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Supplementary information

Plasmodium falciparum is evolving to escape malaria rapid diagnostic tests in Ethiopia

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SUPPLEMENTARY INFORMATION

Plasmodium falciparum is evolving to escape malaria rapid diagnostic tests in Ethiopia

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SUPPLEMENTARY NOTE

Samples subjected to molecular analysis

820 samples with complete demographic and clinical data underwent molecular analysis, including a randomly selected 248/361 (68.7%) of those with the discordant RDT profile of interest (HRP2-, Pf-LDH+), as well as 465/2115 (22.0%) randomly selected *P. falciparum* RDT HRP2 positives (HRP2+, Pf-LDH+) as controls. The remaining 107 samples included 90 with inconclusive HRP2 results (HRP2+ by only 1 RDT, of which 67 were Pf-LDH- and 23 were Pf-LDH+) and 17 negative controls (HRP2-, Pf-LDH-). Quantitative real-time PCR (qPCR) targeting the *P. falciparum* lactate dehydrogenase (*pfldh*) gene confirmed parasitemia in 731/820 (89%) samples, with a geometric mean (GM) of 1,390.7 parasites/μL (geometric standard deviation [geoSD]: 9.8).

Comparison of pfhrp2/3 PCR, RDT, and HRP2 bead-based assays

Concordance between *pfhrp2*-negative PCR results and the discordant RDT profile was good (Cohen's kappa 0.66). Overall, among samples with the discordant RDT profile, 64.8% (95% CI 57-72) were *pfhrp2-/3-* and 8.0% (95% CI 5-13) *pfhrp2-/3+*, with an additional 15.9% (95% CI 11-22) *pfhrp2+/3-* (**Extended Data Figure 2**). Interestingly, of samples HRP2+ by both RDTs, *pfhrp3* could not be amplified in 42.6% (95% CI 38-48).

We observed expected agreement between the results of *pfhrp2/3* PCR assays, RDTs, and a bead-based immunoassay applied to a subset of 456 samples. 93% (95% CI 86-96) of samples *pfhrp2+/3+* by PCR tested positive for HRP2 antigen (GM 40,284 pg/mL HRP2, geoSD 7.5). In comparison, 19% (12-29) of *pfhrp2-/3-* samples were HRP2+, with a GM of 2,089 pg/mL HRP2 (geoSD 5.5).

HRP2+ but *pfhrp2*- PCR results are expected in a subset of subjects because HRP2 antigenemia can persist for weeks after clearance of parasitemia[1]. 92% (95% CI 88-95) of samples HRP2+, Pf-LDH+ by RDT were HRP2+ by the antigen assay (GM 34,536 pg/mL, geoSD 6.5), compared to 24% (95% CI 18-31) of those with the discordant HRP2-, Pf-LDH+ RDT profile of interest (GM 2,455 pg/mL, geoSD: 7.2) (**Table 2**).

Pf-LDH RDT performance

Despite the prevalence of *pfhrp2*-deleted parasites in this study, use of the SD Bioline's Pf-LDH RDT band rather than its HRP2 band did not improve RDT performance. Among 820 samples with RDT results and *pfldh* real-time PCR results available, overall agreement with PCR was slight regardless of test band used (Cohen's kappa 0.04 for the Pf-LDH band and 0.15 for the HRP2 band). Using *pfldh* PCR as the gold standard, the sensitivity and specificity of the Pf-LDH RDT band were 69% and 38%, respectively. The sensitivity and specificity of the HRP2 RDT band were 62% and 72%, respectively. The poor performance of the Pf-LDH RDT band was unexpected, as the RDTs used in this study passed WHO lot testing prior to shipment. Comparison of RDT results within the larger cohort (**Supplementary Table 11**) suggests several explanations, including decreased performance due to inappropriate storage conditions, operational or administrative user error (Pf-LDH test bands are often fainter than HRP2, especially at lower parasite densities), cross-reactivity with other species (though only in a minority of cases as outlined below, co-infections, and/or immunological factors.

For overall detection of *P. falciparum* parasitemia using any falciparum-specific antigen, the SD and CareStart products had similar levels of agreement with

pfldh PCR. Compared to PCR, the sensitivity and specificity of the SD RDT (HRP2+ and/or Pf-LDH+) were 93% and 20% (Cohen's kappa 0.14), respectively; the sensitivity and specificity of the CareStart RDT (HRP2+) were 69% and 60% (Cohen's kappa 0.15), respectively. However, because this study purposefully oversampled subjects at high risk for infection by *pfhrp2/3*-deleted parasites for molecular testing, these estimates should not be generalized to routine care in these regions.

Plasmodium vivax co-infection and pfhrp2/3 deletion

Though analysis of *P. vivax* co-infection was not an objective of this study, analysis of available RDT data did not reveal evidence of selection for *pfhrp2* deletion in the presence of *P. vivax* co-infection. First, the frequency of *pfhrp2* deletion was similar among subjects with versus without *P. vivax* co-infection. Among subjects who underwent *pfhrp2/3* PCR genotyping, *P. vivax* co-infection was identified by the CareStart RDT (Pv-LDH+) in 56 subjects. Of these, 41 (73.2%) were *pfhrp2*+ and 15 (26.8%) were *pfhrp2-.* Among all 608 samples with CareStart RDT results who were subjected to *pfhrp2/3* PCR genotyping, 445 (73.2%) were *pfhrp2*+ and 163 (26.8%) were *pfhrp2-.* Second, we did not observe an association between *P. vivax* co-infection and subtelomeric deletion structural profile. While there was only a single *pfhrp2* deletion profile observed in this study, three distinct *pfhrp3* deletion profiles were observed. The frequency of *P. vivax* co-infection was similar in the two dominant *pfhrp3* deletion subtelomeric structural profiles. 14 of 134 (10.4%) subjects with the *P. falciparum* chr13-P4 (*pfhrp3* deletion) profile and 6 of 106 (5.7%) with the chr13-P3 (*pfhrp3* deletion) profile had co-infection with *P. vivax.*

Subtelomeric profiling and variant calling using MIPs

The MIP panel was designed using a tiled strategy that involved multiple, overlapping probes spanning each gene target. We detected 244 of 273 targets with sufficient mapping quality and depth across multiple segments of both *pfhrp2* and *pfhrp3* and their flanking regions, spanning positions 1,344,451 to 1,397,773 and 2,780,863 to 2,853,533 of chromosomes 8 and 13, respectively. Fourteen total probes were used to target different segments of *pfhrp2* (n = 8 probes) and *pfhrp3* (n = 6). 241 MIPs mapped to 273 targeted loci on the reference genome, including 32 extra loci accounting for the multicopy genes on chromosome 11.

In total, 43,541,045 reads were devoted to this sample set, or roughly half of a single NextSeq 550 mid-output flow cell. Probes failing to amplify in >90% of the samples were removed from the analysis, leaving 244 loci. 841 of 1014 samples and controls had sequence data after read mapping. 20 of 841 belonged to control strains (positive controls). None of the 20 negative controls had any sequence mapping to the reference genome. Deletion calls were only made in samples with sufficient depth of UMI coverage (see Methods), leaving 375 high-coverage samples from the study cohort and 6 controls in the final call set.

The median parasite density for samples successfully called using MIP sequencing was 5,077 p/μL (SD: 1.6×10^4), compared to 264 p/μL (SD: 5.9×10^3) for samples with failed MIP calls. Among 367 (97.9%) MIP-called samples with matching PCR data, 85 (23.2%) were *pfhrp2-/3-* by PCR. Receiver-operator curve analysis indicated the optimal parasite density threshold above which samples had sufficient coverage for MIP calling was approximately 925 p/μL, although this threshold is project-specific and expected to improve with additional sequencing effort (**Extended Data Figure 4**).

Comparison of pfhrp2/3 MIP sequencing to PCR, HRP2 immunoassay, and whole-genome sequencing results

Among 367 (97.9%) MIP-called samples with matching PCR data, 85 (23.2%) were *pfhrp2-/3-* by PCR. MIP sequencing results indicated that 126/367 (34.3%; 95% CI 30-39) were *pfhrp2-,* 264/367 (71.9%; 95% CI 67-76) *pfhrp3-,* and 116/367 (31.6%; 95% CI 27-37) *pfhrp2-/3-* by MIP sequencing. Of samples called *pfhrp2-* by MIP sequencing, 82.0% were *pfhrp2-* by PCR and 73.3% had the discordant RDT profile. Similarly, of samples called *pfhrp3-* by MIP sequencing, 76.7% were *pfhrp3-* by PCR. Differences between genotyping results were apparent and expected due to differences in targets and methodologies (PCR is better suited for samples with low parasite density than MIP sequencing). Comparison of results from MIP and PCR *pfhrp2/3* deletion genotyping revealed excellent agreement between the two approaches for *pfhrp2* (Cohen's kappa 0.82) and good agreement for *pfhrp3* (Cohen's kappa 0.63).

Comparison to the bead-based HRP2 immunoassay results provided additional confidence in the validity of our *pfhrp2/3* deletion calls using MIP sequencing. 175 MIP-called samples also had bead-based antigen detection results available. Despite fundamental differences in the targets of these two approaches (*pfhrp2* gene versus HRP2 antigen, which can linger after clearance of infection),[1] observed agreement between the two methods was consistent with expectation. Of those samples *pfhrp2+* by MIP sequencing, 94.1% were HRP2+ by bead-based antigen immunoassay, whereas 79.5% of those *pfhrp2-* by MIPs were also HRP2- by the immunoassay.

We used whole-genome sequencing (WGS) to evaluate *pfhrp2/3* MIP sequencing results and breakpoint regions in a small validation subset. Among 14

samples subjected to WGS and with MIP calls, median WGS depth of coverage was 20 reads/locus (range 4-38). While the distribution of aligned reads was uneven in the regions flanking *pfhrp2* and *pfhrp3*, visual inspection of WGS coverage supported 13 (93%) *pfhrp2* and 14 (100%) *pfhrp3* deletion calls made using MIP sequencing data (**Figure 4**). For the single discordant *pfhrp2* deletion call (lab ID: 1314), *pfhrp2* PCR results were consistent with the MIP sequencing result. Precise mapping of breakpoint regions using WGS was not possible due to regions of very high coverage ("jackpotting") resulting from selective whole-genome amplification and low coverage due to ambiguous read mapping to repetitive and paralogous loci. However, breakpoint regions identified using MIPs were consistent with WGS coverage centromeric to *pfhrp2* and *pfhrp3* on chromosomes 8 and 13, respectively, with the exception of calls in chromosome 13's multi-copy 28S rRNA gene. Discordance in these calls was expected due to ambiguous mapping of short-read sequences to a multi-copy gene. MIP results from well-characterized lab strains 3D7 (*pfhrp2+/3+*), DD2 (*pfhrp2-/3+*), and HB3 (*pfhrp2+/3-*) were consistent with whole-genome alignments of published short-read data. Telomeric deletion breakpoint assessment was limited by a small number of successful MIP targets telomeric to both genes. However, the concordance in *pfhrp2/3* deletion calls and centromeric deletion breakpoint regions by MIP and WGS techniques confirmed the utility of MIPs for identifying *pfhrp2/3* deletions and determining their extent and breakpoint regions.

Association between malaria symptoms, geographical location, and subtelomeric structural variants

We did not observe an association between subtelomeric deletion profile and

the number of symptoms experienced by subjects (**Extended Data Figure 5**). Because the majority of subjects (96.5%, 2620/2714) who tested positive for *P. falciparum* by RDT were febrile, fever alone was not sufficient to evaluate disease severity. Therefore, as a crude metric of disease severity, we calculated the total number of symptoms (six total were assessed: fever, headache, joint pain, feeling cold, nausea, and lack of appetite). No significant differences in the total number of symptoms by deletion profile were revealed for chromosome 8 ($F(3, 334) = 0.29$, $p = 0.83$) or chromosome 13 ($F(2, 335) = 0.33$, $p = 0.72$) by one-way ANOVA. No obvious spatial patterns in subtelomeric deletion profiles were apparent at the regional level (**Supplementary Table 2**).

Extended haplotype homozygosity analysis

91 and 17 biallelic SNPs within the 28kb and 27kb regions centromeric to *pfhrp2* and *pfhrp3* deletions, respectively, were used to calculate EHH statistics. 327 samples with *pfhrp2* deletion calls using MIP sequencing and sufficient variant data were included in the EHH analysis, including 212 *pfhrp2*-intact and 115 *pfhrp2*-deleted haplotypes. 162 samples with *pfhrp3* deletion calls using MIP sequencing and sufficient variant data were included in the EHH analysis, including 37 *pfhrp3*-intact and 125 *pfhrp3*-deleted haplotypes with three distinct subtelomeric structural profiles. No variant calls were made in the 15.5 kb region immediately centromeric to *pfhrp3* to avoid ambiguity in read mapping to the duplicated DNA segment containing multicopy genes including 5.8S, 28S rRNA.

REFERENCES

1 Markwalter CF, Gibson LE, Mudenda L, Kimmel DW, Mbambara S, Thuma PE *et al.* Characterization of Plasmodium Lactate Dehydrogenase and Histidine-Rich Protein 2 Clearance Patterns via Rapid On-Bead Detection from a Single Dried Blood Spot. *Am J Trop Med Hyg* 2018; **98**: 1389–1396.

Supplementary Table 1. PCR results by age, sex, and parasite density. P values were calculated using chi-square (gender) and the non-parametric Kruskal-Wallis test (age, parasitemia).

	PCR-based deletion calls				**p value***	**test statistic**
	pfhrp2+/3+	***pfhrp2-/3-***	***pfhrp2-/3+***	***pfhrp2+/3-***		
N	253	136	27	192		
Sex = Female, N (%)	72 (29%)	48 (35%)	7 (26%)	59 (31%)	0.53	$X^2(3, N=610) = 2.24$
Age, Median (IQR)	19 (13)	18 (14)	16 (14)	19 (14)	0.76	$X^2(3, N=608) = 1.16$
Parasitemia (p/µL), Median (IQR)	2824 (7712)	3877 (8191)	2112 (6828)	2946 (8340)	0.14	$X^2(3, N=608) = 5.54$

Supplementary Table 2. RDT profile by district for individuals *P. falciparum*-positive by RDT (n=2,714). Abbreviations: Pf, *P. falciparum*; HRP2, histidine-rich protein 2; Pf-LDH, *P. falciparum*-specific lactate dehydrogenase; RDT, rapid diagnostic test.

		RDT results		
Region / District	**Total Pf+, n**	2 HRP2+, 1 PfLDH+	2 HRP2-, 1 PfLDH+	1 HRP2+, 1 HRP2-
Tigray	**689**	**460 (67%)**	**140 (20%)**	**85 (12%)**
Ahferom	117	83 (71%)	18 (15%)	16 (14%)
Atseged Tsimbila	160	86 (54%)	48 (30%)	26 (16%)
Gulomekeda	21	14 (67%)	5 (24%)	2 (10%)
K. Humera	176	115 (65%)	39 (22%)	21 (12%)
L. Adiabo	145	111 (77%)	22 (15%)	11 (8%)
T. Adiabo	69	51 (74%)	10 (14%)	6 (9%)
Amhara	**1,342**	**997 (74%)**	**211 (16%)**	**131 (10%)**
Metema	233	178 (76%)	30 (13%)	24 (10%)
Quara	516	435 (84%)	39 (8%)	42 (8%)
Tegede	296	197 (67%)	65 (22%)	33 (11%)
West Armachiho	295	187 (63%)	75 (25%)	32 (11%)
Gambella	**683**	**658 (96%)**	**10 (1%)**	**15 (2%)**
Itang	151	144 (95%)	2 (1%)	5 (3%)
Kule Refugee Camp	472	461 (98%)	4 (1%)	7 (1%)

Supplementary Table 3. Prevalence estimate sensitivity analysis. Abbreviations: CI, confidence interval; RDT, rapid diagnostic test; Pf-Pos, *P. falciparum*-positive by RDT.

Approach #1 (primary): Ci.impt function within asbio package, which calculates 95% CI of product of 2 proportions

	Pf-Pos, n	Discordant RDTs, n*	Discordant RDT prevalence, % (95% CI)	*pfhrp2*- PCR concordance (overall), %*	ci.impt prevalence estimate, % (95% CI)
Amhara	1342	211	15.8 (13.9-17.8)	72.7	11.5 (9.8-13.4)
Tigray	689	140	20.4 (17.5-23.7)	72.7	14.9 (12.5-17.7)
Gambella	683	10	1.5 (0.7-2.8)	72.7	1.1 (0.6-2.0)

Approach #2: Bootstrapping (1000 iterations)

	Pf-Pos, n	Discordant RDTs, n*	Discordant RDT prevalence, % (95% CI)	*pfhrp2*- PCR concordance (overall), %*	Estimated N with discordant RDT and pfhrp2- PCR result	Prevalence estimate, %	Bootstrap 95% CI
Amhara	1342	211	15.8 (13.9-17.8)	72.7	153.397	11.5	9.7-13.2
Tigray	689	140	20.4 (17.5-23.7)	72.7	101.78	14.9	12.2-17.4
Gambella	683	10	1.5 (0.7-2.8)	72.7	7.27	1.1	0.2-1.8

* Cases Pf-LDH-positive but HRP2-negative on both RDTs were considered potential candidates for pfhrp2/3 gene deletion and defined as 'discordant.'
** Overall proportion of 'discordant RDT profile' infections with *pfhrp2* deletion calls by PCR.

