the k13 gene at amino acid 258.	L   M   L/M   Not genotyped   Genotyping Failure			
Molecular	k13_281	This is the genotype of the k13 gene at amino acid 281.	D   V   D/V   Not genotyped   Genotyping Failure			
Molecular	k13_287	This is the genotype of the k13 gene at amino acid 287.	G   C   G/C   Not genotyped   Genotyping Failure			
Molecular	k13_334	This is the genotype of the k13 gene at amino acid 334.	F   L   F/L   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	k13_352	This is the genotype of the k13 gene at amino acid 352.	I   T   I/T   Not genotyped   Genotyping Failure			
Molecular	k13_438	This is the genotype of the k13 gene at amino acid 438.	K   N   K/N   Not genotyped   Genotyping Failure			
Molecular	k13_441	This is the genotype of the k13 gene at amino acid 441.	P   L   P/L   Not genotyped   Genotyping Failure			
Molecular	k13_442	This is the genotype of the k13 gene at amino acid 442.	F   V   F/V   Not genotyped   Genotyping Failure			
Molecular	k13_443	This is the genotype of the k13 gene at amino acid 443.	P   S   P/S   Not genotyped   Genotyping Failure			
Molecular	k13_446	This is the genotype of the k13 gene at amino acid 446.	F   I   F/I   Not genotyped   Genotyping Failure			
Molecular	k13_449	This is the genotype of the k13 gene at amino acid 449.	G   A   D   G/A   G/A/D   Not genotyped   Genotyping Failure			
Molecular	k13_452	This is the genotype of the k13 gene at amino acid 452.	D   E   D/E   Not genotyped   Genotyping Failure			
Molecular	k13_458	This is the genotype of the k13 gene at amino acid 458.	N   Y   N/Y   Not genotyped   Genotyping Failure			
Molecular	k13_469	This is the genotype of the k13 gene at amino acid 469.	C   F   Y   C/F   C/Y/F   Not genotyped   Genotyping Failure			
Molecular	k13_470	This is the genotype of the k13 gene at amino acid 470.	W   X   W/X   Not genotyped   Genotyping Failure			
Molecular	k13_471	This is the genotype of the k13 gene at amino acid 471.	R   Not genotyped   Genotyping Failure			
Molecular	k13_474	This is the genotype of the k13 gene at amino acid 474.	T   I   T/I   Not genotyped   Genotyping Failure			
Molecular	k13_476	This is the genotype of the k13 gene at amino acid 476.	M   I   M/I   Not genotyped   Genotyping Failure			
Molecular	k13_478	This is the genotype of the k13 gene at amino acid 478.	T   Not genotyped   Genotyping Failure			
Molecular	k13_479	This is the genotype of the k13 gene at amino acid 479.	K   I   K/I   Not genotyped   Genotyping Failure			
Molecular	k13_481	This is the genotype of the k13 gene at amino acid 481.	A   V   A/V   Not genotyped   Genotyping Failure			
Molecular	k13_483	This is the genotype of the k13 gene at amino acid 483.	F   S   F/S   Not genotyped   Genotyping Failure			
Molecular	k13_485	This is the genotype of the k13 gene at amino acid 485.	S   N   S/N   Not genotyped   Genotyping Failure			
Molecular	k13_490	This is the genotype of the k13 gene at amino acid 490.	N   T   N/T   Not genotyped   Genotyping Failure			
Molecular	k13_492	This is the genotype of the k13 gene at amino acid 492.	L   S   L/S   Not genotyped   Genotyping Failure			
Molecular	k13_493	This is the genotype of the k13 gene at amino acid 493.	Y   H   T   Y/H   Y/H/T   Not genotyped   Genotyping Failure			
Molecular	k13_494	This is the genotype of the k13 gene at amino acid 494.	V   I   V/I   Not genotyped   Genotyping Failure			
Molecular	k13_495	This is the genotype of the k13 gene at amino acid 495.	F   L   F/L   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	k13_496	This is the genotype of the k13 gene at amino acid 496.	G   Not genotyped   Genotyping Failure			
Molecular	k13_508	This is the genotype of the k13 gene at amino acid 508.	T   N   T/N   Not genotyped   Genotyping Failure			
Molecular	k13_511	This is the genotype of the k13 gene at amino acid 511.	Y   H   Y/H   Not genotyped   Genotyping Failure			
Molecular	k13_513	This is the genotype of the k13 gene at amino acid 513.	R   Not genotyped   Genotyping Failure			
Molecular	k13_515	This is the genotype of the k13 gene at amino acid 515.	R   K   T   R/K   R/K/T   Not genotyped   Genotyping Failure			
Molecular	k13_516	This is the genotype of the k13 gene at amino acid 516.	D   Y   D/Y   Not genotyped   Genotyping Failure			
Molecular	k13_520	This is the genotype of the k13 gene at amino acid 520.	V   A   V/A   Not genotyped   Genotyping Failure			
Molecular	k13_522	This is the genotype of the k13 gene at amino acid 522.	S   C   S/C   Not genotyped   Genotyping Failure			
Molecular	k13_525	This is the genotype of the k13 gene at amino acid 525.	N   D   N/D   Not genotyped   Genotyping Failure			
Molecular	k13_527	This is the genotype of the k13 gene at amino acid 527.	P   H   L   P/H   Not genotyped   Genotyping Failure			
Molecular	k13_528	This is the genotype of the k13 gene at amino acid 528.	R   G   T   R/G   R/G/T   Not genotyped   Genotyping Failure			
Molecular	k13_532	This is the genotype of the k13 gene at amino acid 532.	C   A   C/A   Not genotyped   Genotyping Failure			
Molecular	k13_533	This is the genotype of the k13 gene at amino acid 533.	G   A   G/A   Not genotyped   Genotyping Failure			
Molecular	k13_537	This is the genotype of the k13 gene at amino acid 537.	N   I   N/I   Not genotyped   Genotyping Failure			
Molecular	k13_538	This is the genotype of the k13 gene at amino acid 538.	G   V   G/V   Not genotyped   Genotyping Failure			
Molecular	k13_539	This is the genotype of the k13 gene at amino acid 539.	R   T   R/T   Not genotyped   Genotyping Failure			
Molecular	k13_542	This is the genotype of the k13 gene at amino acid 542.	C   Y   C/Y   Not genotyped   Genotyping Failure			
Molecular	k13_543	This is the genotype of the k13 gene at amino acid 543.	I   T   I/T   Not genotyped   Genotyping Failure			
Molecular	k13_544	This is the genotype of the k13 gene at amino acid 544.	G   R   G/R   Not genotyped   Genotyping Failure			
Molecular	k13_545	This is the genotype of the k13 gene at amino acid 545.	G   E   G/E   Not genotyped   Genotyping Failure			
Molecular	k13_552	This is the genotype of the k13 gene at amino acid 552.	I   C   I/C   Not genotyped   Genotyping Failure			
Molecular	k13_553	This is the genotype of the k13 gene at amino acid 553.	P   L   P/L   Not genotyped   Genotyping Failure			
Molecular	k13_554	This is the genotype of the k13 gene at amino acid 554.	N   S   N/S   Not genotyped   Genotyping Failure			
Molecular	k13_556	This is the genotype of the k13 gene at amino acid 556.	E   D   E/D   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	k13_557	This is the genotype of the k13 gene at amino acid 557.	A   S   A/S   Not genotyped   Genotyping Failure			
Molecular	k13_558	This is the genotype of the k13 gene at amino acid 558.	Y   H   Y/H   Not genotyped   Genotyping Failure			
Molecular	k13_561	This is the genotype of the k13 gene at amino acid 561.	R   H   C   R/H   R/H/C   Not genotyped   Genotyping Failure			
Molecular	k13_564	This is the genotype of the k13 gene at amino acid 564.	A   V   A/V   Not genotyped   Genotyping Failure			
Molecular	k13_566	This is the genotype of the k13 gene at amino acid 566.	V   I   V/I   Not genotyped   Genotyping Failure			
Molecular	k13_568	This is the genotype of the k13 gene at amino acid 568.	V   G   V/G   Not genotyped   Genotyping Failure			
Molecular	k13_569	This is the genotype of the k13 gene at amino acid 569.	A   T   S   A/T/S   Not genotyped   Genotyping Failure			
Molecular	k13_574	This is the genotype of the k13 gene at amino acid 574.	P   L   P/L   Not genotyped   Genotyping Failure			
Molecular	k13_575	This is the genotype of the k13 gene at amino acid 575.	R   K   R/K   Not genotyped   Genotyping Failure			
Molecular	k13_576	This is the genotype of the k13 gene at amino acid 576.	S   L   S/L   Not genotyped   Genotyping Failure			
Molecular	k13_578	This is the genotype of the k13 gene at amino acid 578.	A   S   A/S   Not genotyped   Genotyping Failure			
Molecular	k13_580	This is the genotype of the k13 gene at amino acid 580.	C   Y   C/Y   Not genotyped   Genotyping Failure			
Molecular	k13_584	This is the genotype of the k13 gene at amino acid 584.	D   V   D/V   Not genotyped   Genotyping Failure			
Molecular	k13_612	This is the genotype of the k13 gene at amino acid 612.	E   D   E/D   Not genotyped   Genotyping Failure			
Molecular	k13_613	This is the genotype of the k13 gene at amino acid 613.	Q   E   Q/E   Not genotyped   Genotyping Failure			
Molecular	k13_614	This is the genotype of the k13 gene at amino acid 614.	F   L   F/L   Not genotyped   Genotyping Failure			
Molecular	k13_617	This is the genotype of the k13 gene at amino acid 617.	A   T   A/T   Not genotyped   Genotyping Failure			
Molecular	k13_619	This is the genotype of the k13 gene at amino acid 619.	L   S   L/S   Not genotyped   Genotyping Failure			
Molecular	k13_621	This is the genotype of the k13 gene at amino acid 621.	A   F   A/F   Not genotyped   Genotyping Failure			
Molecular	k13_637	This is the genotype of the k13 gene at amino acid 637.	V   D   V/D   Not genotyped   Genotyping Failure			
Molecular	k13_667	This is the genotype of the k13 gene at amino acid 667.	P   Q   R   T   L   P/L   P/Q/R/T/L   Not genotyped   Genotyping Failure			
Molecular	k13_675	This is the genotype of the k13 gene at amino acid 675.	A   V   A/V   Not genotyped   Genotyping Failure			
Molecular	k13_676	This is the genotype of the k13 gene at amino acid 676.	A   D   A/D   Not genotyped   Genotyping Failure			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Molecular	k13_701	This is the genotype of the k13 gene at amino acid 701.	P   R   P/R   Not genotyped   Genotyping Failure			
Molecular	k13_719	This is the genotype of the k13 gene at amino acid 719.	H   N   H/N   Not genotyped   Genotyping Failure			
Molecular	k13_725	This is the genotype of the k13 gene at amino acid 725.	N   Y   N/Y   Not genotyped   Genotyping Failure			
<b>OUTCOMES TABLE</b>						
Outcome	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Outcome	site	This is the name of the study site for the subject.				
