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P. vivax microhaplotype deep sequencing assays

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We use this protocol and it's working

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Abstract

This SOP is adapted from a high throughput rhAmpSeq library preparation protocol by integrated DNA technologies (IDT) and has been optimized at the Australian Genomic Research Facility. The SOP describes the laboratory procedures for amplifying a panel of 98 *Plasmodium vivax* markers, using high-throughput multiplex PCR, for downstream genotyping by sequencing on the Illumina platform. The 98 markers include a panel of 93 microhaplotype loci (loci comprising of 3 or more globally high diversity SNPs) distributed across the *P. vivax* genome, as well as one *Plasmodium* species confirmation marker and 4 putative drug resistance markers. Further information on potential use cases for *P. vivax* microhaplotype genotyping, including recurrence classification, characterization of infection diversity, and spatiotemporal monitoring, can be found in Siegel et al [\[1\]](#).

Materials

	Item	Supplier	Size	Catalog#
	Reagents			
	IDTE, pH 7.5	IDT	10 × 2 mL	11-01-02-02
	IDTE pH 8.0	IDT	10 × 2 mL	11-01-02-05
	Nuclease-Free Water	IDT	10 × 2 mL	11-04-02-01
	rhAmpSeq Library Kit	IDT	16 rxn 100 rxn 500 rxn 5000 rxn	10000064 10000065 10000066 10000067
	rhAmpSeq <i>pv</i> custom PCR panel	IDT	0.4nmole (1.6mL)	Sales Order# 9413072 WO#3363760
	xGen 10nt UDI Index Primer Plates	IDT	Plate 1-4 Plate 1-8 Plate 1-16	10008052 10008053 10008054
	SPRIselect	Beckman Coulter	5 mL 60 mL 450 mL	B23317 B23318 B23319
	Ethanol (200 proof)			
	High Sensivity D1000 ScreenTape	Agilent	7 ScreenTape s	AG 5067- 5584
	High Sensitivity D1000 Reagents	Agilent	112 reactions	AG 5067- 5585
	Colibri™ Library Quantification Kit	Invitrogen		A38524500
	Consumables			



Item	Supplier	Size	Catalog#
DNA LoBind Tubes	Eppendorf	250 pcs (1.5 mL) 250 pcs (2 mL)	022431021 022431048
Eppendorf twin.tec [®] microbiology PCR Plate 96, semi-skirted, 250 µL	Eppendorf	10 pcs	0030129326
Axygen [™] 8-Strip PCR Tubes, 0.2 mL	Thermo Fisher Scientific	125 pcs	14-222-251
Microseal 'B' PCR Plate Sealing Film	Bio-Rad	100 pcs	MSB1001
Agilent Loading Tips	Agilent	112 pcs	AG 5067-5598
Agilent Strip caps	Agilent	120 pcs	AG 401425
Agilent Optical tube strip	Agilent	120 pcs	AG 401428
Equipment			
DynaMag [™] 2 Magnet or equivalent	Thermo Fisher Scientific		12321D
Agilent 4150 TapeStation	Agilent		
96-well thermocycler			
Microcentrifuge			
Vortex			
Centrifuge with plate adapter			

Before start

The only safe stopping point in the procedure is **after** clean-up (Step 48).



Sample Preparation

- 1 Input DNA does not require prior quantification or normalization. Using a *cox1* *P. vivax* qPCR assay (Gruenberg et al., 2018), input DNA with a CT value of <30 (roughly ≥ 100 parasites/ μL) yielded a read depth of ≥ 100 reads/marker. If DNA amount is limited (11 μL of DNA is required for this protocol), gDNA can be diluted using IDTE, pH 8.0.

Rebalanced Working Primer Preparation

- 2 Thaw an aliquot of Rebalanced rhAmpSeq PCR Panel (Forward and Reverse Stock Primer Pool from -20°C storage.
- 3 After thawing the primers, briefly vortex, then centrifuge.
- 4 Prepare working primer pools using a 1 in 5 dilution.
To sequence 96-samples, add 42 μL of Forward/Reverse **Stock** Pool to 168 μL of IDTE, pH 7.5.
Tip: Prepare multiple aliquots of rhAmpSeq forward/reverse primer pools and store at -20°C to avoid multiple freeze-thaw cycles.

Perform Targeted rhAmpSeq PCR₁

- 5 Thaw 4X rhAmpSeq Library Mix 1 and Rebalanced rhAmpSeq Working PCR Panel (Forward and Reverse **Working** Pool) completely to room temperature (15– 20°C).
- 6 After thawing the reagents, briefly vortex and then centrifuge.
- 7 Prepare the following **PCR₁** master mix in a Lo-bind Eppendorf tube for the number of samples being processed:

Component	Per reaction
4X rhAmpSeq Library Mix 1	5 μL



Component	Per reaction
rhAmpSeq pv custom PCR Panel – Forward Working Pool	2µL
rhAmpSeq pv custom PCR Panel – Reverse Working Pool	9µL
Total	9µL

Targeted rhAmp PCR_1 master mix

- 8 Briefly vortex and centrifuge down the mastermix.
- 9 In a new 96-well plate, add 9µL of PCR_1 master mix to each reaction well.
- 10 Add 11µL of gDNA to each reaction well.
- 11 Seal the plate, then briefly vortex and centrifuge.
- 12 Place the plate in a thermocycler and run the following program (Lid set to 105°C):

Step	Cycle	Temperature	Duration
Activate enzyme	1	95°C	10 min
Amplify	14	95°C	15 sec
		61°C	8 min
Deactivate enzyme	1	99.5°C	15 min
		4°C	Hold

Targeted rhAmp PCR_1 Program



- 13 Once the program is complete, remove the plate from the thermocycler and proceed immediately to **Dilute PCR_1 product.**

Dilute PCR_1 product

- 14 Briefly vortex the PCR_1 product, then centrifuge.
- 15 In a new 96-well plate, add 95µL of Nuclease-Free Water to each well.
- 16 Transfer 5µL of the PCR_1 product to each well (To prepare a final dilution of 1 in 20 dilution). Pipette up and down to ensure the entire volume is dispensed.
- 17 Seal the plate and thoroughly vortex to mix, then centrifuge before proceeding immediately to Perform Indexing PCR_2.