Supplementary Table 4. MIP subtelomeric structural profiles by region for 367 samples with both MIP calls and PCR data.

	Region		
MIP call	Tigray (n=128)	Amhara (n=208)	Gambella (n=31)
pfhrp2+	**79**	**143**	**19**
chr8-P1	40 (51%)	84 (59%)	13 (68%)
chr8-P2	18 (23%)	27 (19%)	3 (16%)
chr8-P3	21 (27%)	32 (22%)	3 (16%)
pfhrp2-	**49**	**65**	**12**
chr8-P4	49 (100%)	65 (100%)	12 (100%)
pfhrp3+	**31**	**59**	**13**
chr13-P1	31 (100%)	59 (100%)	13 (100%)
pfhrp3-	**97**	**149**	**18**
chr13-P3	41 (42%)	70 (47%)	7 (39%)
chr13-P4	56 (58%)	79 (53%)	11 (61%)

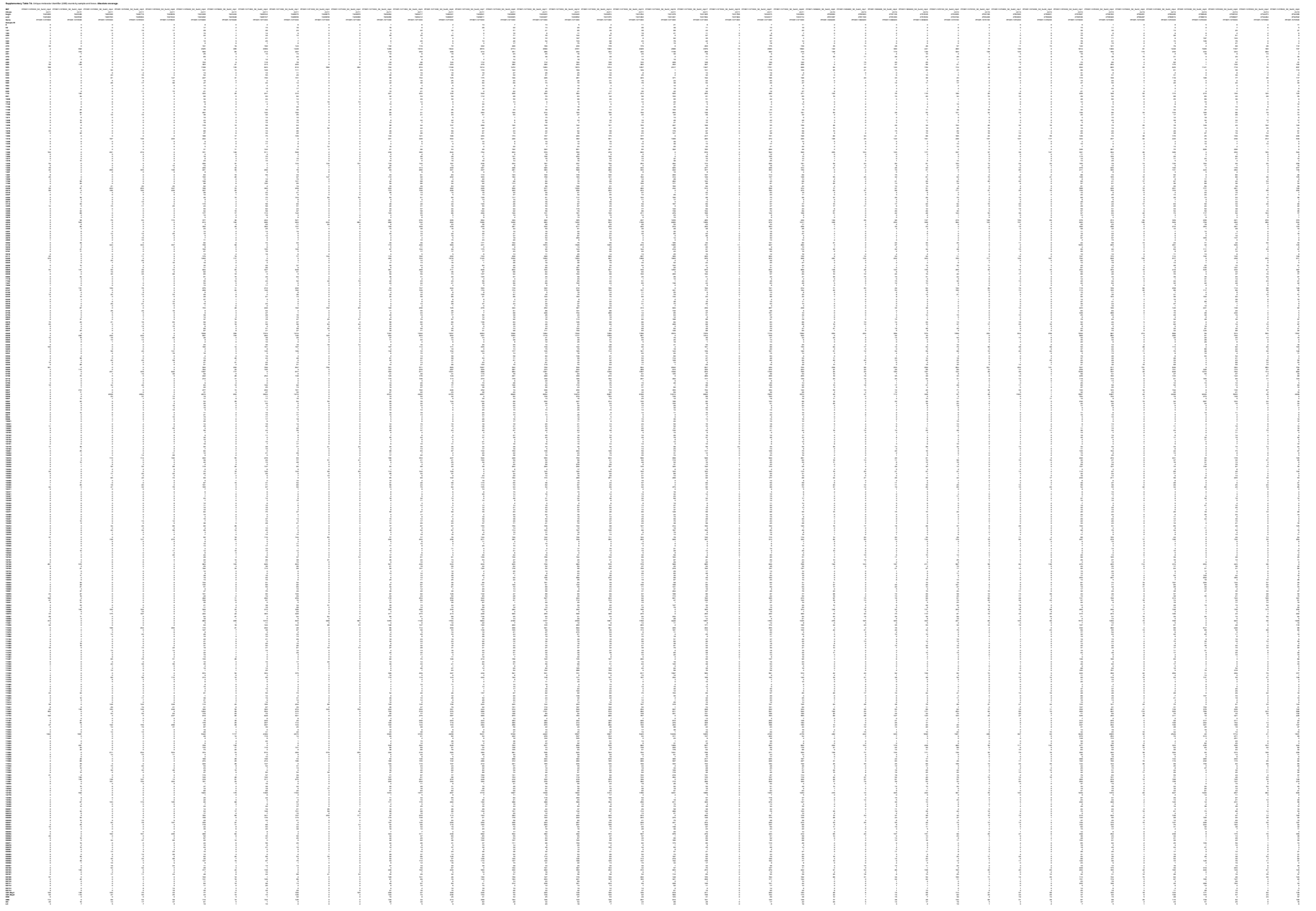
Supplementary Table 5. Pfhrp2/3 MIP panel design overview, including genes targeted, MIPs designed, and genomic coordinates.
Key: Target Group: An identifier for the MIP target region. It is possible and preferred to design probes for multiple genes within a single target group if they are in close proximity; Gene ID: targeted gene's identifier; annotation: target gene annotation; MIP: MIP ID; Copy: Target copy ID for paralogous/multicopy genes; orientation: probe orientation relative to the reference genome; chrom: MIP target chromosome; capture_start: genomic coordinate of the start of captured sequence; capture_end: genomic coordinate of the end of captured sequence; gene_start: starting position of the target gene; gene_end: end position of the target gene; multicopy: whether the gene has a paralog on another location in the genome.
Genes for which MIP design failed are still retained in the table to provide an overview of the entire target region.
Alternating shading of rows are demarcating targeted genes.