Outcome	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Outcome	etf	This indicates whether the subject had Early Treatment Failure (ETF) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	lcf	This indicates whether the subject had Late Clinical Failure (LCF) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	ltf	This indicates whether the subject had Late Treatment Failure (LTF) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	lcpf	This indicates whether the subject had Late Clinical or Parasitological Failure (LCPF) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	acpr	This indicates whether the subject had Adequate Clinical and Parasitological Response (ACPR) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	sevmalaria	This indicates whether the subject developed severe malaria as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	death	This indicates whether the subject died, as reported by the data contributor.	1=Yes   0=No			
Outcome	amlr	This indicates whether the subject had a protocol violation by taking any other medications with antimalarial activity (other than indicated study drug) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	lfu	This indicates whether the subject was Lost to Follow-up (LFU) as defined and reported by the data contributor.	1=Yes   0=No			
Outcome	danger	This indicates whether the subject had any symptoms defined as Danger Signs by the WHO as reported by the data contributor.	1=Yes   0=No			
Outcome	wdraw	This indicates whether the subject was withdrawn from the study as defined and reported by the data contributor.	1=Yes   0=No			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Outcome	outcome	This indicates the subject's outcome at the end of the study as defined and reported by the data contributor.	ACPR=Adequate Clinical and Parasitological Response   ETFD=ETF with Death   ETFS=ETF with Severe Malaria   ETFDS=ETF with Danger Signs   ETP=ETF with Parasitological Criteria   ETFC=ETF with Clinical Criteria   ETF=Early Treatment Failure - Not otherwise specified   LCFD=LCF with Death   LCFS=LCF with Severe Malaria   LCFDS=LCF with Danger Signs   LCFF=LCF with Fever (measured or subjective)   LCF=Late Clinical Failure - Not otherwise specified   LPF=Late Parasitological Failure   LCFLPF=LCF/LPF indistinguishable   AE=Adverse Event requiring change in antimalarial therapy prior to completion of full dose of study drug   PD=Treatment Protocol Deviation   D=Death Not Due to Malaria   LFU=Lost to Follow-up   AMLR=Use of other antimalarials outside of study protocol   CW=Withdrawal of Consent by Patient   IW=Investigator-initiated Withdrawal from further follow-up   O=Patient does not complete follow-up for other reason   ED=Enrollment Deviation			
<b>CONCENTRATION TABLE</b>						
Concentration	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Concentration	site	This is the name of the study site for the subject.				
Concentration	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Concentration	obsdate	For this table this is the timing information of the blood draw for the analyte concentration measurement. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Concentration	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the blood draw for the analyte concentration measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
Concentration	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the blood draw for the analyte concentration measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
Concentration	matrix	This describes the sample matrix for all analytes measured. <b>Note:</b> this variable is only populated if the same matrix was used for all measurements. If different analytes used a different matrix, this information will be in the appropriate <b>sample_matrix*</b> variable.	Venous plasma   Capillary plasma   Whole blood			
Concentration	concname1	This is the name of analyte 1 measured.	Amodiaquine   Lumefantrine   Sulfadoxine   Artemether   Dihydroartemisinin   Pyrimethamine   Mefloquine   Desethylamodiaquine   Piperaquine   Desbutyl lumefantrine   Chloroquine   Primaquine   Artesunate			
Concentration	metconcname1	This is the name of metabolite 1 measured.	Desbutyl lumefantrine   Desethylamodiaquine   Desethyl-chloroquine   Dihydroartemisinin   Carboxy-primaquine			
Concentration	sample_matrix1	This describes the sample matrix for the analyte named in <b>concname1</b> or <b>metconcname1</b> .	Venous plasma   Capillary plasma   Whole blood			
Concentration	concentration1	This is the concentration of the analyte named in <b>concname1</b> .		ng/ml	1.00E+09	0
Concentration	metconcentration1	This is the concentration of the metabolite named in <b>metconcname1</b> .		ng/ml	1.00E+09	0
Concentration	loq1	This is the lowest level of quantification of the analyte named in <b>concname1</b> .		ng/ml	100	1
Concentration	mloq1	This is the lowest level of quantification of the metabolite named in <b>metconcname1</b> .		ng/ml	100	1
Concentration	bloq1	This indicates the sample for the analyte named in <b>concname1</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	mbloq1	This indicates the sample for the metabolite named in <b>metconcname1</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	concname2	This is the name of analyte 2 measured.	Amodiaquine   Lumefantrine   Sulfadoxine   Artemether   Dihydroartemisinin   Pyrimethamine   Mefloquine   Desethylamodiaquine   Piperaquine   Desbutyl lumefantrine   Chloroquine   Primaquine   Artesunate			
Concentration	metconcname2	This is the name of metabolite 2 measured.	Desbutyl lumefantrine   Desethylamodiaquine   Desethyl-chloroquine   Dihydroartemisinin   Carboxy-primaquine			
Concentration	sample_matrix2	This describes the sample matrix for the analyte named in <b>concname2</b> or <b>metconcname2</b> .	Venous plasma   Capillary plasma   Whole blood			
Concentration	concentration2	This is the concentration of the analyte named in <b>concname2</b> .		ng/ml	1.00E+09	0
Concentration	metconcentration2	This is the concentration of the metabolite named in <b>metconcname2</b> .		ng/ml	1.00E+09	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Concentration	loq2	This is the lowest level of quantification of the analyte named in <b>concname2</b> .		ng/ml	100	1
Concentration	mloq2	This is the lowest level of quantification of the metabolite named in <b>metconcname2</b> .		ng/ml	100	1
Concentration	bloq2	This indicates the sample for the analyte named in <b>concname2</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	mbloq2	This indicates the sample for the metabolite named in <b>metconcname2</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	concname3	This is the name of analyte 3 measured.	Amodiaquine   Lumefantrine   Sulfadoxine   Artemether   Dihydroartemesinin   Pyrimethamine   Mefloquine   Desethylamodiaquine   Piperaquine   Desbutyl lumefantrine   Chloroquine   Primaquine   Artesunate			
Concentration	metconcname3	This is the name of metabolite 3 measured.	Desbutyl lumefantrine   Desethylamodiaquine   Desethyl-chloroquine   Dihydroartemesinin   Carboxy-primaquine			
Concentration	sample_matrix3	This describes the sample matrix for the analyte named in <b>concname3</b> or <b>metconcname3</b> .	Venous plasma   Capillary plasma   Whole blood			
Concentration	concentration3	This is the concentration of the analyte named in <b>concname3</b> .		ng/ml	1.00E+09	0
Concentration	metconcentration3	This is the concentration of the metabolite named in <b>metconcname3</b> .		ng/ml	1.00E+09	0
Concentration	loq3	This is the lowest level of quantification of the analyte named in <b>concname3</b> .		ng/ml	100	1
Concentration	mloq3	This is the lowest level of quantification of the metabolite named in <b>metconcname3</b> .		ng/ml	100	1
Concentration	bloq3	This indicates the sample for the analyte named in <b>concname3</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	mbloq3	This indicates the sample for the metabolite named in <b>metconcname3</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	concname4	This is the name of analyte 4 measured.	Amodiaquine   Lumefantrine   Sulfadoxine   Artemether   Dihydroartemesinin   Pyrimethamine   Mefloquine   Desethylamodiaquine   Piperaquine   Desbutyl lumefantrine   Chloroquine   Primaquine   Artesunate			