Perform Indexing PCR

- 18 Thaw 4X rhAmpSeq Library Mix 2 and xGen 10nt UDI Index Primer **Working** Plate completely to room temperature (15-20°C).
- 19 Briefly vortex, then centrifuge the reagents.
- 20 Prepare the following **PCR_2** master mix in a Lo-bind Eppendorf tube for the number of samples being processed:

	Component	Per reaction
	4x rhAmpSeq Library Mix 2	5µL
	Nuclease Free Water	2µL
	Total	7µL



- 21 In a new 96-well plate, add 7 μ L of PCR_2 master mix to each reaction well.
- 22 Add 2 μ L of xGen 10nt UDI Index Primer Working Concentration to each corresponding well using a multichannel pipette.
- 23 Add 11 μ L of diluted rhAmpSeq PCR_1 product to each reaction well in a 96-well plate using a multichannel pipette.
- 24 Important! Note down the index plate and well position used for each sample.
- 25 Seal the plate, then briefly vortex and centrifuge.

- 26 Place the plate in a thermocycler and run the following program (lid set to 105°C):

	Step	Cycle	Temperature	Duration
	Activate enzyme	1	95°C	3 min
	Amplify	24	95°C	15 sec
			60°C	30 sec
			72°C	30 sec
	Final extension	1	72°C	1 min
			4°C	Hold

Indexing PCR Cycling Condition

- 27 Once the program is complete, remove the plate from the thermocycler and proceed immediately to **Pool libraries**.

Pool libraries

- 28 Using a multichannel pipette, pool each row by transferring 5 μ L of each indexed library into an 8-well strip tube (use 10 μ L if the total number of individual libraries processed is less than 20 samples).



- 29 Cap the strip tube, briefly vortex, then centrifuge down.
- 30 Combine all libraries from the strip tube into a single 2mL LoBind tube.
- 31 Important! Pool the complete volume from each well for an even sample coverage.
- 32 Properly seal and store the plate with remaining individual indexed libraries at -20°C then proceed immediately to clean up the pooled libraries.

Clean up library

- 33 Prepare 2mL of fresh 80% ethanol solution by combining 400μL of molecular-grade water and 1,600μL of molecular-grade ethanol (Absolute ethanol).
- 34 Transfer 100μL of the rhAmpSeq library pool to a new 1.5mL tube.
- 35 Vortex the SPRI beads thoroughly before use.
- 36 Add 70μL of SPRI (0.7X) to the library pool.
- 37 Thoroughly mix the contents of the tube by pipetting up and down.
- 38 Incubate for 10 minutes at room temperature.
- 39 Briefly pulse spin down the tube then place it on a magnetic rack for 5 minutes, or until the solution is clear.
- 40 Keeping the tube on the magnet, do the following:
 - 40.1 Aspirate with the pipette, then discard the supernatant.



- 40.2 Add 1000 μ L of 80% ethanol to the tube.
- 40.3 Incubate at room temperature for 30 seconds.
- 40.4 Aspirate, then discard the supernatant.
- 40.5 Repeat the 80% ethanol wash one more time (steps 40.1 - 40.4).
- 40.6 Using a new P200 pipette tip, remove the remaining ethanol from the tube.
- 40.7 Allow the beads to dry for 3 minutes at room temperature.
- 41 Remove the tube from the magnet.
- 42 Add 22 μ L of IDTE, pH 8.0, to elute the library pool.
- 43 Thoroughly vortex to fully resuspend the beads, then briefly pulse spin down the tube.
- 44 Incubate at room temperature for 3 minutes.
- 45 Place the tube on the magnet to collect the beads for 1 minute, or until the solution is clear.
- 46 While keeping the tube on the magnet, transfer 20 μ L of the final library pool elution into a new 1.5mL LoBind tube, ensuring no beads are carried over.
- 47 Proceed to quantify and check the size of the library.



- 48 Store any remaining library pool at -20°C for **up to 3 weeks**.

Library QC

- 49 Quantify the library concentration using Illumina NGS library quantification kit (such as The Invitrogen Colibri Library Quantification Kit)
- 50 Using capillary electrophoresis, check the fragment size of the library before and after beads clean-up to ensure that adapter dimers have been successfully removed.

Sequencing

- 51 Follow Illumina's recommended protocol for a 2 × 150bp paired-end sequencing run on your Illumina platform

Protocol references

[1] Siegel, S.V., Trimarsanto, H., Amato, R. *et al.* Lineage-informative microhaplotypes for recurrence classification and spatio-temporal surveillance of *Plasmodium vivax* malaria parasites. *Nat Commun* **15**, 6757 (2024). <https://doi.org/10.1038/s41467-024-51015-3>

[2] Gruenberg et al:
Plasmodium vivax molecular diagnostics in community surveys: pitfalls and solutions. *Malaria Journal* (2018), 17:55.
<https://doi.org/10.1186/s12936-018-2201-0>



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