Target Group	Gene ID	annotation	MIP	Copy	orientation	chrom	capture_start	capture_end	gene_start	gene_end	multicopy
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	forward	chr8	1344451	1344645	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	reverse	chr8	1344498	1344701	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	forward	chr8	1344701	1344906	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	reverse	chr8	1344779	1344968	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	forward	chr8	1344968	1345115	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	reverse	chr8	1345114	1345327	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	forward	chr8	1345238	1345442	1344405	1345487	FALSE
PF3D7-0831400	PF3D7_0831400	Plasmodium exported protein, unknown function	PF3D7-0831400_S0_Sub0_	C0	forward	chr8	1345510	1345689	1344405	1345487	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	forward	chr8	1353428	1353627	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	reverse	chr8	1353580	1353743	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	forward	chr8	1353726	1353924	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	reverse	chr8	1353887	1354058	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	forward	chr8	1354006	1354194	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	reverse	chr8	1354153	1354316	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	forward	chr8	1354246	1354421	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	reverse	chr8	1354391	1354562	1353456	1354669	FALSE
PF3D7-0831500	PF3D7_0831500	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831500_S0_Sub0_	C0	forward	chr8	1354535	1354733	1353456	1354669	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1358227	1358416	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1358417	1358620	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1358512	1358684	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1358685	1358896	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1358866	1359070	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1359316	1359495	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1359452	1359625	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1359601	1359789	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1360022	1360201	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1360210	1360415	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1360426	1360635	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1360699	1360912	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1360950	1361117	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1361101	1361299	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1361271	1361441	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1361516	1361685	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1361679	1361888	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1361770	1361964	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1362282	1362464	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1362452	1362651	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1362686	1362852	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	reverse	chr8	1362870	1363048	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1362995	1363185	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1363201	1363415	1358314	1363618	FALSE
PF3D7-0831600	PF3D7_0831600	cytoadherence linked asexual protein 8	PF3D7-0831600_S0_Sub0_	C0	forward	chr8	1363389	1363584	1358314	1363618	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1365415	1365577	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1365517	1365690	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1365668	1365855	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1365845	1366018	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1365922	1366112	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1366111	1366306	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1366184	1366356	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1366347	1366532	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1366443	1366638	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1366597	1366801	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1366771	1366959	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1366886	1367107	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1367010	1367187	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1367148	1367355	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	reverse	chr8	1367243	1367422	1365467	1367506	FALSE
PF3D7-0831700	PF3D7_0831700	heat shock protein 70	PF3D7-0831700_S0_Sub0_	C0	forward	chr8	1367406	1367616	1365467	1367506	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	forward	chr8	1371664	1371848	1371847	1372720	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	reverse	chr8	1371800	1371998	1371847	1372720	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	forward	chr8	1371969	1372175	1371847	1372720	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	reverse	chr8	1372168	1372367	1371847	1372720	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	forward	chr8	1372345	1372509	1371847	1372720	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	reverse	chr8	1372430	1372615	1371847	1372720	FALSE
PF3D7-0831750	PF3D7_0831750	Plasmodium exported protein (PHISTa), unknown func	PF3D7-0831750_S0_Sub0_	C0	forward	chr8	1372614	1372807	1371847	1372720	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip0	C0	reverse	chr8	1374269	1374450	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip1	C0	forward	chr8	1374297	1374521	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip2	C0	forward	chr8	1374297	1374498	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip3	C0	reverse	chr8	1374430	1374625	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip4	C0	reverse	chr8	1374468	1374661	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip5	C0	reverse	chr8	1374619	1374805	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip6	C0	forward	chr8	1374630	1374822	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip7	C0	forward	chr8	1374763	1374985	1374236	1375299	FALSE
hrp2	PF3D7_0831800	histidine-rich protein II	hrp2_S0_Sub0_mip8	C0	reverse	chr8	1374871	1375047	1374236	1375299	FALSE
PF3D7-0831900	PF3D7_0831900	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831900_S0_Sub0_	C0	forward	chr8	1380756	1380927	1380834	1381835	FALSE
PF3D7-0831900	PF3D7_0831900	Plasmodium exported protein (PHIST), unknown functi	PF3D7-0831900_S0_Sub0_	C0	reverse	chr8	1380948	1381125	1380834	1381835	FALSE
PF3D7-0832000	PF3D7_0832000	stevor	PF3D7-0832000_S0_Sub0_	C0	forward	chr8	1383785	1383949	1383349	1384377	FALSE
PF3D7-0832000	PF3D7_0832000	stevor	PF3D7-0832000_S0_Sub0_	C0	reverse	chr8	1383870	1384053	1383349	1384377	FALSE
PF3D7-0832000	PF3D7_0832000	stevor	PF3D7-0832000_S0_Sub0_	C0	forward	chr8	1384048	1384225	1383349	1384377	FALSE
PF3D7-0832000	PF3D7_0832000	stevor	PF3D7-0832000_S0_Sub0_	C0	reverse	chr8	1384194	1384363	1383349	1384377	FALSE
PF3D7-0832000	PF3D7_0832000	stevor	PF3D7-0832000_S0_Sub0_	C0	forward	chr8	1384364	1384560	1383349	1384377	FALSE
PF3D7-0832000	PF3D7_0832000	stevor	PF3D7-0832000_S0_Sub0_	C0	reverse	chr8	1384390	1384585	1383349	1384377	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	forward	chr8	1386570	1386754	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	reverse	chr8	1386610	1386808	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	forward	chr8	1386788	1386973	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	reverse	chr8	1386959	1387131	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	forward	chr8	1387025	1387224	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	reverse	chr8	1387189	1387362	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	forward	chr8	1387281	1387480	1386625	1387882	FALSE
PF3D7-0832100	PF3D7_0832100	rifin, pseudogene	PF3D7-0832100_S0_Sub0_	C0	reverse	chr8	1387448	1387625	1386625	1387882	FALSE
PF3D7-0832200-2	PF3D7_0832200	Plasmodium exported protein (PHISTa-like), unknown	PF3D7-0832200-2_S0_Sub0	C0	reverse	chr8	1392258	1392431	1392168	1393491	FALSE
PF3D7-0832200-2	PF3D7_0832200	Plasmodium exported protein (PHISTa-like), unknown	PF3D7-0832200-2_S0_Sub0	C0	forward	chr8	1392429	1392612	1392168	1393491	FALSE
PF3D7-0832200-2	PF3D7_0832200	Plasmodium exported protein (PHISTa-like), unknown	PF3D7-0832200-2_S0_Sub0	C0	forward	chr8	1392665	1392854	1392168	1393491	FALSE
PF3D7-0832200-2	PF3D7_0832200	Plasmodium exported protein (PHISTa-like), unknown	PF3D7-0832200-2_S0_Sub0	C0	forward	chr8	1392878	1393071	1392168	1393491	FALSE
PF3D7-0832200-2	PF3D7_0832200	Plasmodium exported protein (PHISTa-like), unknown	PF3D7-0832200-2_S0_Sub0	C0	reverse	chr8	1392909	1393108	1392168	1393491	FALSE
PF3D7-0832300	PF3D7_0832300	Plasmodium exported protein (PHISTa-like), unknown	PF3D7-0832300_S0_Sub0_	C0	forward	chr8	1397685	1397861	1397014	1397885	FALSE
PF3D7-0832500	PF3D7_0832500	rifin	PF3D7-0832500_S0_Sub0_	C0	forward	chr8	1402717	1402904	1402567	1403711	FALSE
PF3D7-0832400	PF3D7_0832400	stevor,PIR protein				chr8			1399559	1400583	FALSE
PF3D7-0832600	PF3D7_0832600	stevor,PIR protein				chr8			1405834	1406999	FALSE
PF3D7-0832700	PF3D7_0832700	Plasmodium exported protein (PHISTa-like), unknown				chr8			1408570	1409356	FALSE
PF3D7-0832800	PF3D7_0832800	rifin,PIR protein (RIF)				chr8			1411057	1412141	FALSE
PF3D7-0832900	PF3D7_0832900	stevor,PIR protein				chr8			1414282	1415293	FALSE
PF3D7-0833000	PF3D7_0833000	rifin,PIR protein (RIF)				chr8			1417437	1418625	FALSE
PF3D7-0833100	PF3D7_0833100	rifin,PIR protein (RIF)				chr8			1420817	1422077	FALSE
PF3D7-0833200	PF3D7_0833200	rifin,PIR protein (RIF)				chr8			1426883	1428135	FALSE
PF3D7-0833300	PF3D7_0833300	erythrocyte membrane protein 1 (PfEMP1), exon 2, ps				chr8			1429329	1430514	FALSE
PF3D7-0833400	PF3D7_0833400	rifin,PIR protein (RIF)				chr8			1432695	1433932	FALSE
PF3D7-0833500	PF3D7_0833500	erythrocyte membrane protein 1, PfEMP1 (VAR)				chr8			1435793	1443449	FALSE
PF3D7-1369900	PF3D7_1369900	tRNA Tryptophan	PF3D7-1369900_S0_Sub0_	C0	reverse	chr13	2780863	2781067	2781080	2781151	FALSE
PF3D7-1369900	PF3D7_1369900	tRNA Tryptophan	PF3D7-1369900_S0_Sub0_	C0	forward	chr13	2780963	2781160	2781080	2781151	FALSE
PF3D7-1369900	PF3D7_1369900	tRNA Tryptophan	PF3D7-1369900_S0_Sub0_	C0	reverse	chr13	2781106	2781280	2781080	2781151	FALSE
PF3D7-1369900	PF3D7_1370000	tRNA Arginine	PF3D7-1369900_S0_Sub0_	C0	reverse	chr13	2781638	2781839	2781622	2781695	FALSE
PF3D7-1370100	PF3D7_1370100	tRNA Cysteine	PF3D7-1370100_S0_Sub0_	C0	forward	chr13	2783006	2783199	2783150	2783221	FALSE
PF3D7-1370100	PF3D7_1370100	tRNA Cysteine	PF3D7-1370100_S0_Sub0_	C0	reverse	chr13	2783188	2783408	2783150	2783221	FALSE
PF3D7-1370200	PF3D7_1370200	tRNA Glycine	PF3D7-1370200_S0_Sub0_	C0	forward	chr13	2783580	2783800	2783766	2783836	FALSE
PF3D7-1370200	PF3D7_1370200	tRNA Glycine	PF3D7-1370200_S0_Sub0_	C0	reverse	chr13	2783801	2783989	2783766	2783836	FALSE
PF3D7-1370300	PF3D7_1370300	membrane associated histidine-rich protein 1	PF3D7-1370300_S0_Sub0_	C0	reverse	chr13	2787987	2788186	2787972	2788913	FALSE
PF3D7-1370300	PF3D7_1370300	membrane associated histidine-rich protein 1	PF3D7-1370300_S0_Sub0_	C0	forward	chr13	2788160	2788346	2787972	2788913	FALSE
PF3D7-1370300	PF3D7_1370300	membrane associated histidine-rich protein 1	PF3D7-1370300_S0_Sub0_	C0	reverse	chr13	2788281	2788487	2787972	2788913	FALSE
PF3D7-1370300	PF3D7_1370300	membrane associated histidine-rich protein 1	PF3D7-1370300_S0_Sub0_	C0	forward	chr13	2788486	2788674	2787972	2788913	FALSE
PF3D7-1370300	PF3D7_1370300	membrane associated histidine-rich protein 1	PF3D7-1370300_S0_Sub0_	C0	reverse	chr13	2788646	2788819	2787972	2788913	FALSE
PF3D7-1370300	PF3D7_1370300	membrane associated histidine-rich protein 1	PF3D7-1370300_S0_Sub0_	C0	forward	chr13	2788740	2788907	2787972	2788913	FALSE
PF3D7-1370500	PF3D7_1370500	unspecified product	PF3D7-1370500_S0_Sub0_	C0	reverse	chr13	2794273	2794464	2794237	2794851	TRUE
PF3D7-1370500	PF3D7_1370500	unspecified product	PF3D7-1370500_S0_Sub0_	C0	forward	chr13	2794388	2794592	2794237	2794851	TRUE
PF3D7-1370500	PF3D7_1370500	unspecified product	PF3D7-1370500_S0_Sub0_	C0	reverse	chr13	2794590	2794763	2794237	2794851	TRUE
PF3D7-1370500	PF3D7_1370500	unspecified product	PF3D7-1370500_S0_Sub0_	C0	forward	chr13	2794718	2794887	2794237	2794851	TRUE
PF3D7-1370500	PF3D7_1370500	unspecified product	PF3D7-1370500_S0_Sub0_	C0	reverse	chr13	2794812	2795027	2794237	2794851	TRUE
PF3D7-1370900	PF3D7_1370900	unspecified product	PF3D7-1370900_S0_Sub0_	C0	forward	chr13	2797288	2797472	2797507	2798103	TRUE
PF3D7-1370900	PF3D7_1370900	unspecified product	PF3D7-1370900_S0_Sub0_	C0	reverse	chr13	2797384	2797578	2797507	2798103	TRUE
PF3D7-1370900	PF3D7_1370900	unspecified product	PF3D7-1370900_S0_Sub0_	C0	forward	chr13	2797866	2798036	2797507	2798103	TRUE
PF3D7-1370900	PF3D7_1370900	unspecified product	PF3D7-1370900_S0_Sub0_	C0	reverse	chr13	2798027	2798194	2797507	2798103	TRUE
PF3D7-1371000	PF3D7_1371200	5.8S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2802545	2802759	2802527	2802686	TRUE
PF3D7-1371000	PF3D7_1371200	5.8S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2802681	2802868	2802527	2802686	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2802887	2803071	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2802890	2803101	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2803077	2803279	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2803230	2803425	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2803404	2803620	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2803604	2803824	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2803821	2804038	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2803985	2804201	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2804128	2804329	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2804236	2804420	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2804453	2804665	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2804733	2804952	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2804887	2805088	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2805067	2805275	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2805291	2805504	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	reverse	chr13	2805378	2805597	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2805781	2805997	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2806111	2806300	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2806117	2806319	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2806228	2806430	2802945	2807159	TRUE
PF3D7-1371000	PF3D7_1371300	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C0	forward	chr13	2806917	2807127	2802945	2807159	TRUE
PF3D7-1371500	PF3D7_1371500	probable protein, unknown function	PF3D7-1371500_S0_Sub0_	C0	forward	chr13	2808585	2808762	2808563	2809222	FALSE
PF3D7-1371500	PF3D7_1371500	probable protein, unknown function	PF3D7-1371500_S0_Sub0_	C0	reverse	chr13	2808671	2808855	2808563	2809222	FALSE
PF3D7-1371500	PF3D7_1371500	probable protein, unknown function	PF3D7-1371500_S0_Sub0_	C0	forward	chr13	2808809	2808983	2808563	2809222	FALSE
PF3D7-1371500	PF3D7_1371500	probable protein, unknown function	PF3D7-1371500_S0_Sub0_	C0	reverse	chr13	2808964	2809134	2808563	2809222	FALSE
PF3D7-1371500	PF3D7_1371500	probable protein, unknown function	PF3D7-1371500_S0_Sub0_	C0	forward	chr13	2809086	2809265	2808563	2809222	FALSE
PF3D7-1371500	PF3D7_1371500	probable protein, unknown function	PF3D7-1371500_S0_Sub0_	C0	reverse	chr13	2809250	2809438	2808563	2809222	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2811767	2811979	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2811977	2812173	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2812266	2812441	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2812420	2812618	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2812590	2812799	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2812837	2813043	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2813009	2813224	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2813244	2813443	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2813421	2813614	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2814557	2814756	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2814849	2815025	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2815114	2815330	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2815719	2815912	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2816090	2816295	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2816383	2816585	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2817675	2817894	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2817881	2818091	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2818001	2818208	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	reverse	chr13	2818179	2818356	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2818278	2818498	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2818563	2818774	2811706	2820270	FALSE
PF3D7-1371600	PF3D7_1371600	erythrocyte binding like protein 1, pseudogene	PF3D7-1371600_S0_Sub0_	C0	forward	chr13	2818861	2819039	2811706	2820270	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2820938	2821144	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	reverse	chr13	2821099	2821304	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2821300	2821493	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	reverse	chr13	2821460	2821668	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2821662	2821870	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	reverse	chr13	2821820	2822011	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2822011	2822216	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	reverse	chr13	2822205	2822373	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2822308	2822491	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	reverse	chr13	2822469	2822659	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2822584	2822761	2821078	2823292	FALSE
PF3D7-1371700	PF3D7_1371700	serine/threonine protein kinase, FIKK family	PF3D7-1371700_S0_Sub0_	C0	forward	chr13	2823252	2823451	2821078	2823292	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	forward	chr13	2824238	2824413	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	reverse	chr13	2824387	2824571	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	forward	chr13	2824557	2824756	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	reverse	chr13	2824720	2824924	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	forward	chr13	2824862	2825065	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	reverse	chr13	2825044	2825213	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	forward	chr13	2825212	2825411	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	reverse	chr13	2825286	2825480	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	reverse	chr13	2825484	2825680	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	forward	chr13	2825578	2825774	2824302	2825852	FALSE
PF3D7-1371800	PF3D7_1371800	Plasmodium exported protein, unknown function	PF3D7-1371800_S0_Sub0_	C0	reverse	chr13	2825791	2825996	2824302	2825852	FALSE
PF3D7-1371900	PF3D7_1371900	Plasmodium exported protein, unknown function	PF3D7-1371900_S0_Sub0_	C0	forward	chr13	2829900	2830069	2829856	2830669	FALSE
PF3D7-1371900	PF3D7_1371900	Plasmodium exported protein, unknown function	PF3D7-1371900_S0_Sub0_	C0	reverse	chr13	2829964	2830171	2829856	2830669	FALSE
PF3D7-1371900	PF3D7_1371900	Plasmodium exported protein, unknown function	PF3D7-1371900_S0_Sub0_	C0	forward	chr13	2830165	2830368	2829856	2830669	FALSE
PF3D7-1371900	PF3D7_1371900	Plasmodium exported protein, unknown function	PF3D7-1371900_S0_Sub0_	C0	reverse	chr13	2830343	2830520	2829856	2830669	FALSE
PF3D7-1371900	PF3D7_1371900	Plasmodium exported protein, unknown function	PF3D7-1371900_S0_Sub0_	C0	forward	chr13	2830434	2830643	2829856	2830669	FALSE
PF3D7-1371900	PF3D7_1371900	Plasmodium exported protein, unknown function	PF3D7-1371900_S0_Sub0_	C0	reverse	chr13	2830641	2830843	2829856	2830669	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	forward	chr13	2832906	2833066	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	reverse	chr13	2833052	2833251	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	forward	chr13	2833241	2833442	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	reverse	chr13	2833330	2833507	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	forward	chr13	2833491	2833682	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	reverse	chr13	2833575	2833782	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	forward	chr13	2833764	2833939	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	reverse	chr13	2833883	2834055	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	reverse	chr13	2834183	2834346	2832952	2834322	FALSE
PF3D7-1372000	PF3D7_1372000	Plasmodium exported protein (PHISTa), unknown func	PF3D7-1372000_S0_Sub0_	C0	forward	chr13	2834232	2834431	2832952	2834322	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2836945	2837114	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2837011	2837176	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2837149	2837347	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2837337	2837545	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2837460	2837631	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2837604	2837816	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2837734	2837933	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2837874	2838075	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2838030	2838197	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2838146	2838330	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2838293	2838492	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2838437	2838650	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2838545	2838757	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2838704	2838871	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	forward	chr13	2838819	2839006	2837053	2839058	FALSE
PF3D7-1372100	PF3D7_1372100	Plasmodium exported protein (PHISTb), unknown func	PF3D7-1372100_S0_Sub0_	C0	reverse	chr13	2838998	2839199	2837053	2839058	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip0	C0	forward	chr13	2840643	2840859	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip2	C0	forward	chr13	2840751	2840954	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip3	C0	reverse	chr13	2840794	2841015	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip4	C0	forward	chr13	2841009	2841205	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip5	C0	reverse	chr13	2841140	2841341	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip6	C0	forward	chr13	2841246	2841436	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip7	C0	reverse	chr13	2841420	2841635	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip9	C0	forward	chr13	2841464	2841653	2840727	2841703	FALSE
hrp3	PF3D7_1372200	histidine-rich protein III	hrp3_S0_Sub0_mip10	C0	reverse	chr13	2841663	2841862	2840727	2841703	FALSE
PF3D7-1372400	PF3D7_1372400	acyl-CoA synthetase	PF3D7-1372400_S0_Sub0_	C0	forward	chr13	2852540	2852728	2850891	2853482	FALSE
PF3D7-1372400	PF3D7_1372400	acyl-CoA synthetase	PF3D7-1372400_S0_Sub0_	C0	reverse	chr13	2852715	2852915	2850891	2853482	FALSE
PF3D7-1372400	PF3D7_1372400	acyl-CoA synthetase	PF3D7-1372400_S0_Sub0_	C0	forward	chr13	2852916	2853119	2850891	2853482	FALSE
PF3D7-1372400	PF3D7_1372400	acyl-CoA synthetase	PF3D7-1372400_S0_Sub0_	C0	reverse	chr13	2853114	2853312	2850891	2853482	FALSE
PF3D7-1372400	PF3D7_1372400	acyl-CoA synthetase	PF3D7-1372400_S0_Sub0_	C0	forward	chr13	2853213	2853379	2850891	2853482	FALSE
PF3D7-1372400	PF3D7_1372400	acyl-CoA synthetase	PF3D7-1372400_S0_Sub0_	C0	reverse	chr13	2853355	2853533	2850891	2853482	FALSE
PF3D7-1372300	PF3D7_1372300	Plasmodium exported protein (PHIST), unknown functi				chr13			2845766	2846538	FALSE
PF3D7-1372500	PF3D7_1372500	stevor, pseudogene,PIR protein, pseudogene				chr13			2854543	2855568	FALSE
PF3D7-1372600	PF3D7_1372600	rifin,PIR protein (RIF)				chr13			2856585	2858026	FALSE
PF3D7-1372700	PF3D7_1372700	rifin,PIR protein (RIF)				chr13			2860162	2861441	FALSE
PF3D7-1372800	PF3D7_1372800	stevor,PIR protein				chr13			2863865	2864869	FALSE
PF3D7-1372900	PF3D7_1372900	erythrocyte membrane protein 1 (PfEMP1), exon 2, ps				chr13			2865892	2867226	FALSE
PF3D7-1373000	PF3D7_1373000	rifin,PIR protein (RIF)				chr13			2868922	2870165	FALSE
PF3D7-1373100	PF3D7_1373100	rifin,PIR protein (RIF)				chr13			2871859	2873088	FALSE
PF3D7-1373200	PF3D7_1373200	Plasmodium exported protein, unknown function, fragr				chr13			2875990	2876203	FALSE
PF3D7-1373300	PF3D7_1373300	rifin,PIR protein (RIF)				chr13			2877907	2879141	FALSE
PF3D7-1373400	PF3D7_1373400	rifin,PIR protein (RIF)				chr13			2881590	2882956	FALSE
PF3D7-1373500	PF3D7_1373500	erythrocyte membrane protein 1, PfEMP1 (VAR)				chr13			2884785	2892340	FALSE
PF3D7-1370500	PF3D7_1148200	unspecified product	PF3D7-1370500_S0_Sub0_	C1	reverse	chr11	1920280	1920462	1920268	1920811	TRUE
PF3D7-1370500	PF3D7_1148200	unspecified product	PF3D7-1370500_S0_Sub0_	C1	forward	chr11	1920386	1920590	1920268	1920811	TRUE
PF3D7-1370500	PF3D7_1148200	unspecified product	PF3D7-1370500_S0_Sub0_	C1	reverse	chr11	1920588	1920760	1920268	1920811	TRUE
PF3D7-1370500	PF3D7_1148200	unspecified product	PF3D7-1370500_S0_Sub0_	C1	forward	chr11	1920716	1920884	1920268	1920811	TRUE
PF3D7-1370500	PF3D7_1148200	unspecified product	PF3D7-1370500_S0_Sub0_	C1	reverse	chr11	1920809	1921024	1920268	1920811	TRUE
PF3D7-1370900			PF3D7-1370900_S0_Sub0_	C1	forward	chr11	1923308	1923492			TRUE
PF3D7-1370900			PF3D7-1370900_S0_Sub0_	C1	reverse	chr11	1923404	1923648			TRUE
PF3D7-1370900			PF3D7-1370900_S0_Sub0_	C1	forward	chr11	1923884	1924054			TRUE
PF3D7-1370900			PF3D7-1370900_S0_Sub0_	C1	reverse	chr11	1924045	1924210			TRUE
PF3D7-1371000	PF3D7_1148620	5.8S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1928534	1928747	1928510	1928677	TRUE
PF3D7-1371000	PF3D7_1148620	5.8S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1928670	1928856	1928510	1928677	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1928875	1929058	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1928878	1929088	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1929064	1929266	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1929217	1929412	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1929391	1929607	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1929591	1929811	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1929808	1930025	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1929972	1930188	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1930115	1930316	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1930223	1930407	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1930440	1930652	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1930720	1930939	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1930874	1931075	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1931054	1931262	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1931278	1931491	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	reverse	chr11	1931365	1931584	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1931768	1931984	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1932098	1932287	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1932104	1932306	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1932215	1932417	1928934	1933138	TRUE
PF3D7-1371000	PF3D7_1148640	28S ribosomal RNA	PF3D7-1371000_S0_Sub0_	C1	forward	chr11	1932904	1933114	1928934	1933138	TRUE

Supplementary Table 6. *Pfhrp2/3* MIP panel probe sequences.