Concentration	metconcname4	This is the name of metabolite 4 measured.	Desbutyl lumefantrine   Desethylamodiaquine   Desethyl-chloroquine   Dihydroartemesinin   Carboxy-primaquine			
Concentration	sample_matrix4	This describes the sample matrix for the analyte named in <b>concname4</b> or <b>metconcname4</b> .	Venous plasma   Capillary plasma   Whole blood			
Concentration	concentration4	This is the concentration of the analyte named in <b>concname4</b> .		ng/ml	1.00E+09	0
Concentration	metconcentration4	This is the concentration of the metabolite named in <b>metconcname4</b> .		ng/ml	1.00E+09	0
Concentration	loq4	This is the lowest level of quantification of the analyte named in <b>concname4</b> .		ng/ml	100	1
Concentration	mloq4	This is the lowest level of quantification of the metabolite named in <b>metconcname4</b> .		ng/ml	100	1
Concentration	bloq4	This indicates the sample for the analyte named in <b>concname4</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	mbloq4	This indicates the sample for the metabolite named in <b>metconcname4</b> was below its stated lowest level of quantification.	1=Yes   0=No			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Concentration	concname5	This is the name of analyte 5 measured.	Amodiaquine   Lumefantrine   Sulfadoxine   Artemether   Dihydroartemisinin   Pyrimethamine   Mefloquine   Desethylamodiaquine   Piperaquine   Desbutyl lumefantrine   Chloroquine   Primaquine   Artesunate			
Concentration	metconcname5	This is the name of metabolite 5 measured.	Desbutyl lumefantrine   Desethylamodiaquine   Desethyl-chloroquine   Dihydroartemisinin   Carboxy-primaquine			
Concentration	sample_matrix5	This describes the sample matrix for the analyte named in <b>concname5</b> or <b>metconcname5</b> .	Venous plasma   Capillary plasma   Whole blood			
Concentration	concentration5	This is the concentration of the analyte named in <b>concname5</b> .		ng/ml	1.00E+09	0
Concentration	metconcentration5	This is the concentration of the metabolite named in <b>metconcname5</b> .		ng/ml	1.00E+09	0
Concentration	loq5	This is the lowest level of quantification of the analyte named in <b>concname5</b> .		ng/ml	100	1
Concentration	mloq5	This is the lowest level of quantification of the metabolite named in <b>metconcname5</b> .		ng/ml	100	1
Concentration	bloq5	This indicates the sample for the analyte named in <b>concname5</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	mbloq5	This indicates the sample for the metabolite named in <b>metconcname5</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	concname6	This is the name of analyte 6 measured.	Amodiaquine   Lumefantrine   Sulfadoxine   Artemether   Dihydroartemisinin   Pyrimethamine   Mefloquine   Desethylamodiaquine   Piperaquine   Desbutyl lumefantrine   Chloroquine   Primaquine   Artesunate			
Concentration	metconcname6	This is the name of metabolite 6 measured.	Desbutyl lumefantrine   Desethylamodiaquine   Desethyl-chloroquine   Dihydroartemisinin   Carboxy-primaquine			
Concentration	sample_matrix6	This describes the sample matrix for the analyte named in <b>concname1</b> or <b>metconcname1</b> .	Venous plasma   Capillary plasma   Whole blood			
Concentration	concentration6	This is the concentration of the analyte named in <b>concname6</b> .		ng/ml	1.00E+09	0
Concentration	metconcentration6	This is the concentration of the metabolite named in <b>metconcname6</b> .		ng/ml	1.00E+09	0
Concentration	loq6	This is the lowest level of quantification of the analyte named in <b>concname6</b> .		ng/ml	100	1
Concentration	mloq6	This is the lowest level of quantification of the metabolite named in <b>metconcname6</b> .		ng/ml	100	1
Concentration	bloq6	This indicates the sample for the analyte named in <b>concname6</b> was below its stated lowest level of quantification.	1=Yes   0=No			
Concentration	mbloq6	This indicates the sample for the metabolite named in <b>metconcname6</b> was below its stated lowest level of quantification.	1=Yes   0=No			
<b>ADVERSE EVENTS TABLE</b>						
AdverseEvents	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
AdverseEvents	site	This is the name of the study site for the subject.				

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
AdverseEvents	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
AdverseEvents	raw_term	This is the name/term of the adverse event as provided by the data contributor. This is recorded directly from the raw data and may contain a mixture of words from various languages, spelling mistakes, and multiple AEs recorded together (e.g., "headache and vomiting"). <b>Note:</b> This table will only contain Adverse Events as defined by the contributor (i.e., clinical symptoms not defined as "adverse events" in the raw data will not be placed in this table).				
AdverseEvents	raw_term_details	This contains more details about the adverse event named in <b>raw_term</b> . This is recorded directly from the raw data and may contain a mixture of words from various languages, spelling mistakes, and multiple AEs recorded together (e.g., "headache and vomiting").				
AdverseEvents	preferred_term	This is the MedDRA coded Preferred Term used to describe the adverse event named in <b>raw_term</b> . <b>Note:</b> This MedDRA coding was completed by WWARN.				
AdverseEvents	llt	This is the MedDRA coded Lowest Level Term (LLT) used to describe the adverse event named in <b>raw_term</b> . <b>Note:</b> This MedDRA coding was completed by WWARN.				
AdverseEvents	soc	This is the MedDRA coded System Organ Class (SOC) used to describe the adverse event named in <b>raw_term</b> . <b>Note:</b> This MedDRA coding was completed by WWARN.				
AdverseEvents	hlgt	This is the MedDRA coded Higher Level Group Term (HLGT) used to describe the adverse event named in <b>raw_term</b> . <b>Note:</b> This MedDRA coding was completed by WWARN.				
AdverseEvents	hlt	This is the MedDRA coded Higher Level Term (HLT) used to describe the adverse event named in <b>raw_term</b> . <b>Note:</b> This MedDRA coding was completed by WWARN.				
AdverseEvents	AE_start_date	This is the date the adverse event named in <b>raw_term</b> was reported to have started.		YYYY-MM-DD		
AdverseEvents	AE_start_time	This is the time the adverse event named in <b>raw_term</b> was reported to have started.		HH:MM:SS		
AdverseEvents	AE_stop_date	This is the date the adverse event named in <b>raw_term</b> was reported to have ended.		YYYY-MM-DD		
AdverseEvents	AE_stop_time	This is the time the adverse event named in <b>raw_term</b> was reported to have ended.		HH:MM:SS		
AdverseEvents	AE_continuing	This indicates the adverse event named in <b>raw_term</b> was still occurring at the time the question was asked of the subject.	1=Yes   0=No			
AdverseEvents	AE_severity_grade	This indicates the severity grading of the adverse even named in <b>raw_term</b> .	mild   moderate   severe   life-threatening			
AdverseEvents	AE_primaquine_related	This indicates if the adverse event named in <b>raw_term</b> was determined to be related to the use of Primaquine.	not related   unlikely   possible   probable   definitely   Unassessable/Unclassified   N/A			
AdverseEvents	AE_act_related	This indicates if the adverse event named in <b>raw_term</b> was determined to be related to the use of the ACT administered in the study.	not related   unlikely   possible   probable   definitely   Unassessable/Unclassified   N/A			
AdverseEvents	AE_drug_related	This indicates if the adverse event named in <b>raw_term</b> was determined to be related to the use of the study drug administered.	not related   unlikely   possible   probable   definitely   Unassessable/Unclassified   N/A			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
AdverseEvents	AE_is_SAE	This indicates if the adverse event named in <b>raw_term</b> was considered to be a Serious Adverse Event (SAE).	1=Yes   0=No			
AdverseEvents	SAE_type	This indicates why the adverse event named in <b>raw_term</b> was considered to be a SAE.	results in death   is life-threatening   requires in-patient hospitalisation or prolongation of hospitalisation   results in permanent or significant disability/incapacity   congenital anomaly/birth defect   medically significant   other			
AdverseEvents	SAE_other	This is a further text description of the reason expressed as "other" in the variable <b>SAE_type</b> .				
AdverseEvents	AE_prescribed_drug	This is a text description of any drug prescribed to treat the adverse event named in <b>raw_term</b> . This is recorded directly from the raw data and may contain a mixture of words from various languages, spelling mistakes, and multiple drugs recorded together (e.g., "Clindamycin and Paracetamol").				
AdverseEvents	AE_action_taken	This indicates any action taken to address the adverse event named in <b>raw_term</b> .	none   stopped ACT   prescribed drug   blood transfusion   hospitalisation   other			
AdverseEvents	AE_other_action_taken	This is a further text description of the reason expressed as "other" in the variable <b>AE_action_taken</b> . This is recorded directly from the raw data and may contain a mixture of words from various languages and spelling mistakes.				
AdverseEvents	AE_outcome	This indicates the outcome of the adverse event named in <b>raw_term</b> .	recovered/resolved   recovered/resolved with sequela   recovering/resolving   not recovered/not resolved   fatal   DK			
AdverseEvents	date_of_death	This is the date of the subject's death as a result of the SAE.		YYYY-MM-DD		
AdverseEvents	meddra_version	This is a description of the version of MedDRA used to code the adverse event named in <b>raw_term</b> .				
AdverseEvents	haemoglobinuria	This contains information about the specific Adverse Event - "Presence or absence of free haemoglobin in the subject's urine". The result depends on the raw data provided: if raw data contains "yes" or "no" for presence then it is recorded as such. If the data is reported as a count on the Hillmen Scale (1-10) then the number is recorded.	Yes   No   1   2   3   4   5   6   7   8   9   10			
<b>PCR TABLE</b>						
PCR	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
PCR	site	This is the name of the study site for the subject.				
PCR	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
PCR	pcr	This is the result for the PCR testing to distinguish between reinfection and recrudescence.	RI=reinfection   RC=recrudescence   NA=not applicable   NR=no result available   NPF=non-Pf malaria   IND=indeterminate   O=other			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
<b>BIOCHEMISTRY TABLE</b>						
Biochemistry	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Biochemistry	site	This is the name of the study site for the subject.				
Biochemistry	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Biochemistry	obsdate	For this table this is the timing information of the biochemistry measurement. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> Note: These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		
Biochemistry	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the biochemistry measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
Biochemistry	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the biochemistry measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
Biochemistry	glucose	This is the subject's Glucose result at the visit. The default unit for the repository is milligrams per decilitre.		mg/dL	1000	0
Biochemistry	sodium	This is the subject's Sodium result at the visit. The default unit for the repository is millimoles per litre.		mmol/L	191	100
Biochemistry	potassium	This is the subject's Potassium result at the visit. The default unit for the repository is millimoles per litre.		mmol/L	10	0
Biochemistry	calcium	This is the subject's Calcium result at the visit. The default unit for the repository is milligrams per decilitre.		mg/dL	20	0
Biochemistry	magnesium	This is the subject's Magnesium result at the visit. The default unit for the repository is millimoles per litre.		mmol/L	9.9	0
Biochemistry	bun	This is the subject's Blood Urea Nitrogen (BUN) result at the visit. The default unit for the repository is milligrams per decilitre.		mg/dL	200	0
Biochemistry	creatinine	This is the subject's Creatinine result at the visit. The default unit for the repository is milligrams per decilitre.		mg/dL	20	0
Biochemistry	bilirubin	This is the subject's Total Bilirubin result at the visit. The default unit for the repository is milligrams per decilitre.		mg/dL	75	0
Biochemistry	alatrans	This is the subject's Alanine Transaminase (also referred to as ALT, alanine aminotransferase, ALAT, or SGPT) result at the visit. The default unit for the repository is units per litre.		units/L	5000	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Biochemistry	aspmamtrans	This is the subject's Aspartate Aminotransferase (also referred to as AST, aspartate transaminase, or SGOT) result at the visit. The default unit for the repository is units per litre.		units/L	5000	0
Biochemistry	alkphos	This is the subject's Alkaline Phosphatase (ALP) result at the visit. The default unit for the repository is units per litre.		units/L	10000	0
Biochemistry	albumin	This is the subject's Albumin result at the visit. The default unit for the repository is grams per decilitre.		g/dL	10	0
Biochemistry	totprot	This is the subject's Total Protein result at the visit. The default unit for the repository is grams per decilitre.		g/dL	15	0
<b>ECG TABLE</b>						
ECG	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
ECG	site	This is the name of the study site for the subject.				
ECG	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
ECG	obsdate	For this table this is the timing information of the ECG measurement. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> Note: These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		
ECG	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the ECG measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
ECG	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the ECG measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
ECG	qt	This is the QT interval from the subject's ECG measurement. The default unit for the repository is milliseconds.		ms	900	0
ECG	qtcf	This is the corrected QT interval (using Fredericia's correction formula) from the subject's ECG measurement. The default unit for the repository is milliseconds.		ms	900	0
ECG	qtcb	This is the corrected QT interval (using Bazett's correction formula) from the subject's ECG measurement. The default unit for the repository is milliseconds.		ms	900	0
ECG	heartrate	This is the subject's heart rate from the subject's ECG measurement. The default unit for the repository is beats per minute.		bpm	250	40
ECG	rrinterval	This is the RR interval from the subject's ECG measurement. The default unit for the repository is milliseconds.		ms	2000	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
ECG	printerval	This is the PR interval from the subject's ECG measurement. The default unit for the repository is milliseconds.		ms	500	0
ECG	qrsinterval	This is the QRS interval from the subject's ECG measurement. The default unit for the repository is milliseconds.		ms	500	0
ECG	twaveheight	This is the height of the T Wave from the subject's ECG measurement. The default unit for the repository is millimetres.		mm	15	0
ECG	paperspeed	This is the paper speed of the ECG machine used for the subject's ECG measurement. The default unit for the repository is millimetres per second.		mm/sec	100	10
ECG	reviewmethod	This is the method used to review the subject's ECG measurement (e.g., threshold, tangent).	threshold   tangent   superimposed median beat   automated global median beat   longest QT method   other			
ECG	ecgcategory	This is the category of the ECG machine used for the subject's ECG measurement (e.g. 12-lead, Holter).	Standard 12-lead resting   1-lead (single trace)   3-lead   Holter			
ECG	ecgreadtype	This is the type of read used to review the subject's ECG measurement (e.g. manual, automated).	Manual read   Automated read   Central lab manual   Central lab automatic   Mixed read			
ECG	patientposition	This is the subject's position during the ECG measurement.	Supine   Left-lateral   Upright   Other			
ECG	leadchoice	This is the lead chosen for the ECG measurement recording.	I   II   III   aVR   aVL   aVF   V1   V2   V3   V4   V5   V6   multiple			
ECG	morphologicalchanges	This is a text description of any morphological changes found in the ECG measurement. This is recorded directly from the raw data and may contain a mixture of words from various languages and spelling mistakes.				
ECG	ecgmachinespecification	This is a text description of the ECG machine used for the measurement. This is recorded directly from the raw data and may contain a mixture of words from various languages and spelling mistakes.				
<b>TREATMENT TABLE</b>						
Treatment	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Treatment	site	This is the name of the study site for the subject.				
Treatment	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Treatment	obsdate	For this table this is the timing information of the drug administration. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> Note: These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	dayoftreat	This is a WWARN-calculation of the <u>relative day number</u> of the drug administration. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
Treatment	houroftreat	This is a WWARN-calculation of the <u>relative hour number</u> of the drug administration. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
Treatment	treat	This is the name of the intervention/treatment regimen that the subject received.				
Treatment	superv	This indicates to what level the treatment/intervention named in <b>treat</b> was supervised. Supervised = every drug and every dose was supervised. Unsupervised = nothing at all was supervised. Partial = one drug was supervised or only some doses were supervised.	supervised   unsupervised   partial   unknown			
Treatment	fatamt	This is the amount of fat, in grams, given with each administration of the treatment named in <b>treat</b> .		g	100	0
Treatment	fatdes	This is a text description of the fat administration listed in <b>fatamt</b> (e.g., "given with a snack").				