MIP	probe_id	Probe Sequence
PF3D7-0831400_	ref	CTTGGGTATCTTTTCCATATATAATAACGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTATCTTTCCTTGCTTTTTCTCTC
PF3D7-0831400_	ref	GATACAGCAGTGAATACTAAAAGAAGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATAGATTCCATGAAACTTACAGATAAA
PF3D7-0831400_	ref	TAAGGTATTTGTATAGGCATCGATAGATAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACGCATGAATTCTTTAAATATATCTTTTA
PF3D7-0831400_	ref	AAGCAGGTAAATATATAAACGAGGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAACAAAATGATGAATCTAAATGTGAA
PF3D7-0831400_	ref	TTTGTCATTTAATCTGAATCCATTTAAAGAACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAGCTTGATCAGTATTATTTGACT
PF3D7-0831400_	ref	TGGAGAACATGATGAAGAAGAAGAACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTCATTCAGATATAACTTTATGAATTT
PF3D7-0831400_	ref	TACAGCAATAAATAGAAATACGTTGGTATATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTCTTTTATTTCAACATATTTATGGAGTG
PF3D7-0831400_	ref	ACAAAAATTCGTTATCCTGTGGTTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATTCTCATCATTATAATAAAATGAATATATATA
PF3D7-0831500_	ref	CAGCATTATATATACAATTCAAAGTAAGTTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCACCGTTTATAGGAAATATTATAAAA
PF3D7-0831500_	ref	TCCATGATGTCTTTTTCTTATATCCATTATTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGATATATACAGTTCAACCATATAATTAATATATA
PF3D7-0831500_	ref	TGTACAAGTAGAAAATTTTCCTTCTTTAAATCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTAGTATTATTTTTATTTACATATACCCAATAT
PF3D7-0831500_	ref	AACACATGAACTATTCTCCCCATATTTATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTCTTACTATTATTATTACTATTATTATTGTTTT
PF3D7-0831500_	ref	TAATGATATGACAAAACAATTAACAAAGGAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAAAAAGACGAATCGAATAA
PF3D7-0831500_	ref	TTTCCTGAATCATTACTAACATTACTTATATTATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATTTAGATCAATTAATTTTTCATCTAATATAT
PF3D7-0831500_	ref	GTTTAATGGAAAAATATTTAGATGAATTTGATGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAAAGGAAGAATTATTTTATGTTCTTGA
PF3D7-0831500_	ref	ACGTTTACTTTCATATTTCTTTTTATATTTCTGTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCATACATATAATTTATTAACTTTTCTAAAT
PF3D7-0831500_	ref	TAATATGTGTTTAAAGTGTAACATAAAGTAATAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATAAAAGTCCTTCATTAGATGATATA
PF3D7-0831600_	ref	AAAATGTACAGGAAATATGACAACCATAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATTTGGATTTGAATCTCCATTTAAAT
PF3D7-0831600_	ref	TTTCATTCACATTTTTACTTCTCATTAATGGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTACAATATATATATCATCATCTGCAT
PF3D7-0831600_	ref	ATGTAAGTCGAAATCCGTATCTTCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATTCCGTAAGAACTATAACGTTT
PF3D7-0831600_	ref	ATAAGCCCTAGTATCGTAATCTATGAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAAATTAAGTCTTACATTCCAAAGAAT
PF3D7-0831600_	ref	CAAAGAATGATCAAATAATGTAGGAAGTTCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCATTCATAAAATTACTATCTAAGGGAATAT
PF3D7-0831600_	ref	AAGGGAATATGTTTCATGAATGAGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGTAACATGGAAGGAACATTATC
PF3D7-0831600_	ref	TTGGAGCTTAAGACCTTGAGTTACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACGTAAAAAGTGAAAAATAGACAAATA
PF3D7-0831600_	ref	TTCTAGTATCGTTAAATTCTTATGTAGTTCATCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTATTGATTGTTCCTTTAATAAATTTTCA
PF3D7-0831600_	ref	TGCAATTTCTACGTAAAAAGTGAAAAATAGACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAATAATAACATGTCTTGAATACATTTAGT
PF3D7-0831600_	ref	TCACGTTTTTAGTACATGTTAATTCATTTTTACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAACATCTCCCAAATAATTTATTGGATG
PF3D7-0831600_	ref	TTACGCATTTGTCTCAATAATTCTAAAATAACCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATAATTTGAGAAATAAAAACCTGCA
PF3D7-0831600_	ref	TCAGATCTAATACTCGATTATGTAATTCTCTTCTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAATAAAATATCGTCAACATTCTTTCT
PF3D7-0831600_	ref	TGAGCTCTTTTCAATTTATAATTTCAATACAGACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGCTAATGAGAGATGCATATGA
PF3D7-0831600_	ref	CTTTTTAACTAAAGGTGTTGCTGTTAAATATTTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTTGTAAGTGTCTTCTATTTTTCTAAA
PF3D7-0831600_	ref	AATTGTGTATTTCTAATTCCCTTTGTTCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTGTAATAAACTATTAGTTATGCTAT
PF3D7-0831600_	ref	GTTTATTGAATAGCCATAGCGAAACATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAATCAAGTTTTTATGATATTGCAAAATA
PF3D7-0831600_	ref	TAAAAAGGTAGATCAATTCCTTGGTAGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCATATCTTACTTTTGCTTATGTATATAAT
PF3D7-0831600_	ref	TGGAGGTTTTTCGACTTCTTTAAGAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGATCAATTCCTTGGTAGAAAATTT
PF3D7-0831600_	ref	AAGTCGAAAAACCTCCAGGAAAATANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATATCTCTCAAGGAAACGAAAATT
PF3D7-0831600_	ref	TGGTTATCTTGATGAGGCAATGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATGTATGCCCTTTGTTTTATG
PF3D7-0831600_	ref	AATCCGATGAAGATGATCAAAAGGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGAAAACGTGGTTATCTTGATGA
PF3D7-0831600_	ref	ACTGATGATTACAAAAATACCTGAAGATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTAAAAATGAGGAATTTCTAAATGATA
PF3D7-0831600_	ref	TGGAAGAATTAGATAACATATCAAATCAATATGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTGCACTAGAAGAATTAAATAAAGTATTT
PF3D7-0831600_	ref	TAATTTTAATATCATAAAATGTCCCAGAGCTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCAGGATATTACATTCCATATTTGTATT
PF3D7-0831600_	ref	AAGATGGATTCTTTTCATATATATGTAATGATCCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTGTTTTCAGAATGCTGTATATTATT
PF3D7-0831700_	ref	TGCAATTTATTGTCTATCAAAAAGGAATAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAGTATATAATCCTATAATGACTAAAATATATCAA
PF3D7-0831700_	ref	AAATGTTCCTCCTCCTAAATCGAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTTGTGCGGATGATGATAATA
PF3D7-0831700_	ref	TTTTTGAAGTTAAAGCTACCTCAGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTGTTCCAGCTTATTTCAATGATT
PF3D7-0831700_	ref	AATCATTGGTTTCCATCAGAACCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACCATATGCTATAGCTGCTGC
PF3D7-0831700_	ref	AAAACCAGTTAAAAATGCTGTTATTACTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATGCAAAAAGATTAATAGGAAGAAAAT
PF3D7-0831700_	ref	TACATATACCAACACATGAATAGGTGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCAGAACCACCTTTTACAGTAAAT
PF3D7-0831700_	ref	TCCAGGAATCCAGAAAATACAGTTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACAGTACATACAGCAAGTAACAAT
PF3D7-0831700_	ref	AGGCTTGATTTTGACAATAACTGACTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTACCTAAATCAATACCAATTGCA
PF3D7-0831700_	ref	TAACTGTTTTCATACATTTTTCTGAATCATCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTCCATTATTTTGTGCTTCTTATTTTT
PF3D7-0831700_	ref	AAAAATCAAACAGCAGAAACTGAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAGATGATATCGATCGTATGGTAA
PF3D7-0831700_	ref	TGGGATACCTTCTAATTGAAATTTTCCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATTTTGTTCATCCTCTTCTTTATATTT
PF3D7-0831700_	ref	AAAACCAAATTACTATTACAAATGATAAAGGAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAAATCTTTACAACATATGCTGATAA
PF3D7-0831700_	ref	AACAGCTTCATCTGGATTAATGGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAACTTGAATTAAAACACCTGGTT
PF3D7-0831700_	ref	ACCAAATTAATTGAAAGAAATACAACTATACCAACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCAAAAATACAACAACTTATCAAAGATT
PF3D7-0831700_	ref	TTATAATCGATTCCATCAAATAAAGAATCAACTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAATGGCTTTACATGGTTCTTTT
PF3D7-0831700_	ref	AAAAATGGATAAAAGCCAAGTACATGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTAAAGATGTTTCCAAAAATTCAAAAT
PF3D7-0831750_	ref	TGTACATATGAATGATGAAAATATTATCTTAGATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTATCGTATGTGTAAAACTTTTGATTT
PF3D7-0831750_	ref	TTTGTATTCAAAAACATTTTAAAGACCTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATAGCATATGTCTTTCTTAAGTTTT
PF3D7-0831750_	ref	AATACTGATGTAAATAAACATAAACTTAATGATTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCACTCAGAAATTATTATCGTCAACA
PF3D7-0831750_	ref	TTTTTATAATACTATCAACTTTTCCATACCTTAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTACATATTATATCATCCCCTCCTAATTT
PF3D7-0831750_	ref	AAAATTTATATGTTATTGGAGTGAAATTATTGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATATAGCACGTAAAGTTTTAATTAATATAT
PF3D7-0831750_	ref	TTAGACAAACACACTTCTTCACAAATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATTTACATAAACATGAAAATAAGTATATTT
PF3D7-0831750_	ref	ATGGGACAGGTGTAAATATAGTTTATAATTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTACTTAATAAAAGAGTTAAACTTGTTAAAAT
PF3D7-0831900_	ref	GCTTATGTTTGTATATGATTGGATTTTTATATATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAGCATATTTATATTTCTACATATTTTTAATTTT
PF3D7-0831900_	ref	AATCATATACAAACATAAGCAAAGAAACTTAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTAGTTTTCAACTTTTTCTAAGCT
PF3D7-0832000_	ref	ACTTGTTCACTATTTCTACTTTTAGTTTTTGTTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAATTATCATTTACCTTATTTGATAAAGATAAT
PF3D7-0832000_	ref	ATATATACACCAATGAATATTACAAATCAAATGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAAATTATTTGCTTACCAATTGAACCAG
PF3D7-0832000_	ref	AAGGAATGAATATATTATTGAGTAAATATTGATGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCATTAGATTGTTGGTATGTGTTTAA
PF3D7-0832000_	ref	TTCCTAATAAAACCCTCATAAACAATTACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATAACCACTCTAAAATGTTATTATTTGC
PF3D7-0832000_	ref	AATTAGTATTCATACAAAATGTGCAATAAGTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTGTGATAGTAAAAATTTATTAAATAGAAAG
PF3D7-0832000_	ref	TACCACTCTAAAATGTTATTATTTGCCTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATATTTTCTATCATATTTCTTATAAAACTTATT
PF3D7-0832100_	ref	AATTAGTAGTTATACCTGCTATTTTATTAGTTTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATGTAATATAGGCGAAATAATGAATT
PF3D7-0832100_	ref	CTTATGTTTTGTAATGGTGAGGTTCATANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGACAAAGGAGACAACTGAAACTA
PF3D7-0832100_	ref	TGAACAAGAATATTGGGATTATTGAAATTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTAGTTATACCTGCTATTTTATTAGTTT
PF3D7-0832100_	ref	ATATATTAGAATGTCGCATGCTAATATCATTGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTACAGCAATTTTTGTTACTATTCAATT
PF3D7-0832100_	ref	ACTAATATCCCTCCACATTTCAAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAAATTGTCTGCATTAATAATTGATTTC
PF3D7-0832100_	ref	TACTTTATATGCTATAAGTGTTTAGAAAGATACAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTCAACAAATTATTTTTAAAATGCAAAAT
PF3D7-0832100_	ref	AAATTTTGCATTACTTCTTTCATTTCTGAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTCAACTTTAACTGCTACTGATTT
PF3D7-0832100_	ref	TGACAAACATATGATCAAAAACAGACAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATATATAATACTATATATATCCATATTTTTACTGG
PF3D7-0832200-2	ref	ATTTAAAAATTTTCTCCTAATTAAACGAACATTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAAATACTCCTGCATCATTTGTTT
PF3D7-0832200-2	ref	AAAATATAATGATGTTACAACTAAAAGAAAATGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGTTCAGAATATAATAATATGTGACAAAA
PF3D7-0832200-2	ref	GTTATCATTATTTTGGAGGTAGGAAACCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAACTAAAAGAAAATGTGATAATATAAATTATAAT
PF3D7-0832200-2	ref	ATTTAATACACATAAGAAAATATTTACAGAATGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGTTATCATTATTTTGGAGGTAGG
PF3D7-0832200-2	ref	TTTCACGTACATTTTTCATAGATACAGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTTCTAATCCTTGGAGCTCTTT
PF3D7-0832300_	ref	ATTCTCCTTAAGAAAATGAATTAACATTCTGATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGAACTTGTATATAGGAGTATATGG
PF3D7-0832500_	ref	AACTTGACGGATTAACAATTGATGTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCATGGCAATATTGAAACTAGTAAT
PF3D7-1369900_	ref	CAGAGTGCAATAAACAGTATATATTTTACATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCCTCTGGGCTCAATAAATTTAATA
PF3D7-1369900_	ref	TTTTCCTTGTATTTCTTTCTTGTTCAATTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATTGTTTTTCTTATTTTGCTTAAATATTAAAAA
PF3D7-1369900_	ref	TGGGGGTTCGAATCCCTCTGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATTCTTTTATTTAATTTTAGAATAAGGAAAAA
PF3D7-1369900_	ref	ATTACGCCACTGGTGCTAATTTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTATATTTGTAATATTCAAAAATTTTTACTTTTT
PF3D7-1370100_	ref	TCTACCGCTGAGCTACACGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATATTTATTTATAATCCAGGCCACA
PF3D7-1370100_	ref	AGATCAGCGGGTCCATGGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGAATATCGTTTTAAAGAAGAAATAAACA
PF3D7-1370200_	ref	ATCGAAGTGACCCGGGTTCGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAGAAATAAAAAGAAATGCATGTAATTT
PF3D7-1370200_	ref	GGCAACGAAGTATTCTACCACTAGACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTATTTTATTTATTATTCTTTATTATTTATATGGAAC
PF3D7-1370300_	ref	TGCTTGCTCTGCCATTTTTAGATATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATGTTTTCCTTCACCATCAGTT
PF3D7-1370300_	ref	TTCTTATACCACTCAGTAAGTTCATTATAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTAGGAATTGGTTTACTAATTTTAT
PF3D7-1370300_	ref	TCCATCTAAAGCTTCAGAAAGAGAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTGGGTTTATATATAATAATAAAAAGGTATTTA
PF3D7-1370300_	ref	ATCACGACCATGATCACGAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATATAGTAATATTATTATTTTAAGTGATACATT
PF3D7-1370300_	ref	TAGAAATGAGGTGCATGGTGATAATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTTTATTTTTGCATGTACATACA
PF3D7-1370300_	ref	AATTAAATGCTTCATAAGATTCTTATATGGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCACGCTCATGAACTTGATCAT
PF3D7-1370500_	ref	ATACGTTAAACCTTAAAATGAATTTACTTATTGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTCTTTACTACTACTAATATATATTATATATGTTAC
PF3D7-1370500_	ref	ATGAGAACATATCATATAATATATAGTCCACTATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATTGATAGCATGTTATTGTTTGTTAT
PF3D7-1370500_	ref	AACACAAAAACTATCATAAATCTTTTTACTCTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACTACATGACGTATATACCATAACAAA
PF3D7-1370500_	ref	ATTGGTATCAAATAAAAATGAAAAAGACTACGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTATAAAATTGAACATTGCATTAGAAAA
PF3D7-1370500_	ref	TTAACCCTCCCCGTAGTTAAAACTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACACCTACCCATATACCACTTAC
PF3D7-1370900_	ref	TTTTTGTACGTCTTAAATTCATAATTAAATGTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAATAATTAAAATATATGGGAAGTGTGTG
PF3D7-1370900_	ref	AAACATATATATATTATTTCTTCTGATTTTCAACGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAACACATTTAATTATGAATTTAAGACTAATT
PF3D7-1370900_	ref	GGATTTATTGAAGAAATGAAAATCTATGAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTAATAAGACTTAAATATATAATTAATTGTTACA
PF3D7-1370900_	ref	AATATTTCGTTATCCATCTTCACACATATATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATCTTATTAATAGTTATAATAAAATTATTAGCA
PF3D7-1371000_	ref	CATCCATCGTTAAGATTGTGGCTATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAATCCAAATTCTCTTTTTCTTCTATGA
PF3D7-1371000_	ref	TAGGAATACCACGTTAATTTGCCCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTACATATAAACTTTCTCTCCTCTAGAA
PF3D7-1371000_	ref	ACAATGATTAGAGGGTTTAGGGGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGAGTATGAGTACATTTGTTAGGAC
PF3D7-1371000_	ref	TCACTTTGGCGTAAATAAGATAACTCCAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCATTACAATCACGTTTAGGGG
PF3D7-1371000_	ref	GATACCGGGCCATAAGAAGGTAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCGTAAATAAGATAACTCCAAGTG
PF3D7-1371000_	ref	ATCTTCGTCTCAAAGGGGAAACAGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGCTCAGATCTTTTTATGAGTAGAA
PF3D7-1371000_	ref	GCTAACTCTTGTACAAACATAGTTGACAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTCCAAGGTTGCTATAAAATTAAAGT
PF3D7-1371000_	ref	GTAAAACCTATGTCAAGGAGTTCATTTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATAATTAAATTCCCTTCTGTATATGCTC
PF3D7-1371000_	ref	CTTCTGTATATGCTCCGTTCCCTCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCTGTAATTTTATTTTCAACCCCC
PF3D7-1371000_	ref	TGCGGTTATTGGTACACTCATTATTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATAAAATGAAAGCGAAAACAGGAA
PF3D7-1371000_	ref	TTTGTGAAACGACTTAGAAGGTGTAGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCAGTGCTTTGAATGTTAAGT
PF3D7-1371000_	ref	GCTCAATGAGAACAGAAATCTCGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATGAAATACCACTACTTTTACAGTT
PF3D7-1371000_	ref	TAAACTTCTCTCCTCTAGAACCAATCAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTTCCTTATAACAGAACAATTTCTA
PF3D7-1371000_	ref	CTCGTGTAGACTAAAAGGGGAAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATACCACTACTTTTACAGTTGTTTTA
PF3D7-1371000_	ref	ATTCTGACTGTGCATATAAAGGTGTCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTTTCTTATATTTCTCCCATTTCTATG
PF3D7-1371000_	ref	TGTTGAGGCTTATCTCTTGTGACAATTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACTGCTAATGTAAATGAGAAATTATACA
PF3D7-1371000_	ref	ACTTTCTCTCCTCTAGAACCAATCAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCACATAGTCTTTTACAACTACGATATA
PF3D7-1371000_	ref	AGATTGGAGTACAAAGATGTGTGATACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAAAAGCTCAAGGAGATAATTCTATAT
PF3D7-1371000_	ref	ATATATTTATTAACTACGGGCTTTACCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCTTCTTACATTTTCCTTCTTAATCC
PF3D7-1371000_	ref	TGCTTGTATGTTTGAGTATTCACTGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAGGAATGAGCAGTTTAAATAGTA
PF3D7-1371000_	ref	ACCCTTTTTCTTACTACTCCTCCCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCACTATTGTTTACCTCTTTCCTCA
PF3D7-1371000_	ref	AATAGTGCATTTGGTTTCTGGCTTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCGAAATGCGTATAATTATTCTGT
PF3D7-1371000_	ref	TATGTTTTATTCATATCACATACGCTCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATTGTAATGAACGATTTGCACG
PF3D7-1371500_	ref	CATTGTTTGAATAATTTGAACACTTTTTATAGTTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATAATAATTGCATTATATAATAATAATAGTAAGA
PF3D7-1371500_	ref	CATTCTTCAAAAGATAATAATACAAGTGATTTATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAACGAAAGAATTTAACAAATACCAGT
PF3D7-1371500_	ref	TTATTATATCATATATGTCTGAGTAGTGGAAAGCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTGAACACTTTTATAGTTATTCTTTATATT
PF3D7-1371500_	ref	TAAACCTAATTCCACTACAAACATTAACAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCCTAAAAGTAAGCATCATATTAAAAT
PF3D7-1371500_	ref	TATGTGTATATAGGTTGAATGGTTTAGACTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTAATAAATGATAAACTAAAATATATAAGTACA
PF3D7-1371500_	ref	AAATTACTTGAAATAATAAAACTAAAAATGTTCCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAAAAAGTTTTTCATATAAAATTAATAATTCTT
PF3D7-1371600_	ref	TGGATCAAAATAAGGATATGCTAAAAAGTGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTGTTCTGTTTACATTGTGTATCAT
PF3D7-1371600_	ref	TGGTGGTCCACATACACCTTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTATATCCCTCCAAACATCCAAA
PF3D7-1371600_	ref	AAAACAAAGAAATTCAGACAGTGATGAAAGAAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGAAAGAAAGAGATGAAAAGGAAA
PF3D7-1371600_	ref	ATTTTAGGTAAATTTTCAGACACCACCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTGGTCAGATGGTATTTTAGAAATT
PF3D7-1371600_	ref	TATTGTTTCCTTATTCCCTTGATTAGAGTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGATTGAAAAATATCAGCGCTTTT
PF3D7-1371600_	ref	CTGAAGAATCCTGAACTACACTTTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCCTCAGTCAAACTTTCATAATCA
PF3D7-1371600_	ref	TCTTCAAGTCCTCCTTCTGAAATGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCTTCAGAATTGTTATTCCTTCTGTA
PF3D7-1371600_	ref	TGCCCCAATAAGACGAATACAATTATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTTCGAGATAATAAAGAACAAGATGA
PF3D7-1371600_	ref	TCAGATTCATGAGAGATCATCAGCATTTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCTCTCCACCTGTATTATCTTTAT
PF3D7-1371600_	ref	TAGTTATTACTTCCACACTTTCACTACAGACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTTTTCTTCAATTATTTGTTCATTCCT
PF3D7-1371600_	ref	GGTTATCTGTACAAATCCATTTCATTTCCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACTCCATCTTATATCATCACATAATTTC
PF3D7-1371600_	ref	ATGATTTAGAAGGTTCAATGGACACCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGATACAACCACATCTCATTCT
PF3D7-1371600_	ref	GTTCGTTCTTTATGACTTAATTGAGATGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCACTTTCTGCGCTTTCTTTATT
PF3D7-1371600_	ref	AAAGTTAATTTTGTGGGATTGCCTGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCCTGAAGCTTCAAATACTGATAATAA
PF3D7-1371600_	ref	ATATTGATCTATAACTCCTGCGTTCTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCACAGGATATTCATCTATTCCTTTAGATA
PF3D7-1371600_	ref	ATTTGAAAACGAGAAACAGTTGGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATGTTACAAGGGGAAGTGTT
PF3D7-1371600_	ref	TAAAGAGAAATTGTGGGCGCAATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGGAAACAGAGAAAAATATTGCA
PF3D7-1371600_	ref	TAACAAGTTTGATTCCAGTTTTACAGCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCACCATTCTTTTCGTAACTTTATT
PF3D7-1371600_	ref	AAAGATGTGAAACATGATGATTCCGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAGATGTTAAACAAAATAAGGAGCATA
PF3D7-1371600_	ref	TGTATTTTTCCCACCATTCTTTTCGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTCCTATTTTGCACCCATTTATTAT
PF3D7-1371600_	ref	AAAACCTGAATTAGTATCTGCTGCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGTTTACTTTGAGAAACACATATAATGA
PF3D7-1371600_	ref	ATATATATTTTTGATTCGCGACGGTAACGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTGTAAAGAAAACCTGAATTAGTATCT
PF3D7-1371700_	ref	TTGTTGGGTTGTATATATATTTTTATTAGTAAGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATTCATTAAGAAGGATAAGGGA
PF3D7-1371700_	ref	TGTATTTCTTTCTTTTTCATATTTATCAAATGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATATTATGTAAAACGCACATCATTTTT
PF3D7-1371700_	ref	TCATGAACTGAACAATTTGATAAACGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATATTTCAAACCAAGAGAAGAAA
PF3D7-1371700_	ref	TATTTTCATTTAAATTTGTTATCATATTGTGTGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAGCATAGGAAGACTGTAAAATTAA
PF3D7-1371700_	ref	GGAGAAGATATATAATTTTAAAAGAAGGGAAGTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATATTTTTATAGAATATATTAATTAATCATGGA
PF3D7-1371700_	ref	TCATTAATGTTATCTAATGAATCCCTACATATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATCTTTATTAATGATTTCTGACCTAATT
PF3D7-1371700_	ref	AAAATACCTATTGATATATGGGTAGAACAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAAATGTGAATATGAAATCTTATGTATAT
PF3D7-1371700_	ref	ATACTTTTATATGTTTTATGATCCTTCAAAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTATCTGACTCATATAATATTTTATAAAATTTA
PF3D7-1371700_	ref	TTGTTGTGTCAGATATAAGTAATGAAGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAATGAATATTATCCAGGAATAACTC
PF3D7-1371700_	ref	TTTCCTTTTATATAATCAAATACATTTTCACCAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTATAAATAGGTGTAGATTGAGACAAAT
PF3D7-1371700_	ref	GGAATGTTGGAAAATTGTGTGGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAATGAGATTACATAATGCTGGATTAA
PF3D7-1371700_	ref	TATACAAGGTTCAAATGATTCAAAAGGTTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGATCTGAACATTTCCATATAAAA
PF3D7-1371800_	ref	AAATATATAGAAATACGGTTCCTAAAACAAATCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTGTAATAGAAAAATGAAAAACAATGAA
PF3D7-1371800_	ref	AACCATTACATGAATATTATACCTTTGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTTTTTAAAAATCATATATGAAAACACATTT
PF3D7-1371800_	ref	GCTTACGTGATGAGAGGATGATAAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGGGATCTATTATAAAATAATAAAAAGAAAA
PF3D7-1371800_	ref	CTCTCATCATGCTAAGCACACATTAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGAACTACCTATTATGGAAAATAAAAAT
PF3D7-1371800_	ref	TGAAAAGAAAAGATCTAAAAGAACTGCTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAAGACTCAGTAATGGAAAATGAA
PF3D7-1371800_	ref	TTTTTATAGACAATTTAATCCTGTTATACTTTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTTCCTATCAAACATGCAAATAAAAA
PF3D7-1371800_	ref	TATATACAAAATGTTGGAAAAGATATTTGATCGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATAAAATTGAAAACGTCGATTAAAAA
PF3D7-1371800_	ref	TGTTCATTTCTCTAATATCTTTTGTATCTTCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTGTTCTTTATATTCATCTGATAAATT
PF3D7-1371800_	ref	ATTAAATCAATTAATAAAAGGATTCCTATAGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAATTTTATTACTATTGGAAAATGATGAA
PF3D7-1371800_	ref	ATCTTTATTTCTTTTATATGTTTTAATTGATCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCTACTTTCATCGAAATATTCTGTATTT
PF3D7-1371800_	ref	TACAAATTATTACTTGATAAAGATGAAGAGAAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCCCAATAAGTTCAACACCTATTAAA
PF3D7-1371900_	ref	TATATATATTTGTAAACCTTTCCTCTTCTTTTACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAATCTTCGTTTGGCTTTTTATT
PF3D7-1371900_	ref	AAATACTTCAATTGTGTATGTGTTTTATTTTCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGTAAAACTTTCTGCCATACATCT
PF3D7-1371900_	ref	AATTGGTATGGAAGTAAGTGTTAGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCAGAAATAATAAAAATAACGGATTAATATT
PF3D7-1371900_	ref	TAATATAAGAAAGTCCTGATACATACCATTTAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGATCTTAACTTATCAATTATACCATTAATTA
PF3D7-1371900_	ref	TAGAATTAAATGAAACCTCAGAATAGTAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATTCCCAATGATAATCATAAATACG
PF3D7-1371900_	ref	CAAGTGATGGTAACAATGAAAATAATACACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATAGTTAAACAAGAAAATTATAAAGCATAA
PF3D7-1372000_	ref	TGATGTACGTATCATTTATGGTAATTTATAATTAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTAAAAATTATTATAATGAAATGTTATAATGAATT
PF3D7-1372000_	ref	TTAAATTGCTAAATTCATCTAAACATGAAAATAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTACTTTTCTTATAATTTATTATGTTATTC
PF3D7-1372000_	ref	TCATCTATATTAATCATTGTGATGTTTGATTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGAGTATAAAAATGAATTATATGATAAATATTAT
PF3D7-1372000_	ref	TCAACATATATATATTACGGAATGAAAAGGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTCAGATAAATTTCTTTCAACCAATGA
PF3D7-1372000_	ref	ATCGGAAATGAATATCAGAAAATGATCAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGAATGATGAAAATAATACCTCAGATT
PF3D7-1372000_	ref	AATGATTGGACCATAATAATTTCTGAGTGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTTCAGTTTCATTTTCTGTATCATTTT
PF3D7-1372000_	ref	AAAGGGTGACATTATTAGAAAAACATTAAATANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCAGAAAATGAATCAGAAGATCA
PF3D7-1372000_	ref	TCGCCATCAGATTCATTTTGTGATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACTATTTAATTGTCTTGTAATATCATTATAATT
PF3D7-1372000_	ref	AAAATTATGAAAATCGTGTTTGTCTGAATACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGATAAGTTTAATGATTCAAATAAAGTTTAA
PF3D7-1372000_	ref	ATACATTAACTAAATCTTCATTTGTATATATTTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATATGATGCATTTAATAATTTCACTTC
PF3D7-1372100_	ref	ATTATTTTATATTGTCCTTTTGGTAGGTTGTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGGAGTATTATTTTATTTTTCATTATTCTTA
PF3D7-1372100_	ref	TGTTATTTTATCCTTCCTATATTTCAAAGGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTATATTGATACTTATATAAGAAGAAAAACAA
PF3D7-1372100_	ref	ATGAAGGAATAAAGAAAGAATATGAATTAGATTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATGATATATTGAGTTATAAAAATATAAAAGAT
PF3D7-1372100_	ref	TGCATCAATTCTTCAATTAAAACATCAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCCTCTTTCATTTTTCATTACATTCAA
PF3D7-1372100_	ref	TTTTAATGAATGGACTGAGGTCAATTCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTAGATTTCAATATTGAGAAGAACGA
PF3D7-1372100_	ref	AAATCAGTTATTATATGATTAAATTTTCCTCTTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTATTAATCATAACAAGCATTTTAAATTCT
PF3D7-1372100_	ref	AGTTACAGATAAATACAAGAAGATATATCAAGAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGATTATACATGAAAAATGCAGAAATA
PF3D7-1372100_	ref	TTCGTATTCTCTTCATTTATTTTATCTTGAAATGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTAAAGAATAATGAAATAAACATTTTTATCTAT
PF3D7-1372100_	ref	TAAGAGCTTCATGAGTAGATGTCCTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTGTCCTTTTGGTAGGTTGTAAT
PF3D7-1372100_	ref	TTTCCCATCATATTTACATATGTTCTGTAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGTATGACATTTCGTTTAATTCA
PF3D7-1372100_	ref	ATAATTTGAATGAAGAGAATAATATGAAATCAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGACATGGTTTATGAATCTAGTGTATATTTA
PF3D7-1372100_	ref	ATCATACTCACCTTTGGATGTTTCGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTTCCTCAATTAATAATTTGTCAACATT
PF3D7-1372100_	ref	TTATTGAGAGGTATATCAAATAATGAAGTACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGAAACATTCATTGATTATTATAATGATA
PF3D7-1372100_	ref	TATCTTTGTGGATATATTATCATTTGATTCTTCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCCAATTAGAATCATTTTCTTCATCTA
PF3D7-1372100_	ref	ATTAATATTTCATACGTAAAAGAATACAAACCTAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAGAATCAGAAGATATTGAATTATTTAGA
PF3D7-1372100_	ref	TCAATTTGTACAGTATCATTCATATAATCTTTTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACACATTCTACAATTAGTTTATTAGAAA
PF3D7-1372400_	ref	AACGTTTGTAAATTTTTGTGTTGTATATGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTATTAATTAAAAGTGATTCCATGTTTAG
PF3D7-1372400_	ref	ATTATTTAGCATATCCGTTTCTATATATTCACCTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCATTTTCCCCTTTACATAATCAAT
PF3D7-1372400_	ref	TTAAGTGGAAGTAGCACGGGTAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAAACATTAAATGAGACTATTTAT
PF3D7-1372400_	ref	TTCATATTTCTTTTTAACTGCATCTATGTAAAAGGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACTCCCTGAGTTATGTTCTTCT
PF3D7-1372400_	ref	AAGAGAAGGATCATTATTAAATAGTAATGAAAGAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATGGAAGTGATAATGAAAATAAAAGA
PF3D7-1372400_	ref	TTCTTCTTAATTGTTTTTGTACTCCCTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTTCATGATTCATCCTTTATTCCA
hrp2_S0_Sub0_	malt0	CACGAAGCCGCCACACATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAACCGATGCTCATCATGCAG
hrp2_S0_Sub0_	malt1	CACGAAGCCGCCACACATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATCCGATGCTCATCATGCAG
hrp2_S0_Sub0_	malt2	CACCATGCAGCCGCACACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAGCTGATGCTCATCATGCAG
hrp2_S0_Sub0_	malt3	CACGAAGCCGCCACACATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTGATGCTCACCATGCAG
hrp2_S0_Sub0_	mref	cacgaAGcCGcCACACATTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNaaccgatgctcatcatgcag
hrp2_S0_Sub0_	malt0	GATGGGCATCGGCTGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTGCATGGTGAGCATCG
hrp2_S0_Sub0_	malt1	GATGGGCATCGGCTGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGAGCATCGGCT
hrp2_S0_Sub0_	malt2	GCTGCATGATGAGCATCAGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGGTGAGCATCAGTT
hrp2_S0_Sub0_	malt3	GCTGCATGATGAGCATCGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGGTGAGCATCAGTT
hrp2_S0_Sub0_	mref	gctgcatgatgagcatcggatNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNctgcatggtgagcatcagtt
hrp2_S0_Sub0_	mref	catcggctgcatggtgagcatNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNctgcatggtgagcatcagtt
hrp2_S0_Sub0_	malt0	ATGCAGCTGATGCTCATCATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTCATCATGCAGCCGAT
hrp2_S0_Sub0_	malt1	ATGCTCATCACGCTCACCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTCACCATGCAGCTGAT
hrp2_S0_Sub0_	malt2	ATGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTCATCATGCAGCCGAT
hrp2_S0_Sub0_	malt3	ATGCTCATCACGCTCACCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTCATCATGCAGCCGAT
hrp2_S0_Sub0_	malt4	ATGCTCATCACGCTCACCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCATGCATCCGAT
hrp2_S0_Sub0_	malt5	ATGCTCATCACGCTCACCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCATGCAGCCTAT
hrp2_S0_Sub0_	mref	atgctcatcacgctcaccatgNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNatgctcatcatgcagcctat
hrp2_S0_Sub0_	malt0	CGATGCTCACCATGCAACCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt1	CGATGCTCACCATGCAACCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCCCATCATGCTCACCAT
hrp2_S0_Sub0_	malt10	CGATGGCTCATCATGCAGCCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt11	CGATGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt12	TGATGCTCATCATGCAGCTGATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt2	CGATGCTCACCATGCAACCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt3	GATGCTCATCATGCAGCCGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTCATCATGCATCCGATG
hrp2_S0_Sub0_	malt4	CGATGCTCACCATGCAGCCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt5	CGATGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt6	CGATGCTCACCATGCAACCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt7	TTATGCCCATCACGCTCATCATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCACGCTCATCAT
hrp2_S0_Sub0_	malt8	TTATGCCCATCACGCTCATCATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTCATCACGCTCACCAT
hrp2_S0_Sub0_	malt9	CTCACCATGCAGCCGATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	mref	cgatgctcaccatgcaaccgaNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNatgctcatcacgctcatcat
hrp2_S0_Sub0_	malt0	ATGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt1	ACGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt2	ATGCTCACCATGCAGCTGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt3	TGCATCCGATGCTCATCATGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTCATCATGCAGCCGATG
hrp2_S0_Sub0_	malt4	ACGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTCATCATGCTCACCAT
hrp2_S0_Sub0_	malt5	ACGCTCACCATGCAGCCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt6	ATGCTCATCATGCAGCCTATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCCCATCATGCTCATCAT
hrp2_S0_Sub0_	malt7	ATGCTCATCATGCATCCGATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCCCATCACGCTCATCAT
hrp2_S0_Sub0_	mref	acgctcatcatgcatccgatgNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNatgcccatcatgctcatcat
hrp2_S0_Sub0_	malt0	CATCGGCTGCATGATGAGCGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGATGAGCATGATGGGCATAG
hrp2_S0_Sub0_	malt1	CATCGGCTGCATGATGAGCATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGAGCATGATGGGCATCG
hrp2_S0_Sub0_	malt10	CATCAGCTGCATGGTGAGCATGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAGCGTGATGGGCATAA
hrp2_S0_Sub0_	malt11	CATCGGTTGCATGGTGAGCATCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGATGAGCATGATGGGCATAG
hrp2_S0_Sub0_	malt12	CATCGGCTGCATGATGAGCGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTGAGCATGATGGGCATCG
hrp2_S0_Sub0_	malt13	CATCGGATGCATGATGAGCATGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTGAGCGTGATGAGCATCG
hrp2_S0_Sub0_	malt2	CATCGGCTGCATGGTGAGCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGAGCATGATGGGCATCG
hrp2_S0_Sub0_	malt3	CATCGGCTGCATGGTGAGCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGATGAGCATGATGGGCATAG
hrp2_S0_Sub0_	malt4	CATCGGCTGCATGATGAGCGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAGCGTGATGGGCATAA
hrp2_S0_Sub0_	malt5	CATCGGCTGCATGATGAGCATCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGATGAGCATGATGGGCATAG
hrp2_S0_Sub0_	malt6	CATAGGCTGCATGGTGAGCATGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGATGAGCATGATGGGCATCATAG
hrp2_S0_Sub0_	malt7	CATCGGCTGCATGATGAGCATCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAGCGTGATGAGCATCA
hrp2_S0_Sub0_	malt8	CATCGGCTGCATGATGAGCATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAGCGTGATGAGCATCA
hrp2_S0_Sub0_	malt9	CATCGGCTGCATGATGAGCATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATGAGCGTGATGGGCATAA
hrp2_S0_Sub0_	mref	CATcgGctgcatgatgagcgtNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNgatgagcgtgatgggcataa
hrp2_S0_Sub0_	malt0	ATCATCTACATGTGCTTGAGTTTCGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTGAGCATGATGAGCAT
hrp2_S0_Sub0_	malt1	ATCATCTACATGTGCTTGAGTTTCGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCATGGTGAGCATGATGG
hrp2_S0_Sub0_	mref	ATCATCTACATGTGCTTGAGTTTCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNatggtgagcatgatgagcat
hrp2_S0_Sub0_	malt0	ATGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	malt1	ATGCTCCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	malt2	ATGCTCATCATGTAGCCGATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	malt3	ATGCTCATCATGCAGCCTATGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	malt4	ACGCTCATCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	malt5	TGCAGCCGATGCCCATCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACTTGTGTAGCAAAAATGCAAAAGG
hrp2_S0_Sub0_	malt6	ACGCTCATCATGCCAGCCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	malt7	ATGCTCACCATGCAGCCGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCGCATTTAATAATAACTTGTGTAGCAAAA
hrp2_S0_Sub0_	mref	atgctcatcatgcagccgatgNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGcATTTAATAATAACTTGTGTAGCAAAA
hrp3_S0_Sub0_	mref	tcgtggtgtgctccatcatggNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATTCATCATTCTATATTTACATGGaAGA
hrp3_S0_Sub0_	mref	TTTTGCTTCCGTACTTTTGTTAGATAACGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAATGCTTATTTTTcACATTTTCATGAA
hrp3_S0_Sub0_	malt0	GTGAGAATCATCAAAACAAGCATTAGCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAATGGTGTAAGTGATGCGTAGT
hrp3_S0_Sub0_	mref	GTGAGAATCATCAAAACAaGCATTAGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAATGGTGTAaGTGATGcGTAGT
hrp3_S0_Sub0_	malt0	ACACCATGATGAGCACCACCATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATCACGGATTTCATTTTAACCTTCA
hrp3_S0_Sub0_	mref	acaccatGATGAGCACCACCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCACGGATTTCATTTTAACCTTCA
hrp3_S0_Sub0_	malt0	CATTAGCTGCATGGTGAGCATTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGTAAAGTATGGGAATT
hrp3_S0_Sub0_	malt1	CATTAGCTGCATGATGAGCATTAGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGTAAAGTATGGGAATT
hrp3_S0_Sub0_	malt2	CATCAGCTACATGATGAGCATCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGTAAAGTATGGGAATT
hrp3_S0_Sub0_	malt3	GATGTGCATGATGGGCATCAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATGGTGAGCATTAGCTGCATG
hrp3_S0_Sub0_	malt4	CATCAGCTACATGATGTGCATGATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGTAAAGTATGGGAATT
hrp3_S0_Sub0_	malt5	CATTAGCTGCATGGTGAGCATTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGTAAAGTATGGGAATT
hrp3_S0_Sub0_	mref	cattagctgcatggtgagcattagNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCATGATGTAAAGTATGGGAATT
hrp3_S0_Sub0_	malt0	CTAATGCTCACCATGCAGCTAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCCCATCATGCACATCAT
hrp3_S0_Sub0_	malt1	CTCACCATGCAGCTAATGCTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATGCAGGTGATGCCCAT
hrp3_S0_Sub0_	malt2	CTAATGCTCACCATGCAGCTAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAAGTCAAGCACATGCAGG
hrp3_S0_Sub0_	mref	ctaatgctCAcCATGCAGCTAATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNatgcccatcatgcacatcat
hrp3_S0_Sub0_	malt0	TTTTGCTAAACAAGTTATTGTTAAATTCGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTAGCTGCATGGTGAGCATT
hrp3_S0_Sub0_	malt1	TTTTGCTAAACAAGTTATTGTTAAATTCGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATTAGCTGCATGATGAGCATT
hrp3_S0_Sub0_	malt2	GTCCTTTTGCATTTTTGCTAAACAAGTTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCATTAGCTGCATGATGAGCATT
hrp3_S0_Sub0_	malt3	GTCCTTTTGCATTTTTGCTAAACAAGTTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCCATCATGGTGGGCATC
hrp3_S0_Sub0_	malt4	GTCCTTTTGCATTTTTGCTAAACAAGTTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTAGCTGCATGGTGAGCATT
hrp3_S0_Sub0_	mref	GTCCTTTTGCATTTTTGCtAAACAAGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNttagctgcatggtgagcatt
hrp3_S0_Sub0_	malt0	TCAAATAAGAGATTATTACACGAAAGTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTTCCGTACTTTTGTTAGATAA
hrp3_S0_Sub0_	malt1	TTATTACACGAAAGTCAAGCACATGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCTTCCGTACTTTTGTTAGATAA
hrp3_S0_Sub0_	mref	TTATTACACGAAAGTCAAGCACATgcNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTTCCGTACTTTTGTTAGATAA
hrp3_S0_Sub0_	malt0	GAAGCAAAAACGGCAGCGGATANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTTGCTAAACAAGTTATTGTTAAATT
hrp3_S0_Sub0_	malt1	GAAGCAAAAACGGCAGCGGATANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTTGCATTTTTGCTAAACAAGT
hrp3_S0_Sub0_	malt2	GAAGCAAAAACGGCAGCGGATANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAGTTATTGTTAAATTCGGAGTTATT
hrp3_S0_Sub0_	mref	GAAGCAAAAACGGCAGCGGATAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTTTTGCATTTTTGCtAAACAAGT