Treatment	vomdrug	This is an indicator of whether the subject vomited the dose described in <b>treat</b> . The timing of this (e.g., within 30 mins or within 1 hour) is contributor-defined and available in the study metadata tables.	1=Yes   0=No			
Treatment	trt1	This is the name of drug 1 in the intervention/treatment regimen described in <b>treat</b> .	UNKNOWN   AL=Artemether-Lumefantrine   AM=Artemether   A-PQP   AQ=Amodiaquine   AN=Artemisinin-Naphthoquine   AS=Artesunate   AS-AQ=Artesunate-Amodiaquine   AS-MQ=Artesunate-Mefloquine   ART=Artemisinin   AV=Atovaquone   AV-PG=Atovaquone-Proguanil   CL=Clindamycin   CP=Chlorproguanil   CQ=Chloroquine   DAP=Dapsone   DHA=Dihydroartemisinin   DHA-PQP=Dihydroartemisinin-Piperaquine   DHA-PQP-TR=Dihydroartemisinin-Piperaquine-Triparanol   DOX=Doxycycline   HL=Halofantrine   CP-DAP=Chlorproguanil-Dapsone   LUM=Lumefantrine   MQ=Mefloquine   PG=Proguanil   PQ=Primaquine   PQP=Piperaquine   PYR=Pyrimethamine   QN=Quinine   SP=Sulfadoxine-Pyrimethamine   SX=Sulfadoxine   TET=Tetracycline   SMP=Sulfamethoxypyrazine-Pyrimethamine   PYN-AS=Artesunate-Pyronaridine   IVM=Ivermectin			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	dos1	This is the dose amount of the drug named in <b>trt1</b> . This is a record of the amount of drug <u>given at each administration</u> – either the number of tablets/pills or the amount in mg/ml of the drug (NOT mg/kg). A separate line will appear in the treatment table for EVERY instance of drug given (e.g., a drug given 3 times a day will have 3 entries for each day of treatment).				
Treatment	dostot1	This is the total dose amount for the entire treatment period of the drug named in <b>trt1</b> . It is the <u>total dose for the entire treatment period</u> – either the number of tablets/pills or the amount in mg/ml of the drug. This amounts to the total number of pills taken / the total mg of drug received by the subject (e.g., for a treatment regime of once a day for 3 days – this would be the value of 3 times the daily dose).				
Treatment	mgperKg1	This is the total daily dose amount in mg/kg of the drug named in <b>trt1</b> . It is the <u>total DAILY mg/kg dose for each treatment DAY</u> – (not a per-instance count – must be the cumulative total of the entire treatment day. e.g., a drug given 3 times a day will be added up to get the total dose for that day to calculate the mg/kg for that day).		mg/kg		
Treatment	dosing1	This is the total dose amount in mg/kg of the drug named in <b>trt1</b> . It is the <u>total mg/kg dose for the entire treatment period</u> – (NOT a daily count – must be the cumulative total of the entire treatment time).		mg/kg	1000	0
Treatment	dosunit1	This is the unit (e.g., tablet, mg, mL) of the dose of the drug named in <b>trt1</b> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			
Treatment	route1	This is the route of administration (e.g., oral, IV) of the drug named in <b>trt1</b> .	Inhal=inhalation   Instill=instillation   N=nasal   O=oral   P=parenteral   R=rectal   SL=sublingual/buccal   TD=transdermal   V=vaginal			
Treatment	dosrepeat1	This is an indicator of whether the dose for <b>trt1</b> was repeated after vomiting. This will be mapped to the time and date of the ORIGINAL dose that was vomited since it is a measure of IF the dose was repeated (not of the time and date of the redose).	1=Yes   0=No			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	trt2	This is the name of drug 2 in the intervention/treatment regimen described in <b>treat</b> .	UNKNOWN   AL=Artemether-Lumefantrine   AM=Artemether   A-PQP   AQ=Amodiaquine   AN=Artemisinin-Naphthoquine   AS=Artesunate   AS-AQ=Artesunate-Amodiaquine   AS-MQ=Artesunate-Mefloquine   ART=Artemisinin   AV=Atovaquone   AV-PG=Atovaquone-Proguanil   CL=Clindamycin   CP=Chlorproguanil   CQ=Chloroquine   DAP=Dapsone   DHA=Dihydroartemisinin   DHA-PQP=Dihydroartemisinin-Piperaquine   DHA-PQP-TR=Dihydroartemisinin-Piperaquine-Trimethoprim   DOX=Doxycycline   HL=Halofantrine   CP-DAP=Chlorproguanil-Dapsone   LUM=Lumefantrine   MQ=Mefloquine   PG=Proguanil   PQ=Primaquine   PQP=Piperaquine   PYR=Pyrimethamine   QN=Quinine   SP=Sulfadoxine-Pyrimethamine   SX=Sulfadoxine   TET=Tetracycline   SMP=Sulfamethoxypyrazine-Pyrimethamine   PYN-AS=Artesunate-Pyronaridine   IVM=Ivermectin			
Treatment	dos2	This is the dose amount of the drug named in <b>trt2</b> . This is a record of the amount of drug <u>given at each administration</u> – either the number of tablets/pills or the amount in mg/ml of the drug (NOT mg/kg). A separate line will appear in the treatment table for EVERY instance of drug given (e.g., a drug given 3 times a day will have 3 entries for each day of treatment).				
Treatment	dostot2	This is the total dose amount for the entire treatment period of the drug named in <b>trt2</b> . It is the total dose for <u>the entire treatment period</u> – either the number of tablets/pills or the amount in mg/ml of the drug. This amounts to the total number of pills taken / the total mg of drug received by the subject (e.g., for a treatment regime of once a day for 3 days – this would be the value of 3 times the daily dose).				
Treatment	mgperKg2	This is the total daily dose amount in mg/kg of the drug named in <b>trt2</b> . It is the <u>total DAILY mg/kg dose for each treatment DAY</u> – (not a per-instance count – must be the cumulative total of the entire treatment day. e.g., a drug given 3 times a day will be added up to get the total dose for that day to calculate the mg/kg for that day).		mg/kg		
Treatment	dosing2	This is the total dose amount in mg/kg of the drug named in <b>trt2</b> . It is the <u>total mg/kg dose for the entire treatment period</u> – (NOT a daily count – must be the cumulative total of the entire treatment time).		mg/kg	1000	0
Treatment	dosunit2	This is the unit (e.g., tablet, mg, mL) of the dose of the drug named in <b>trt2</b> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	route2	This is the route of administration (e.g., oral, IV) of the drug named in <i>trt2</i> .	Inhal=inhalaion   Instill=instillation   N=nasal   O=oral   P=parenteral   R=rectal   SL=sublingual/buccal   TD=transdermal   V=vaginal			
Treatment	dosrepeat2	This is an indicator of whether the dose for <i>trt2</i> was repeated after vomiting. This will be mapped to the time and date of the ORIGINAL dose that was vomited since it is a measure of IF the dose was repeated (not of the time and date of the redose).	1=Yes   0=No			
Treatment	trt3	This is the name of drug 3 in the intervention/treatment regimen described in <i>treat</i> .	UNKNOWN   AL=Artemether-Lumefantrine   AM=Artemether   A-PQP   AQ=Amodiaquine   AN=Artemisinin-Naphthoquine   AS=Artesunate   AS-AQ=Artesunate-Amodiaquine   AS-MQ=Artesunate-Mefloquine   ART=Artemisinin   AV=Atovaquone   AV-PG=Atovaquone-Proguanil   CL=Clindamycin   CP=Chlorproguanil   CQ=Chloroquine   DAP=Dapsone   DHA=Dihydroartemisinin   DHA-PQP=Dihydroartemisinin-Piperaquine   DHA-PQP-TR=Dihydroartemisinin-Piperaquine-Trimethoprim   DOX=Doxycycline   HL=Halofantrine   CP-DAP=Chlorproguanil-Dapsone   LUM=Lumefantrine   MQ=Mefloquine   PG=Proguanil   PQ=Primaquine   PQP=Piperaquine   PYR=Pyrimethamine   QN=Quinine   SP=Sulfadoxine-Pyrimethamine   SX=Sulfadoxine-Tetracline   SMP=Sulfamethoxypyrazine-Pyrimethamine   PYN-AS=Artesunate-Pyronaridine   IVM=Ivermectin			
Treatment	dos3	This is the dose amount of the drug named in <i>trt3</i> . This is a record of the amount of drug <u>given at each administration</u> – either the number of tablets/pills or the amount in mg/ml of the drug (NOT mg/kg). A separate line will appear in the treatment table for EVERY instance of drug given (e.g., a drug given 3 times a day will have 3 entries for each day of treatment).				
Treatment	dostot3	This is the total dose amount for the entire treatment period of the drug named in <i>trt3</i> . It is the total dose for <u>the entire treatment period</u> – either the number of tablets/pills or the amount in mg/ml of the drug. This amounts to the total number of pills taken / the total mg of drug received by the subject (e.g., for a treatment regime of once a day for 3 days – this would be the value of 3 times the daily dose).				