Supplementary Table 7A. Unique molecular identifier (UMI) counts by sample and locus. **Allelotype coverage.**



PF3D7-1371600_S0_Sub0_mip33	PF3D7-1371600_S0_Sub0_mip42	PF3D7-1371600_S0_Sub0_mip43	PF3D7-1371600_S0_Sub0_mip44	PF3D7-1371600_S0_Sub0_mip45	PF3D7-1371600_S0_Sub0_mip46	PF3D7-1371600_S0_Sub0_mip50	PF3D7-1371700_S0_Sub0_mip0	PF3D7-1371700_S0_Sub0_mip2	PF3D7-1371700_S0_Sub0_mip3	PF3D7-1371700_S0_Sub0_mip4	PF3D7-1371700_S0_Sub0_mip5	PF3D7-1371700_S0_Sub0_mip6	PF3D7-1371700_S0_Sub0_mip7	PF3D7-1371700_S0_Sub0_mip8	PF3D7-1371700_S0_Sub0_mip9	PF3D7-1371700_S0_Sub0_mip10	PF3D7-1371700_S0_Sub0_mip11	PF3D7-1371800_S0_Sub0_mip1	PF3D7-1371800_S0_Sub0_mip2	PF3D7-1371800_S0_Sub0_mip3	PF3D7-1371800_S0_Sub0_mip4	PF3D7-1371800_S0_Sub0_mip5	PF3D7-1371800_S0_Sub0_mip6	PF3D7-1371800_S0_Sub0_mip7	PF3D7-1371800_S0_Sub0_mip8	PF3D7-1371900_S0_Sub0_mip0	PF3D7-1371900_S0_Sub0_mip1	PF3D7-1371900_S0_Sub0_mip2	PF3D7-1371900_S0_Sub0_mip3	PF3D7-1371900_S0_Sub0_mip4	PF3D7-1371900_S0_Sub0_mip5	PF3D7-1372000_S0_Sub0_mip1	PF3D7-1372000_S0_Sub0_mip3	PF3D7-1372000_S0_Sub0_mip4	PF3D7-1372000_S0_Sub0_mip5	PF3D7-1372000_S0_Sub0_mip6	PF3D7-1372000_S0_Sub0_mip7	PF3D7-1372000_S0_Sub0_mip8	PF3D7-1372000_S0_Sub0_mip10	PF3D7-1372100_S0_Sub0_mip0
chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13
2816383	2817675	2817881	2818001	2818179	2818278	2818861	2820938	2821300	2821460	2821662	2821820	2822011	2822205	2822308	2822469	2822584	2823252	2824238	2824387	2824557	2824720	2824862	2825044	2825212	2825286	2829900	2829964	2830165	2830343	2830434	2830641	2832906	2833241	2833330	2833491	2833575	2833764	2833883	2834183	2836945
2816585	2817894	2818091	2818208	2818356	2818498	2819039	2821144	2821493	2821668	2821870	2822011	2822216	2822373	2822491	2822659	2822761	2823451	2824413	2824571	2824756	2824924	2825065	2825213	2825411	2825460	2830069	2830171	2830368	2830520	2830643	2830843	2833066	2833442	2833507	2833682	2833782	2833939	2834055	2834346	2837114
PF3D7-1371600	PF3D7-1371600	PF3D7-1371600	PF3D7-1371600	PF3D7-1371600	PF3D7-1371600	PF3D7-1371600	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371700	PF3D7-1371800	PF3D7-1371800	PF3D7-1371800	PF3D7-1371800	PF3D7-1371800	PF3D7-1371800	PF3D7-1371800	PF3D7-1371800	PF3D7-1371900	PF3D7-1371900	PF3D7-1371900	PF3D7-1371900	PF3D7-1371900	PF3D7-1371900	PF3D7-1372000	PF3D7-1372000	PF3D7-1372000	PF3D7-1372000	PF3D7-1372000	PF3D7-1372000	PF3D7-1372000	PF3D7-1372000	PF3D7-1372100