Treatment	mgperKg3	This is the total daily dose amount in mg/kg of the drug named in <i>trt3</i> . It is the <u>total DAILY mg/kg dose for each treatment DAY</u> – (not a per-instance count – must be the cumulative total of the entire treatment day. e.g., a drug given 3 times a day will be added up to get the total dose for that day to calculate the mg/kg for that day).		mg/kg		

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	dosing3	This is the total dose amount in mg/kg of the drug named in <b>trt3</b> . It is the <u>total mg/kg dose for the entire treatment period</u> – (NOT a daily count – must be the cumulative total of the entire treatment time).		mg/kg	1000	0
Treatment	dosunit3	This is the unit (e.g., tablet, mg, mL) of the dose of the drug named in <b>trt3</b> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			
Treatment	route3	This is the route of administration (e.g., oral, IV) of the drug named in <b>trt3</b> .	Inhal=inhalation   Instill=instillation   N=nasal   O=oral   P=parenteral   R=rectal   SL=sublingual/buccal   TD=transdermal   V=vaginal			
Treatment	dosrepeat3	This is an indicator of whether the dose for <b>trt3</b> was repeated after vomiting. This will be mapped to the time and date of the ORIGINAL dose that was vomited since it is a measure of IF the dose was repeated (not of the time and date of the redose).	1=Yes   0=No			
Treatment	trt4	This is the name of drug 4 in the intervention/treatment regimen described in <b>treat</b> .	UNKNOWN   AL=Artemether-Lumefantrine   AM=Artemether   A-PQP   AQ=Amodiaquine   AN=Artemisinin-Naphthoquine   AS=Artesunate   AS-AQ=Artesunate-Amodiaquine   AS-MQ=Artesunate-Mefloquine   ART=Artemisinin   AV=Atovaquone   AV-PG=Atovaquone-Proguanil   CL=Clindamycin   CP=Chlorproguanil   CQ=Chloroquine   DAP=Dapsone   DHA=Dihydroartemisinin   DHA-PQP=Dihydroartemisinin-Piperaquine   DHA-PQP-TR=Dihydroartemisinin-Piperaquine-Trimethoprim   DOX=Doxycycline   HL=Halofantrine   CP-DAP=Chlorproguanil-Dapsone   LUM=Lumefantrine   MQ=Mefloquine   PG=Proguanil   PQ=Primaquine   PQP=Piperaquine   PYR=Pyrimethamine   QN=Quinine   SP=Sulfadoxine-Pyrimethamine   SX=Sulfadoxine   TET=Tetracycline   SMP=Sulfamethoxypyrazine-Pyrimethamine   PYN-AS=Artesunate-Pyronaridine   IVM=Ivermectin			
Treatment	dos4	This is the dose amount of the drug named in <b>trt4</b> . This is a record of the amount of drug <u>given at each administration</u> – either the number of tablets/pills or the amount in mg/ml of the drug (NOT mg/kg). A separate line will appear in the treatment table for EVERY instance of drug given (e.g., a drug given 3 times a day will have 3 entries for each day of treatment).				

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	dostot4	This is the total dose amount for the entire treatment period of the drug named in <b>trt4</b> . It is the <u>total dose for the entire treatment period</u> – either the number of tablets/pills or the amount in mg/ml of the drug. This amounts to the total number of pills taken / the total mg of drug received by the subject (e.g., for a treatment regime of once a day for 3 days – this would be the value of 3 times the daily dose).				
Treatment	mgperKg4	This is the total daily dose amount in mg/kg of the drug named in <b>trt4</b> . It is the <u>total DAILY mg/kg dose for each treatment DAY</u> – (not a per-instance count – must be the cumulative total of the entire treatment day. e.g., a drug given 3 times a day will be added up to get the total dose for that day to calculate the mg/kg for that day).		mg/kg		
Treatment	dosing4	This is the total dose amount in mg/kg of the drug named in <b>trt4</b> . It is the <u>total mg/kg dose for the entire treatment period</u> – (NOT a daily count – must be the cumulative total of the entire treatment time).		mg/kg	1000	0
Treatment	dosunit4	This is the unit (e.g., tablet, mg, mL) of the dose of the drug named in <b>trt4</b> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			
Treatment	route4	This is the route of administration (e.g., oral, IV) of the drug named in <b>trt4</b> .	Inhal=inhalation   Instill=instillation   N=nasal   O=oral   P=parenteral   R=rectal   SL=sublingual/buccal   TD=transdermal   V=vaginal			
Treatment	dosrepeat4	This is an indicator of whether the dose for <b>trt4</b> was repeated after vomiting. This will be mapped to the time and date of the ORIGINAL dose that was vomited since it is a measure of IF the dose was repeated (not of the time and date of the redose).	1=Yes   0=No			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	trt5	This is the name of drug 5 in the intervention/treatment regimen described in <i>treat</i> .	UNKNOWN   AL=Artemether-Lumefantrine   AM=Artemether   A-PQP   AQ=Amodiaquine   AN=Artemisinin-Naphthoquine   AS=Artesunate   AS-AQ=Artesunate-Amodiaquine   AS-MQ=Artesunate-Mefloquine   ART=Artemisinin   AV=Atovaquone   AV-PG=Atovaquone-Proguanil   CL=Clindamycin   CP=Chlorproguanil   CQ=Chloroquine   DAP=Dapsone   DHA=Dihydroartemisinin   DHA-PQP=Dihydroartemisinin-Piperaquine   DHA-PQP-TR=Dihydroartemisinin-Piperaquine-Trimethoprim   DOX=Doxycycline   HL=Halofantrine   CP-DAP=Chlorproguanil-Dapsone   LUM=Lumefantrine   MQ=Mefloquine   PG=Proguanil   PQ=Primaquine   PQP=Piperaquine   PYR=Pyrimethamine   QN=Quinine   SP=Sulfadoxine-Pyrimethamine   SX=Sulfadoxine   TET=Tetracycline   SMP=Sulfamethoxypyrazine-Pyrimethamine   PYN-AS=Artesunate-Pyronaridine   IVM=Ivermectin			
Treatment	dos5	This is the dose amount of the drug named in <i>trt5</i> . This is a record of the amount of drug <u>given at each administration</u> – either the number of tablets/pills or the amount in mg/ml of the drug (NOT mg/kg). A separate line will appear in the treatment table for EVERY instance of drug given (e.g., a drug given 3 times a day will have 3 entries for each day of treatment).				
Treatment	dostot5	This is the total dose amount for the entire treatment period of the drug named in <i>trt5</i> . It is the total dose for <u>the entire treatment period</u> – either the number of tablets/pills or the amount in mg/ml of the drug. This amounts to the total number of pills taken / the total mg of drug received by the subject (e.g., for a treatment regime of once a day for 3 days – this would be the value of 3 times the daily dose).				
Treatment	mgperKg5	This is the total daily dose amount in mg/kg of the drug named in <i>trt5</i> . It is the <u>total DAILY mg/kg dose for each treatment DAY</u> – (not a per-instance count – must be the cumulative total of the entire treatment day. e.g., a drug given 3 times a day will be added up to get the total dose for that day to calculate the mg/kg for that day).		mg/kg		
Treatment	dosing5	This is the total dose amount in mg/kg of the drug named in <i>trt5</i> . It is the <u>total mg/kg dose for the entire treatment period</u> – (NOT a daily count – must be the cumulative total of the entire treatment time).		mg/kg	1000	0
Treatment	dosunit5	This is the unit (e.g., tablet, mg, mL) of the dose of the drug named in <i>trt5</i> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	route5	This is the route of administration (e.g., oral, IV) of the drug named in <i>trt5</i> .	Inhal=inhalaion   Instill=instillation   N=nasal   O=oral   P=parenteral   R=rectal   SL=sublingual/buccal   TD=transdermal   V=vaginal			
Treatment	dosrepeat5	This is an indicator of whether the dose for <i>trt5</i> was repeated after vomiting. This will be mapped to the time and date of the ORIGINAL dose that was vomited since it is a measure of IF the dose was repeated (not of the time and date of the redose).	1=Yes   0=No			
Treatment	trt6	This is the name of drug 6 in the intervention/treatment regimen described in <i>treat</i> .	UNKNOWN   AL=Artemether-Lumefantrine   AM=Artemether   A-PQP   AQ=Amodiaquine   AN=Artemisinin-Naphthoquine   AS=Artesunate   AS-AQ=Artesunate-Amodiaquine   AS-MQ=Artesunate-Mefloquine   ART=Artemisinin   AV=Atovaquone   AV-PG=Atovaquone-Proguanil   CL=Clindamycin   CP=Chlorproguanil   CQ=Chloroquine   DAP=Dapsone   DHA=Dihydroartemisinin   DHA-PQP=Dihydroartemisinin-Piperaquine   DHA-PQP-TR=Dihydroartemisinin-Piperaquine-Trimethoprim   DOX=Doxycycline   HL=Halofantrine   CP-DAP=Chlorproguanil-Dapsone   LUM=Lumefantrine   MQ=Mefloquine   PG=Proguanil   PQ=Primaquine   PQP=Piperaquine   PYR=Pyrimethamine   QN=Quinine   SP=Sulfadoxine-Pyrimethamine   SX=Sulfadoxine-Tetracline   SMP=Sulfamethoxypyrazine-Pyrimethamine   PYN-AS=Artesunate-Pyronaridine   IVM=Ivermectin			
Treatment	dos6	This is the dose amount of the drug named in <i>trt6</i> . This is a record of the amount of drug <u>given at each administration</u> – either the number of tablets/pills or the amount in mg/ml of the drug (NOT mg/kg). A separate line will appear in the treatment table for EVERY instance of drug given (e.g., a drug given 3 times a day will have 3 entries for each day of treatment).				