PF3D7-1372100_S0_Sub0_mip1	PF3D7-1372100_S0_Sub0_mip2	PF3D7-1372100_S0_Sub0_mip3	PF3D7-1372100_S0_Sub0_mip4	PF3D7-1372100_S0_Sub0_mip5	PF3D7-1372100_S0_Sub0_mip6	PF3D7-1372100_S0_Sub0_mip7	PF3D7-1372100_S0_Sub0_mip8	PF3D7-1372100_S0_Sub0_mip9	PF3D7-1372100_S0_Sub0_mip10	PF3D7-1372100_S0_Sub0_mip11	PF3D7-1372100_S0_Sub0_mip12	PF3D7-1372100_S0_Sub0_mip13	PF3D7-1372100_S0_Sub0_mip14	PF3D7-1372100_S0_Sub0_mip15	hrp3_S0_Sub0_mip0	hrp3_S0_Sub0_mip2	hrp3_S0_Sub0_mip3	hrp3_S0_Sub0_mip4	hrp3_S0_Sub0_mip5	hrp3_S0_Sub0_mip6	PF3D7-1372400_S0_Sub0_mip0	PF3D7-1372400_S0_Sub0_mip1	PF3D7-1372400_S0_Sub0_mip2	PF3D7-1372400_S0_Sub0_mip3	PF3D7-1372400_S0_Sub0_mip4	PF3D7-1372400_S0_Sub0_mip5	PF3D7-0831400_S0_Sub0_mip0	PF3D7-0831400_S0_Sub0_mip1	PF3D7-0831400_S0_Sub0_mip2	PF3D7-0831400_S0_Sub0_mip3	PF3D7-0831400_S0_Sub0_mip4	PF3D7-0831400_S0_Sub0_mip5	PF3D7-0831400_S0_Sub0_mip6	PF3D7-0831400_S0_Sub0_mip7	PF3D7-0831500_S0_Sub0_mip1	PF3D7-0831500_S0_Sub0_mip2	PF3D7-0831500_S0_Sub0_mip3	PF3D7-0831500_S0_Sub0_mip4	PF3D7-0831500_S0_Sub0_mip5	PF3D7-0831500_S0_Sub0_mip6	PF3D7-0831500_S0_Sub0_mip7	PF3D7-0831500_S0_Sub0_mip8	PF3D7-0831500_S0_Sub0_mip9
chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8	chr8
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PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	PF3D7-1372100	hrp3	hrp3	hrp3	hrp3	hrp3	hrp3	PF3D7-1372400	PF3D7-1372400	PF3D7-1372400	PF3D7-1372400	PF3D7-1372400	PF3D7-1372400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831400	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500	PF3D7-0831500
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
15	4	24	44	19	22	18	14	12	2	19	6	18	15	2	11	3	13	2	1	18	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2	0	29	19	4	1	3	7	0	0	0	2	0	0	0	0	18	17	5	2	28	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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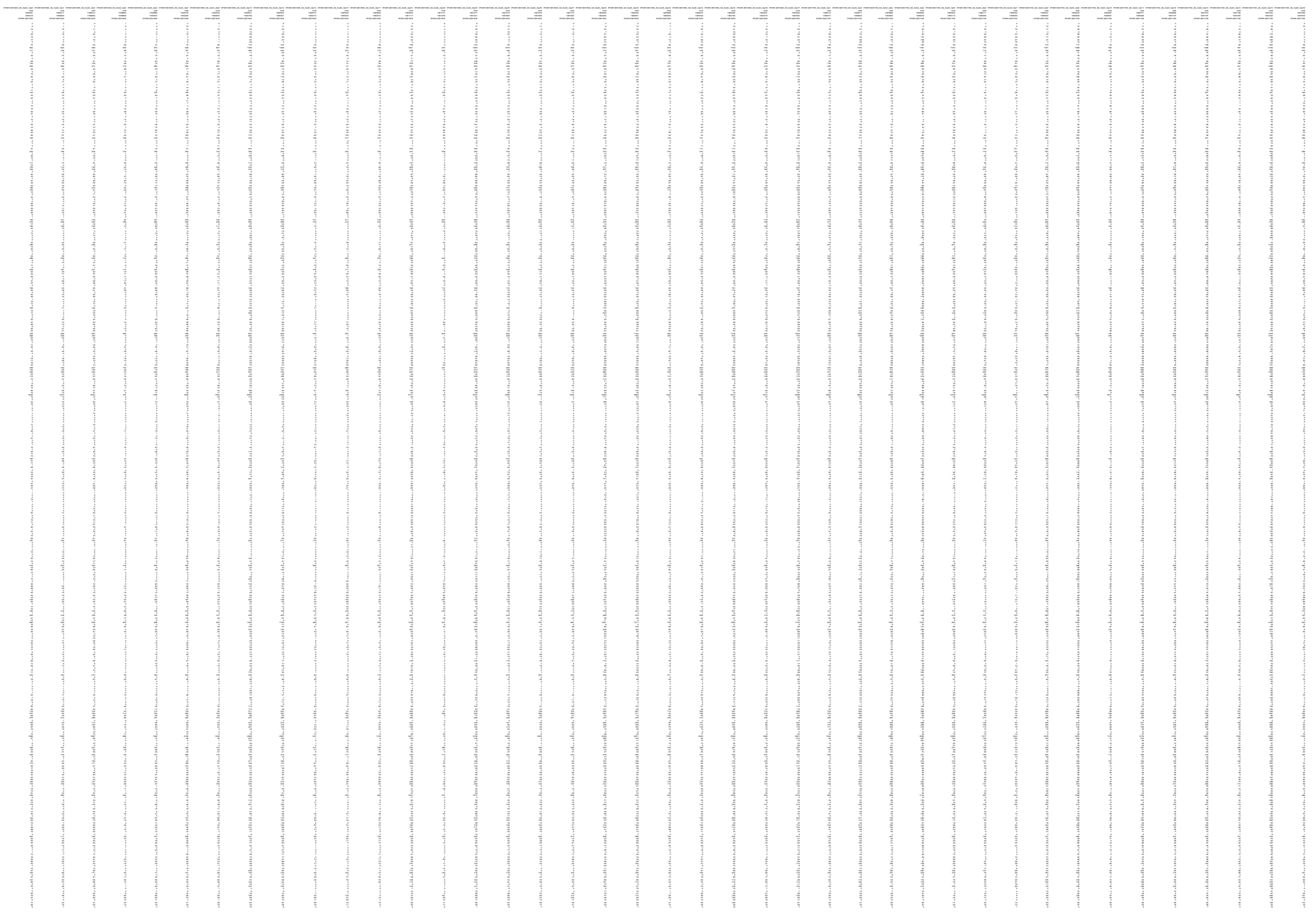
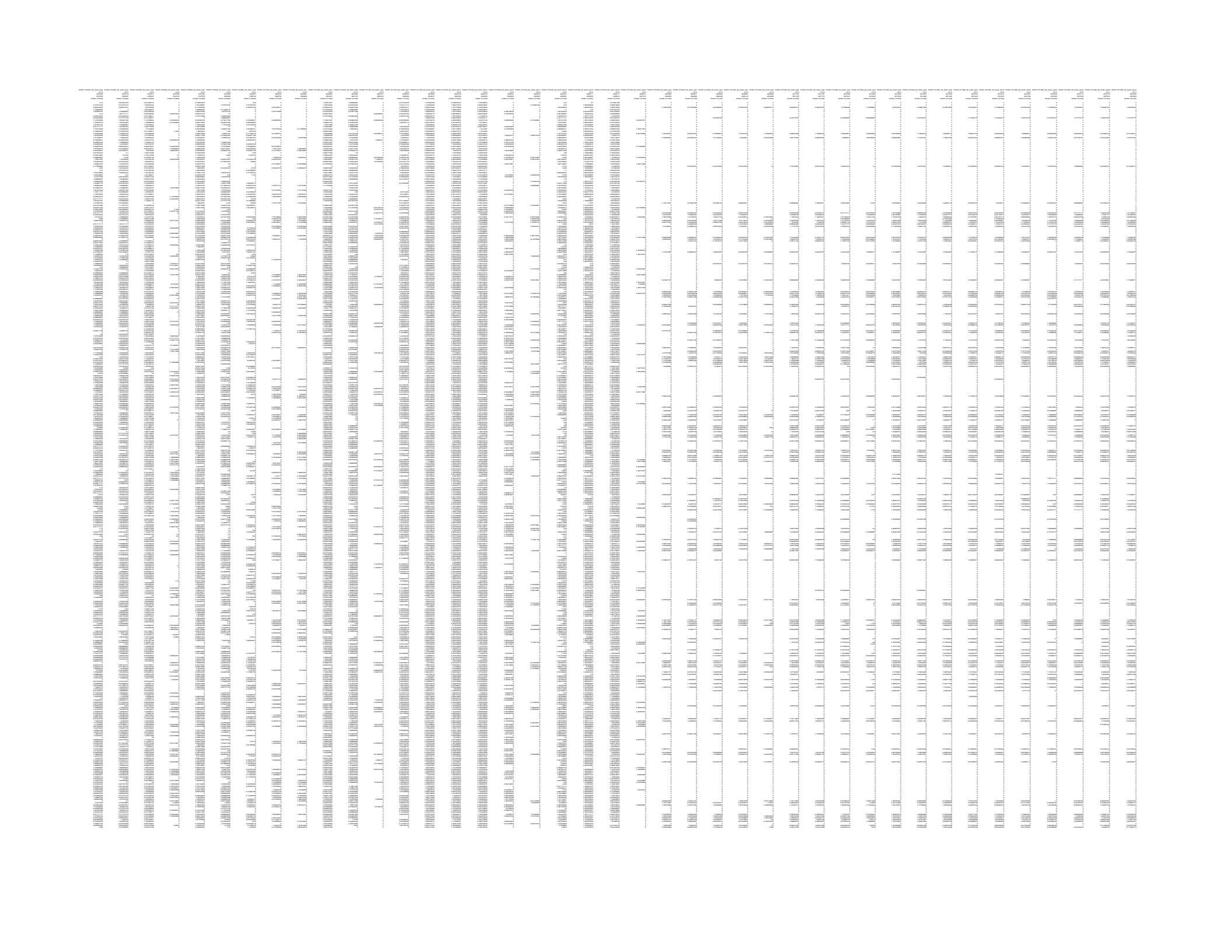
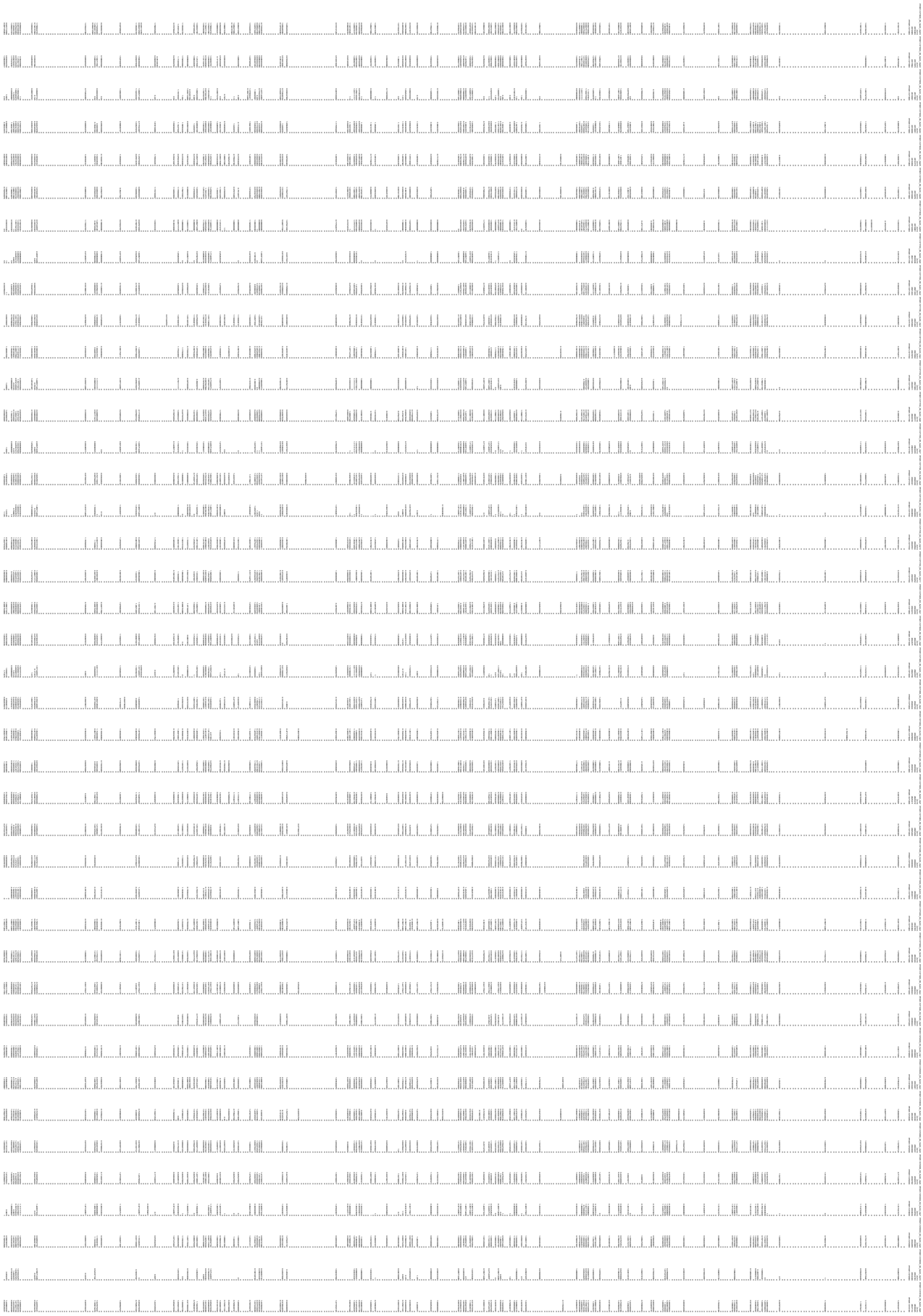
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
29	15	62	101	65	46	68	53	48	15	61	43	81	60	13	12	36	38	3	6	39	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
391	10	677	838	649	554	664	458	408	116	484	350	608	527	5	196	70	1831	255	153	923	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

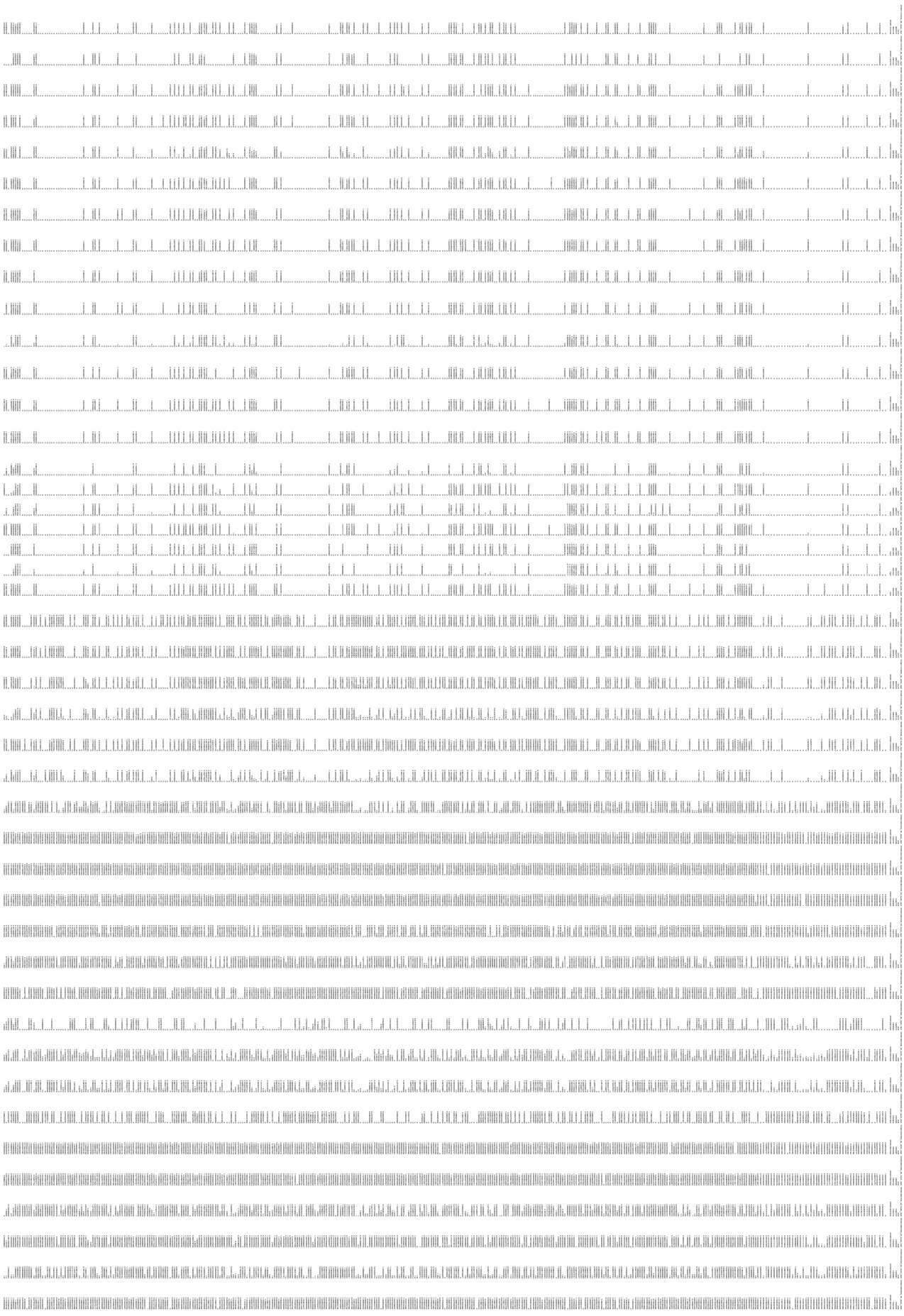


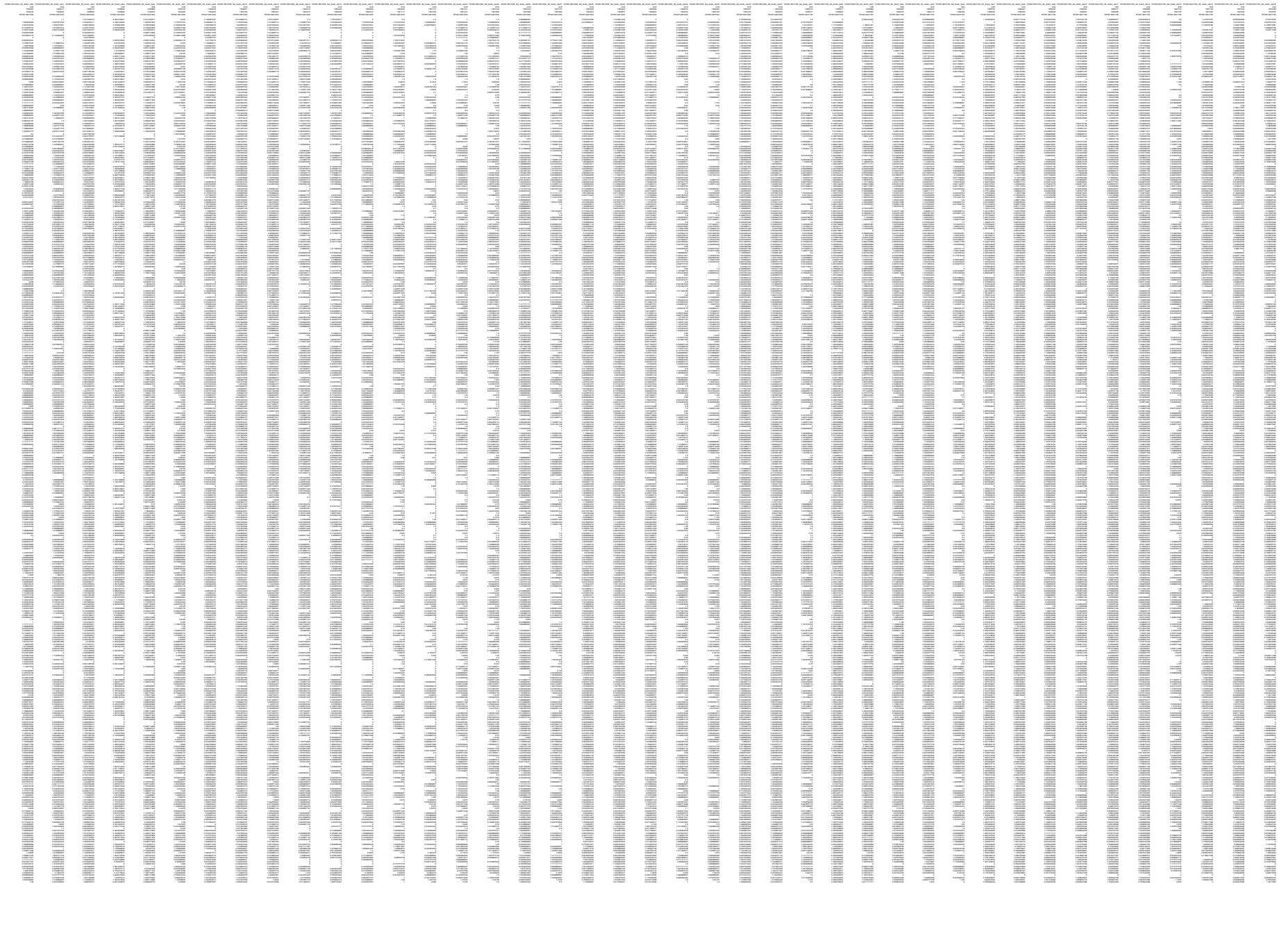
Supplementary Table 7B. Unique molecular identifier (UMI) counts by sample and locus. **Normalized coverage.**