Treatment	dostot6	This is the total dose amount for the entire treatment period of the drug named in <i>trt6</i> . It is the total dose for <u>the entire treatment period</u> – either the number of tablets/pills or the amount in mg/ml of the drug. This amounts to the total number of pills taken / the total mg of drug received by the subject (e.g., for a treatment regime of once a day for 3 days – this would be the value of 3 times the daily dose).				
Treatment	mgperKg6	This is the total daily dose amount in mg/kg of the drug named in <i>trt6</i> . It is the <u>total DAILY mg/kg dose for each treatment DAY</u> – (not a per-instance count – must be the cumulative total of the entire treatment day. e.g., a drug given 3 times a day will be added up to get the total dose for that day to calculate the mg/kg for that day).		mg/kg		

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Treatment	dosing6	This is the total dose amount in mg/kg of the drug named in <b>trt6</b> . It is the <u>total mg/kg dose for the entire treatment period</u> – (NOT a daily count – must be the cumulative total of the entire treatment time).		mg/kg	1000	0
Treatment	dosunit6	This is the unit (e.g., tablet, mg, mL) of the dose of the drug named in <b>trt6</b> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			
Treatment	route6	This is the route of administration (e.g., oral, IV) of the drug named in <b>trt6</b> .	Inhal=inhalation   Instill=instillation   N=nasal   O=oral   P=parenteral   R=rectal   SL=sublingual/buccal   TD=transdermal   V=vaginal			
Treatment	dosrepeat6	This is an indicator of whether the dose for <b>trt6</b> was repeated after vomiting. This will be mapped to the time and date of the ORIGINAL dose that was vomited since it is a measure of IF the dose was repeated (not of the time and date of the redose).	1=Yes   0=No			
<b>HAEMATOLOGY TABLE</b>						
Haematology	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Haematology	site	This is the name of the study site for the subject.				
Haematology	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Haematology	obsdate	For this table this is the timing information of the haematology measurement. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> Note: These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		
Haematology	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the haematology measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
Haematology	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the haematology measurement. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
Haematology	hb	This is the subject's Haemoglobin result at the visit. The default unit for the repository is gm/dl.		gm/dl	30	1
Haematology	ht	This is the subject's Haematocrit result at the visit. The default unit for the repository is %.		%	70	5
Haematology	pt	This is the subject's Platelets result at the visit. The default unit for the repository is billion/L.		billion/L	1200	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Haematology	wbc	This is the subject's White Blood Cell count (WBC) result at the visit. The default unit for the repository is #/ul.		#/ul	99999	0
Haematology	lymph	This is the subject's Lymphocytes result at the visit. The default unit for the repository is %.		%	100	0
Haematology	neu	This is the subject's Neutrophils result at the visit. The default unit for the repository is %.		%	100	0
Haematology	mono	This is the subject's Monocytes result at the visit. The default unit for the repository is %.		%	100	0
Haematology	basophils	This is the subject's Basophils result at the visit. The default unit for the repository is %.		%	100	0
Haematology	eosinophils	This is the subject's Eosinophils result at the visit. The default unit for the repository is %.		%	100	0
Haematology	polymorphs	This is the subject's PMN (Granulocytes) result at the visit. The default unit for the repository is %.		%	100	0
Haematology	red_cell_count	This is the subject's Red Blood Cell count (RBC) result at the visit. The default unit for the repository is million.ul.		million.ul	12	0.1
<b>CONCOMITANT MEDICATIONS TABLE</b>						
ConcMedications	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
ConcMedications	site	This is the name of the study site for the subject.				
ConcMedications	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
ConcMedications	any_conc_meds	This indicates whether the subject took any concomitant medications during the study period.	1=Yes   0=No			
ConcMedications	conc_meds_prior	This indicates whether the concomitant medication named in <b>conc_meds_drugname</b> was started prior to the study period.	1=Yes   0=No			
ConcMedications	conc_meds_drugname	This is the name (as reported by the data contributor) of the concomitant medication taken. This is recorded directly from the raw data and may contain a mixture of words from various languages and spelling mistakes.				
ConcMedications	conc_meds_indication	This is the indication for which the concomitant medication named in <b>conc_meds_drugname</b> was given. This is recorded directly from the raw data and may contain a mixture of words from various languages and spelling mistakes.				
ConcMedications	cm_start_date	This is the date the concomitant medication named in <b>conc_meds_drugname</b> was reported to have started.		YYYY-MM-DD		
ConcMedications	cm_stop_date	This is the date the concomitant medication named in <b>conc_meds_drugname</b> was reported to have stopped.		YYYY-MM-DD		
ConcMedications	conc_meds_dose	This is the dose for the concomitant medication named in <b>conc_meds_drugname</b> .				
ConcMedications	conc_meds_doseunits	This is the dosage unit for the concomitant medication named in <b>conc_meds_drugname</b> .	tablet   g=gram   ml=millilitre   mg=milligram   mcg=microgram   U=unit   TU=thousand units   MU=million units   mmol=millimole   ng=nanogram			

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
ConcMedications	conc_meds_route	This is the route of administration for the concomitant medication named in <b>conc_meds_drugname</b> .	Intralesional   Intramuscular   Intraocular   Intraperitoneal   Subcutaneous   Topical   Nasal   Oral   Rectal   Respiratory   Transdermal   Vaginal   Intravenous   Auricular (Otic)   Respiratory (Inhalation)			
ConcMedications	conc_meds_frequency	This is the frequency of administration for the concomitant medication named in <b>conc_meds_drugname</b> .	BID=twice a day   PRN=as needed   QD=once a day   QID=four times a day   QM=every morning   QOD=every other day   TID=three times a day   Unknown			
<b>PARASITAEMIA TABLE</b>						
Parasitaemia	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Parasitaemia	site	This is the name of the study site for the subject.				
Parasitaemia	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b>sid + pid + site</b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b>pid</b> represents a unique malaria episode for an individual (see also <b>mepid</b> ).				