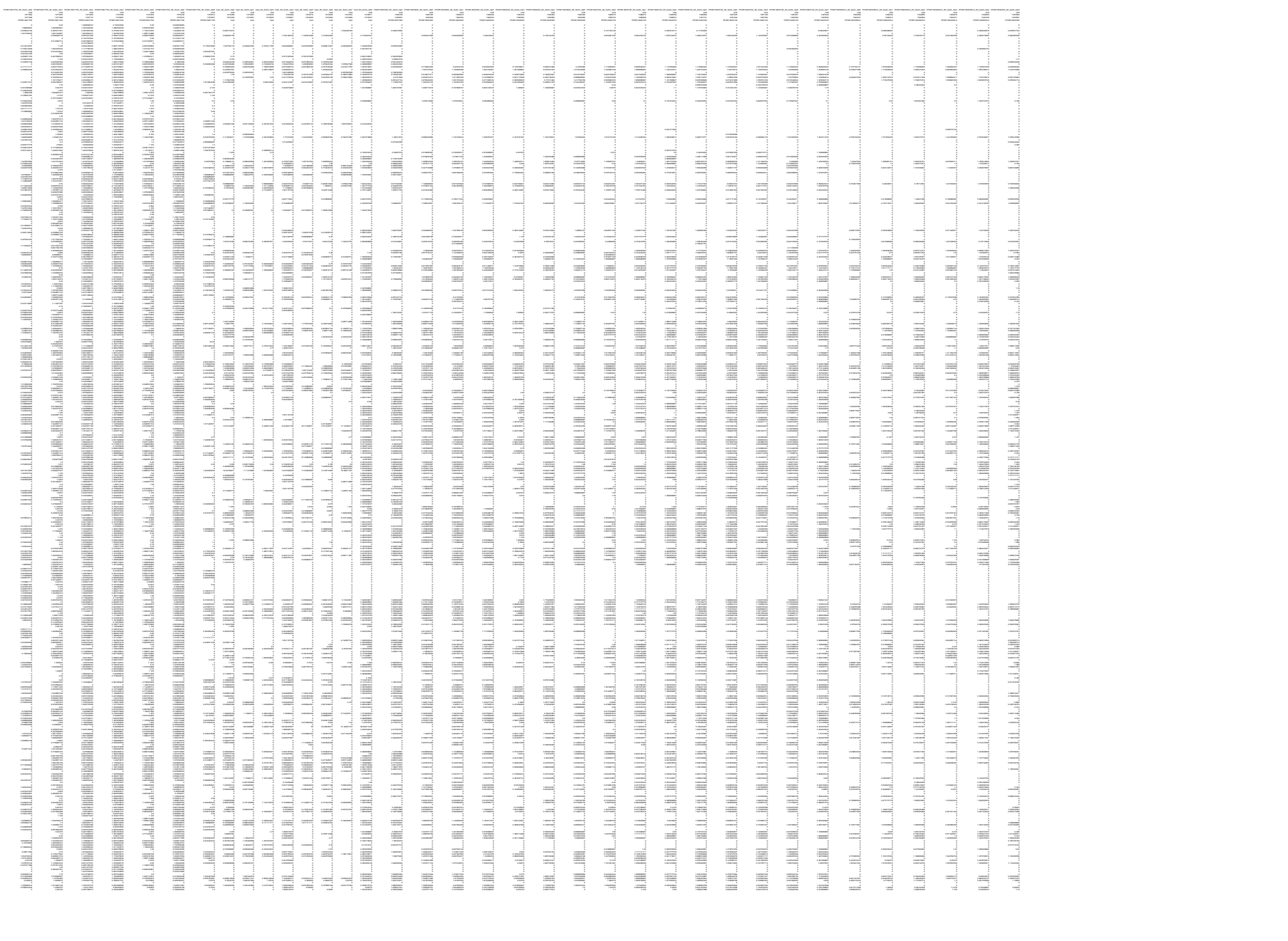
MIP	PF3D7-1370500_S0_Sub0_mip2	PF3D7-1370500_S0_Sub0_mip3	PF3D7-1370500_S0_Sub0_mip4	PF3D7-1370500_S0_Sub0_mip5	PF3D7-1370500_S0_Sub0_mip6	PF3D7-1370900_S0_Sub0_mip0	PF3D7-1370900_S0_Sub0_mip1	PF3D7-1371000_S0_Sub0_mip0	PF3D7-1371000_S0_Sub0_mip1	PF3D7-1371000_S0_Sub0_mip3	PF3D7-1371000_S0_Sub0_mip2	PF3D7-1371000_S0_Sub0_mip4	PF3D7-1371000_S0_Sub0_mip5	PF3D7-1371000_S0_Sub0_mip6	PF3D7-1371000_S0_Sub0_mip7	PF3D7-1371000_S0_Sub0_mip8	PF3D7-1371000_S0_Sub0_mip11	PF3D7-1371000_S0_Sub0_mip12	PF3D7-1371000_S0_Sub0_mip14	PF3D7-1371000_S0_Sub0_mip15	PF3D7-1371000_S0_Sub0_mip16	PF3D7-1371000_S0_Sub0_mip17	PF3D7-1371000_S0_Sub0_mip18	PF3D7-1371000_S0_Sub0_mip21	PF3D7-1371000_S0_Sub0_mip22	PF3D7-1369900_S0_Sub0_mip0	PF3D7-1369900_S0_Sub0_mip1	PF3D7-1369900_S0_Sub0_mip2	PF3D7-1369900_S0_Sub0_mip3	PF3D7-1370100_S0_Sub0_mip0	PF3D7-1370100_S0_Sub0_mip1	PF3D7-1370200_S0_Sub0_mip1	PF3D7-1370200_S0_Sub0_mip2	PF3D7-1370300_S0_Sub0_mip1	PF3D7-1370300_S0_Sub0_mip2	PF3D7-1370300_S0_Sub0_mip3	PF3D7-1370300_S0_Sub0_mip4	PF3D7-1370300_S0_Sub0_mip5	PF3D7-1370300_S0_Sub0_mip6	PF3D7-1370500_S0_Sub0_mip2	PF3D7-1370500_S0_Sub0_mip3
Chrom	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr11	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13	chr13
begin	1920280	1920386	1920588	1920716	1920809	1923308	1923404	1928534	1928670	1928875	1928878	1929064	1929217	1929391	1929591	1929808	1930223	1930440	1930874	1931054	1931278	1931365	1931768	1932215	1932904	2780863	2780963	2781106	2781638	2783006	2783188	2783580	2783801	2787987	2788160	2788281	2788486	2788646	2788740	2794273	2794388
end	1920462	1920590	1920760	1920884	1921024	1923492	1923648	1928747	1928856	1929058	1929088	1929266	1929412	1929607	1929811	1930025	1930407	1930652	1931075	1931262	1931491	1931584	1931984	1932417	1933114	2781067	2781160	2781280	2781839	2783199	2783408	2783800	2783989	2788186	2788346	2788487	2788674	2788819	2788907	2794464	2794592
Gene	PF3D7-1370500	PF3D7-1370500	PF3D7-1370500	PF3D7-1370500	PF3D7-1370500	PF3D7-1370900	PF3D7-1370900	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1371000	PF3D7-1369900	PF3D7-1369900	PF3D7-1369900	PF3D7-1369900	PF3D7-1370100	PF3D7-1370100	PF3D7-1370200	PF3D7-1370200	PF3D7-1370300	PF3D7-1370300	PF3D7-1370300	PF3D7-1370300	PF3D7-1370300	PF3D7-1370300	PF3D7-1370500	PF3D7-1370500
Sample ID																																									
6	0	1.354799391	0	0	0	1.333333333	0	0.356877323	1.224742268	0	0	0.231909055	1.229071332	0.414737529	1.594339623	0.876052948	1.764526244	0.543027006	0.620155039	1.573770492	1.6311019	1.163636364	0	1.008230453	1.844117647	1.333333333	0	2.485714286	2.227126597	3.5	6.3	0	0	1.08952381	0.2	0	2.367309907	0.971428571	1.714285714	3.2	3.188850174
52	0	1.642181079	0	0	0	1.287878788	1.102771851	1.216627239	1.484536082	0	0.318181818	1.686611311	0.558668788	0.659809705	1.560891938	1.251504212	0.802057384	0.987321829	1.40944327	1.690827801	1.376904201	0.727272727	5.045045045	0.982042649	1.371657754	1.515151515	0	0	0.506165136	1.363636364	1.909090909	1.708366668	0	1.238095238	1	0.727272727	0.672531223	0.706493507	0.909090909	2.181818182	0.658853342



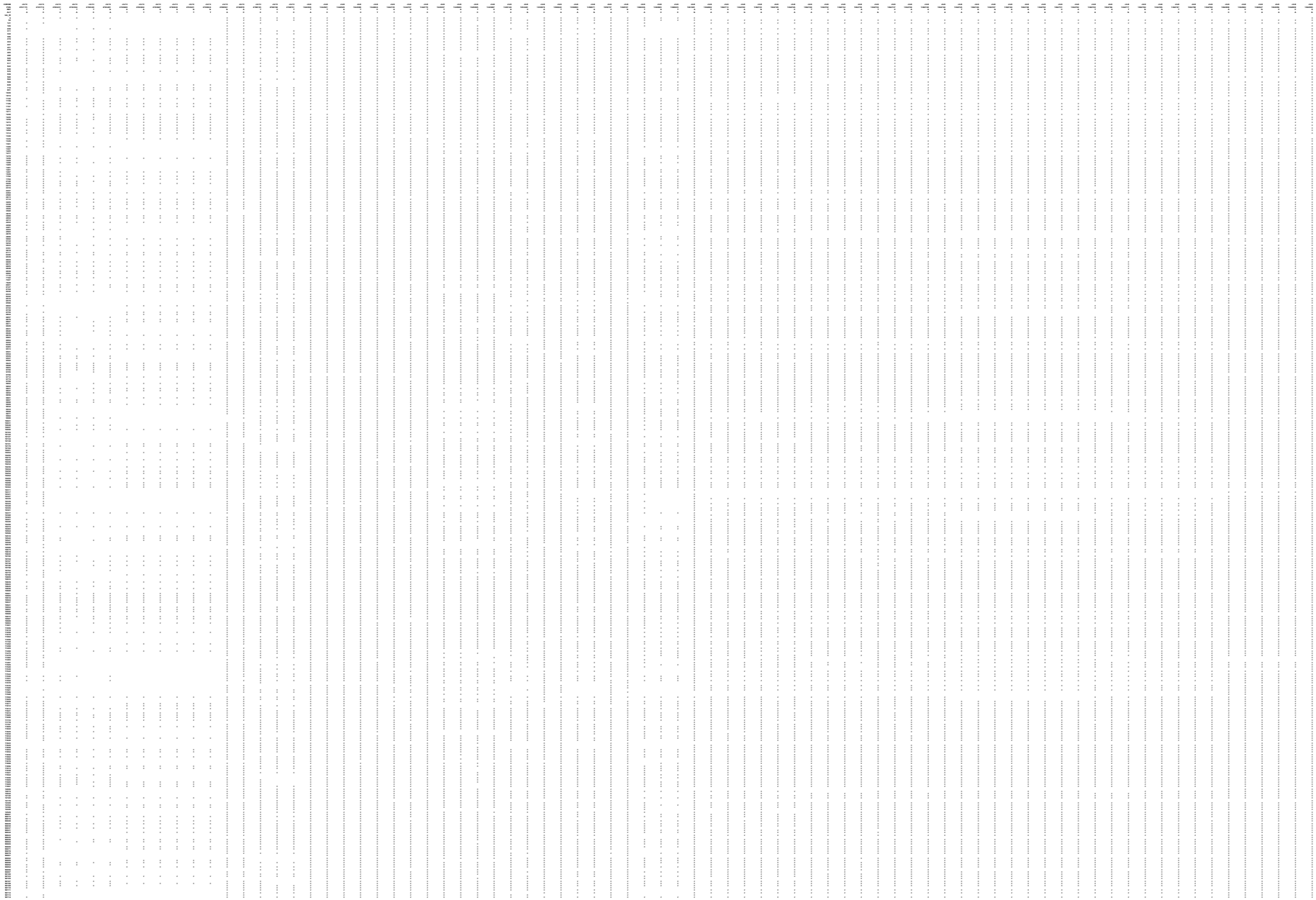








Supplementary Table 8. AMT-variant cells, which were connected for map-and-loop fibers.



Supplementary Table 9. ENA accession numbers of previously published WGS data.

Sample	ENA
QS0056-C	ERR1035493
QS0087-C	ERR1035520
QS0104-C	ERR1035536
QS0109-C	ERR1045266
QS0110-C	ERR1045267
QS0116-C	ERR1045271
QS0126-C	ERR1045280
QS0127-C	ERR1045281
QS0128-C	ERR1045282
QS0129-C	ERR1045283
QS0132-C	ERR1045286
QS0133-C	ERR1045287
QS0135-C	ERR1045288
QS0144-C	ERR1045295
QS0154-C	ERR1106575
QS0155-C	ERR1106606
QS0156-C	ERR1106576
QS0157-C	ERR1106577
QS0159-C	ERR1106579
QS0162-C	ERR1106581
QS0163-C	ERR1106582
QS0166-C	ERR1106584
QS0168-C	ERR1106586
QS0169-C	ERR1106587
QS0170-C	ERR1106590
HB3	ERR012788
DD2	ERR012840
3D7	ERR019061

Supplementary Table 10. Summary statistics of WGS coverage for samples sequenced in this study. Abbreviations: % Coverage, percent of the *P. falciparum* 3D7 (v3) genome with at least 1, 5, or 10 aligned reads per locus.

lab_ID	% Coverage 1X	% Coverage 5X	% Coverage 10X	median coverage value
1156	77.0	46.9	32.5	4
1194	88.1	69.0	53.2	11
1197	91.2	79.3	66.8	20
1208	92.3	84.1	74.7	30
1220	89.4	73.0	58.5	14
1225	79.0	46.6	30.4	4
1268	92.7	87.0	79.3	33
1284	92.2	83.0	72.8	26
1314	90.5	76.8	63.5	17
1333	85.7	60.2	42.2	7
5338	92.4	83.9	73.4	24
9592	93.5	89.2	82.9	36
9821	88.8	70.5	55.4	12
10809	76.3	46.4	33.2	4
10839	46.1	7.9	2.4	0
10885	91.2	78.3	64.1	16
10901	93.3	88.1	81.4	38
10905	91.1	79.4	67.7	21
10924	93.2	88.6	82.0	36
10937	93.0	85.7	76.6	30
10941	87.4	68.0	54.2	12
10957	91.7	80.5	68.5	21
12129	87.5	68.9	55.3	12
99112	92.9	86.7	78.6	31

Supplementary Table 11. RDT results from 12,572 enrolled subjects.

	SD Bioline					
CareStart	HRP2 and Pf-LDH	HRP2 only	Pf-LDH only	Negative	Missing	Invalid
HRP2 and Pv-LDH	536	31	7	18	0	1
HRP2 only	1000	549	49	123	1	3
Pv-LDH only	5	1	39	540	5	0
Negative	6	22	322	9297	0	7
Missing	0	0	0	0	1	0
Invalid	0	1	1	1	0	6

	***P. falciparum* Beta tubulin (*PfBTubulin*)**			***P. falciparum*- specific *pfldh***		
Adapted from:	Primers: Price RN et al. Lancet 2004. 364:438-447. Flap: Afonina I et al. Biotechniques 2007. 770-774. Combined assay: Parr JB et al. Malar J 2018. 17:137.			Pickard AL et al. Antimicrob Agents Chemo 2003. 47(8):2418-2423.		
Forward Primer (5'->3')	AATAAATCATAATGATGTGCGCAAGTGATCC			ACGATTTGGCTGGAGCAGAT		
Reverse Primer (5'->3')	AATAAATCATAATCCTTTGTGGACATTCTTCCTC			TCTCTATTCCATTCTTTGTCACTCTTTC		
Probe (5'->3')				FAM/ AGTAATAGTAACAGCTGGATTTACCAAGGCCCCA /TAMRA		
Cycling conditions:	Temp	Duration	No. Cycles	Temp	Duration	No. Cycles
	50C	2 min	x1	50C	2 min	x1
	95C	10 min	x1	95C	10 min	x1
	95C	15 sec	x45	95C	15 sec	x40
	60C	1 min		60C	1 min	
Reaction conditions:	SYBR Green MM			Roche FastStart Universal Probe Master (Rox)		
	Fwd primer	200 nM		Fwd primer	200 nM	
	Rev primer	200 nM		Rev primer	200 nM	
				Probe	200 nM	
	Template	2 µl		Template	2 µl	
	Total volume	12 µl		Total volume	12 µl	

	***Pfhrp2* - exon 2**			***Pfhrp3* - exon 2 (single-step)**		
Adapted from:	Baker J et al. J Infect Dis 2005. 192:870-877.			Baker J et al. J Infect Dis 2005. 192:870-877.		
Forward Primer (5'->3')	CAAAAGGACTTAATTTAAATAAGAG			AATGCAAAAGGACTTAATTC		
Reverse Primer (5'->3')	AATAAATTTAATGGCGTAGGCA			TGGTGTAAGTGATGCGTAGT		
Cycling conditions:	Temp	Duration	No. Cycles	Temp	Duration	No. Cycles
	94C	10 min	x1	94C	10 min	x1
	94C	50 sec		94C	50 sec	
	55C	50 sec	x45	55C	50 sec	x45
	70C	60 sec		70C	60 sec	
	72C	7 min	x1	72C	7 min	x1
Reaction conditions:	AmpliTaq Gold 360 Master Mix			AmpliTaq Gold 360 Master Mix		
	Fwd primer	200 nM		Fwd primer	200 nM	
	Rev primer	200 nM		Rev primer	200 nM	
	Template	10 µl		Template	10 µl	
	Total volume	25 µl		Total volume	25 µl	