Parasitaemia	obsdate	For this table this is the timing information of the parasitaemia blood smear. It should be composed of the date and time values separated by a space (i.e., YYYY-MM-DD HH:MM:SS). However, please note that in instances where <b>timeinc</b> is not provided <b>obsdate</b> will be populated with the date alone (i.e., YYYY-MM-DD). <b>Note:</b> Note: These may not always be the exact date of the visits depending on what is provided by the contributor (e.g., if they provide a Date of Inclusion and then report presence of fever data as D0 Fever, D1 Fever, D7 Fever with no actual dates of those visits then the date populated in <b>obsdate</b> is calculated relative to the Date of Inclusion: +0 days, +1 days, +7 days).		YYYY-MM-DD HH:MM:SS		
Parasitaemia	dayofobs	This is a WWARN-calculation of the <u>relative day number</u> of the parasitaemia blood smear. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of days since Day0Hour0</u> .		days (cumulative)		
Parasitaemia	hourofobs	This is a WWARN-calculation of the <u>relative hour number</u> of the parasitaemia blood smear. It is based on the <b>obsdate</b> in this table in relation to <b>dateinc</b> and <b>timeinc</b> in the <b>Subject Table</b> being day 0 and hour 0, respectively. The unit is <u>cumulative number of hours since Day0Hour0</u> .		hours (cumulative)		
Parasitaemia	pfbn	This indicates whether there were any asexual forms of <i>Plasmodium falciparum</i> parasites present in the patient's blood smear.	1=Yes   0>No			
Parasitaemia	pfmcl	This is the count of the number of asexual <i>Plasmodium falciparum</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	2000000	0
Parasitaemia	gfbn	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium falciparum</i> parasites present in the patient's blood smear.	1=Yes   0>No			
Parasitaemia	gfmcl	This is the count of the number of sexual (gametocyte) <i>Plasmodium falciparum</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	100000	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Parasitaemia	gfbn2	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium falciparum</i> parasites present in the patient's blood smear. Note: This is only populated if a second method of counting gametocytes is used. See the method in <a href="#"><b>molecular_method_used2</b></a> .	1=Yes   0=No			
Parasitaemia	gfmicl2	This is the count of the number of sexual (gametocyte) <i>Plasmodium falciparum</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre). <b>Note:</b> This is only populated if a second method of counting gametocytes is used. See the method in <a href="#"><b>molecular_method_used2</b></a>		Parasites / Microlitre	100000	0
Parasitaemia	pvbin	This indicates whether there were any asexual forms of <i>Plasmodium vivax</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	pvmicl	This is the count of the number of asexual <i>Plasmodium vivax</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	2000000	0
Parasitaemia	gvbin	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium vivax</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	gvmicl	This is the count of the number of sexual (gametocyte) <i>Plasmodium vivax</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	100000	0
Parasitaemia	gvbin2	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium vivax</i> parasites present in the patient's blood smear. Note: This is only populated if a second method of counting gametocytes is used. See the method in <a href="#"><b>molecular_method_used2</b></a> .	1=Yes   0=No			
Parasitaemia	gvmicl2	This is the count of the number of sexual (gametocyte) <i>Plasmodium vivax</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre). <b>Note:</b> This is only populated if a second method of counting gametocytes is used. See the method in <a href="#"><b>molecular_method_used2</b></a>		Parasites / Microlitre	100000	0
Parasitaemia	pmbin	This indicates whether there were any asexual forms of <i>Plasmodium malariae</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	pmmicl	This is the count of the number of asexual <i>Plasmodium malariae</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	2000000	0
Parasitaemia	gmbin	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium malariae</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	gmmicl	This is the count of the number of sexual (gametocyte) <i>Plasmodium malariae</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	100000	0
Parasitaemia	gmbin2	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium malariae</i> parasites present in the patient's blood smear. Note: This is only populated if a second method of counting gametocytes is used. See the method in <a href="#"><b>molecular_method_used2</b></a> .	1=Yes   0=No			
Parasitaemia	gmmicl2	This is the count of the number of sexual (gametocyte) <i>Plasmodium malariae</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre). <b>Note:</b> This is only populated if a second method of counting gametocytes is used. See the method in <a href="#"><b>molecular_method_used2</b></a>		Parasites / Microlitre	100000	0
Parasitaemia	pobin	This indicates whether there were any asexual forms of <i>Plasmodium ovale</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	pomicl	This is the count of the number of asexual <i>Plasmodium ovale</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	2000000	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Parasitaemia	gobin	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium ovale</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	gomicl	This is the count of the number of sexual (gametocyte) <i>Plasmodium ovale</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	100000	0
Parasitaemia	gobin2	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium ovale</i> parasites present in the patient's blood smear. Note: This is only populated if a second method of counting gametocytes is used. See the method in <b>molecular_method_used2</b> .	1=Yes   0=No			
Parasitaemia	gomicl2	This is the count of the number of sexual (gametocyte) <i>Plasmodium ovale</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre). <b>Note:</b> This is only populated if a second method of counting gametocytes is used. See the method in <b>molecular_method_used2</b>		Parasites / Microlitre	100000	0
Parasitaemia	pkbin	This indicates whether there were any asexual forms of <i>Plasmodium knowlesi</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	pkmicl	This is the count of the number of asexual <i>Plasmodium knowlesi</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	2000000	0
Parasitaemia	gkbin	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium knowlesi</i> parasites present in the patient's blood smear.	1=Yes   0=No			
Parasitaemia	gkmicl	This is the count of the number of sexual (gametocyte) <i>Plasmodium knowlesi</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	100000	0
Parasitaemia	gkbin2	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium knowlesi</i> parasites present in the patient's blood smear. Note: This is only populated if a second method of counting gametocytes is used. See the method in <b>molecular_method_used2</b> .	1=Yes   0=No			
Parasitaemia	gkmicl2	This is the count of the number of sexual (gametocyte) <i>Plasmodium knowlesi</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre). <b>Note:</b> This is only populated if a second method of counting gametocytes is used. See the method in <b>molecular_method_used2</b>		Parasites / Microlitre	100000	0
Parasitaemia	pxbin	This indicates whether there were any asexual forms of <i>Plasmodium</i> mixed infection parasites present in the patient's blood smear. This variable is used when each individual species in the mixed infection is not provided.	1=Yes   0=No			
Parasitaemia	pxmicl	This is the count of the number of asexual <i>Plasmodium</i> parasites in a mixed infection found in the patient's blood smear. This variable is used when the counts for each individual species in the mixed infection are not provided. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	2000000	0
Parasitaemia	gxbin	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium</i> mixed infection parasites present in the patient's blood smear. This variable is used when each individual species in the mixed infection is not provided.	1=Yes   0=No			
Parasitaemia	gxmicl	This is the count of the number of sexual (gametocyte) <i>Plasmodium</i> parasites in a mixed infection found in the patient's blood smear. This variable is used when the counts for each individual species in the mixed infection are not provided. The default unit is parasites/uL (microlitre).		Parasites / Microlitre	100000	0

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Parasitaemia	gxbin2	This indicates whether there were any sexual (gametocyte) forms of <i>Plasmodium</i> mixed infection parasites present in the patient's blood smear. This variable is used when each individual species in the mixed infection is not provided. Note: This is only populated if a second method of counting gametocytes is used. See the method in <b><i>molecular_method_used2</i></b> .	1=Yes   0=No			
Parasitaemia	gxmicl2	This is the count of the number of sexual (gametocyte) <i>Plasmodium vivax</i> parasites found in the patient's blood smear. The default unit is parasites/uL (microlitre). <b>Note:</b> This is only populated if a second method of counting gametocytes is used. See the method in <b><i>molecular_method_used2</i></b>		Parasites / Microlitre	100000	0
Parasitaemia	paramethod	This indicates the method by which the parasites counts were measured (e.g., per 200 White Blood Cells).	WBC   RBC   /500RBC   /1000RBC   /200WBC   /500WBC			
Parasitaemia	Gam_count_method	This indicates the method by which the gametocyte counts were measured (e.g., per 200 White Blood Cells).	/100RBC   /200RBC   /400RBC   /200WBC   /500WBC			
Parasitaemia	Molecular_method_used	When there is more than one method recorded for determining the presence and count of gametocytes - this is the method used to determine the presence and count of the gametocytes listed in the <b><i>g*bin</i></b> and <b><i>g*micl</i></b> columns.	PCR   QT-NASBA   Microscopy			
Parasitaemia	Molecular_method_used2	When there is more than one method recorded for determining the presence and count of gametocytes - this is the method used to determine the presence and count of the gametocytes listed in the <b><i>g*bin2</i></b> and <b><i>g*micl2</i></b> columns.	PCR   QT-NASBA   Microscopy			
<b>MEMBRANE FEEDING TABLE</b>						
Membrane Feeding	sid	This is the WWARN-generated study identifier - it will be the same for all subjects within a unique data contribution.				
Membrane Feeding	site	This is the name of the study site for the subject.				
Membrane Feeding	pid	This is the contributor-provided subject identifier used within the study. This is not unique in the repository as some studies could use the same naming conventions. A concatenation of <b><i>sid+pid+site</i></b> is the best way to generate a unique identifier. In the case of longitudinal studies, <b><i>pid</i></b> represents a unique malaria episode for an individual (see also <b><i>mepid</i></b> ).				
Membrane Feeding	No_mosquitoes_used	This is the total number of mosquitoes selected for feeding.			200	0
Membrane Feeding	No_mosquitoes_fully_fed	This is the total number of mosquitoes which were fully fed.			200	0
Membrane Feeding	No_surviving_to_dissection	This is the total number of mosquitoes which survived to dissection day.			200	0
Membrane Feeding	Unfed_discarded	This indicates whether unfed mosquitoes were discarded.	1=Yes   0=No		200	0
Membrane Feeding	No_dissected	This is the total number of mosquitoes dissected.			200	0
Membrane Feeding	No_infected	This is the total number of mosquitoes found to be infected during dissection.			200	0
Membrane Feeding	Oocysts1	This is the number of oocysts found during dissection of mosquito 1.			50	1
Membrane Feeding	Oocysts2	This is the number of oocysts found during dissection of mosquito 2.			2000	1

Table Name	Variable Name	Variable Definition	Variable's Controlled Terminology	Variable's Default Unit	Range - HIGH value	Range - LOW value
Membrane Feeding	Oocysts3	This is the number of oocysts found during dissection of mosquito 3.			2000	1
Membrane Feeding	Oocysts4	This is the number of oocysts found during dissection of mosquito 4.			2000	1
Membrane Feeding	Oocysts5	This is the number of oocysts found during dissection of mosquito 5.			2000	1
Membrane Feeding	Oocysts6	This is the number of oocysts found during dissection of mosquito 6.			2000	1
Membrane Feeding	DissectionDay	This is the number of days between feeding and dissecting the mosquitoes.		Days	20	1