Standard Operating Procedure

AmpliSeq custom assay for molecular surveillance of *Plasmodium falciparum* and *Plasmodium vivax* parasites from dried blood spot DNA

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1 General information

1.1 Aim and application

The aim of this procedure is to describe the AmpliSeq custom assay library preparation for molecular surveillance of Plasmodium falciparum (Pf) and Plasmodium vivax (Pv). Four different AmpliSeq designs from our lab are publicly available, listed in chronological order of the design:

- AmpliSeq Pf Peru v1
  - Design ID Illumina: IAAQ179763_241
  - https://doi.org/10.21769/bioprotoc.4621
  - https://doi.org/10.1128/spectrum.00960-22
- Pv AmpliSeq v1 Vietnam
  - Design ID Illumina: IAAQ198716_241
  - https://doi.org/10.3389/fcimb.2022.953187
- AmpliSeq Pf Vietnam v2
  - Design ID Illumina: IAAQ200463_241
  - https://doi.org/10.3389/fgene.2024.1478706
- Pv AmpliSeq v2 Peru
  - Design ID Illumina: IAAQ212588_242
  - https://doi.org/10.1371/journal.pntd.0011879

The primer pools of these assay designs are different, but the procedures are the same and described here. Each of the assays has 2 primer pools. The assays can be applied to DNA extracted from DBS or whole blood or white blood cell depleted red blood cells taking into account the criteria for parasitaemia and DNA concentrations specified in the protocol below.

1.2 Background

Malaria molecular surveillance has great potential to support local national malaria control programs (NMCPs) to inform policy for malaria control and elimination. Drug resistance markers have been analyzed using amplicon sequencing strategies, microsatellites or SNP barcodes are used to analyze parasite gene flow, and diagnostic resistance markers are determined with PCR assays. Alternatively, WGS can be used to type all these markers, but is less well suited for high throughput analysis. Here we present a 3-day workflow for targeted resequencing of markers in drug resistance-associated genes, *hrp2&3* (for Pf), country or region-specific SNP-barcodes for population genetic analysis, a worldwide SNP barcode (for Pv) for prediction of origin, and *ama1* using Illumina short-read sequencing technology. The assay applies a multiplex PCR approach to amplify all genomic regions of

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interest in a rapid and easily standardizable procedure, and allows simultaneous amplification of a high number of targets at once, and therefore has great potential for implementation into routine surveillance practice by national malaria control programs (NMCPs). The assay can be performed on routinely collected filter paper blood spots, and can be easily adapted to different regions to investigate either regional trends or in-country epidemiological changes.

1.3 Legislation and standards

These procedures are based on the guidelines in 'AmpliSeq for Illumina On-Demand, Custom, and Community Panels – Reference guide' from Illumina (Document # 1000000036408 v08 November 2019) and is for research use only.

2 Responsibilities

These procedures can only be carried out by a trained researcher or lab technician. These procedures are to be carried out in part in the ITM genome facilities, therefore requires training in the genome regulations, or working under the direct supervision of a trained researcher or lab technician as part of this training.

3 Definitions and abbreviations

96w - 96 wells
CD indexes – combinatorial dual indexes
DNA – Deoxy nucleic acid
dsDNA – double stranded DNA
EtOH – ethanol
PCR grade H_2O – purified molecular biology grade water
RT – room temperature

4 Method

4.1 Materials and Reagents

1. Ampliseq Library PLUS for Illumina (96 reactions; Illumina, # 20019102)

   Contains:

   a) 1X Lib Amp Mix
   b) 10X Library Amp primers
   c) DNA Ligase
   d) 5X Ampliseq HiFi Mix
   e) FuPa Reagent
   f) Low TE
   g) Switch solutions

2. Ampliseq Custom DNA panel for Illumina (see Supplementary manifest files and APPENDIX for oligo sequences. *Note: We order the ready-made pools directly from Illumina, but you could order the oligo's separately and combine them yourself.*)

   Contains:

   a) Primer pool 1 (red cap)
   b) Primer pool 2 (blue cap)

3. Ampliseq CD Indexes Set A for Illumina (96 indexes, 96 samples; Illumina, #20019105)

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Note: optionally you can also use Index Set B, C or D or combine multiple sets when combining more than 96 samples in one run.)

4. Absolute ethanol (Sigma-Aldrich, Merck, #1.00983.1000)
5. Agencourt AMPure XP beads (Beckman Coulter, #A63881)
6. 96 well-PCR plate, 0.2-mL (Greiner Bio-One, #652201)
7. 8-well PCR strips (Greiner Bio-One, #673210)
8. Strip caps for PCR pates (Greiner Bio-One, #373250)
9. Adhesive seals for PCR plates (Westburg Life Science, #WB2-3800)
10. Nuclease free water (Lonza, #BE51200)
11. Qubit® dsDNA HS Assay Kits (Invitrogen, Thermo Fischer Scientific, #Q32851)
12. Thin-wall, clear, 0.5-mL PCR tube strips (*e.g.* Qubit™ Flex Assay Tube Strips, Thermo Fischer Scientific, #Q33252)
13. Pipette filter tips (*e.g.* 10µL of Greiner Bio-One, #771353; Biofil, #PPT150010)
14. Combitips 0.2-mL and 0.5-mL (Eppendorf, # 0030089774 and #0030089421)
15. Miseq Reagent Kit v3 (600-cycle) (Illumina, # MS-102-3003)
    a) Reagent Cartridge
    b) HT1 (Hybridization buffer, 5 mL)
    c) PR2 (Incorporation buffer, 500 mL)
    d) Flowcell
16. Optional to include as controls and take along in the library preparation:
    a) DNA extracted of laboratory strain(s) of *P. falciparum* (e.g. 3D7, Dd2, etc.) as PF positive control
    b) DNA extracted from well-quantified *P. vivax* infected patient samples as PV positive control
    c) DNA extracted from uninfected human blood as negative control

4.2 Equipment

1. Multichannel pipettes 0.10 mL, 0.1 mL and 0.3 mL
2. Electronic Multi-Dispenser Pipette (Eppendorf, Multipette © E3x, #4987000029)
3. Centrifuge (Sigma Laborzentrifugen GmbH, Sigma 4-16KS, serial nr. #150507)
4. Vortex (Scientific Industries, Vortex Genie 2, #SI-0236)
5. 96 well-magnet stand (Invitrogen, ThermoFisher Scientific, Dynamag ™-96 Side Skirted, #12027; RNA Life Technologies, Ambion® Magnetic Stand-96, #1307065)
6. Qubit Flex fluorometer (Invitrogen, ThermoFischer Scientific, #Q33327)
7. Conventional cycler (Biometra, Westburg, Tprofessional Thermocycler Basic 96x0.2-mL, #846-070-701)
8. LichtCycler® 480 Real-Time PCR System (Roche, #04640268001)
9. MiSeq System - benchtop sequencer (Illumina)

   Note: For our panels you need a sequencer than can do 2 × 300 bp reads. Therefore the MiSeq systems or latest NextSeq 2000 sequencers are suitable.

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4.3 Software

1. Illumina experiment Manager (Illumina)
2. Illumina local run manager (on MiSeq system)
3. Microsoft Excel (Microsoft)

4.4. Procedures

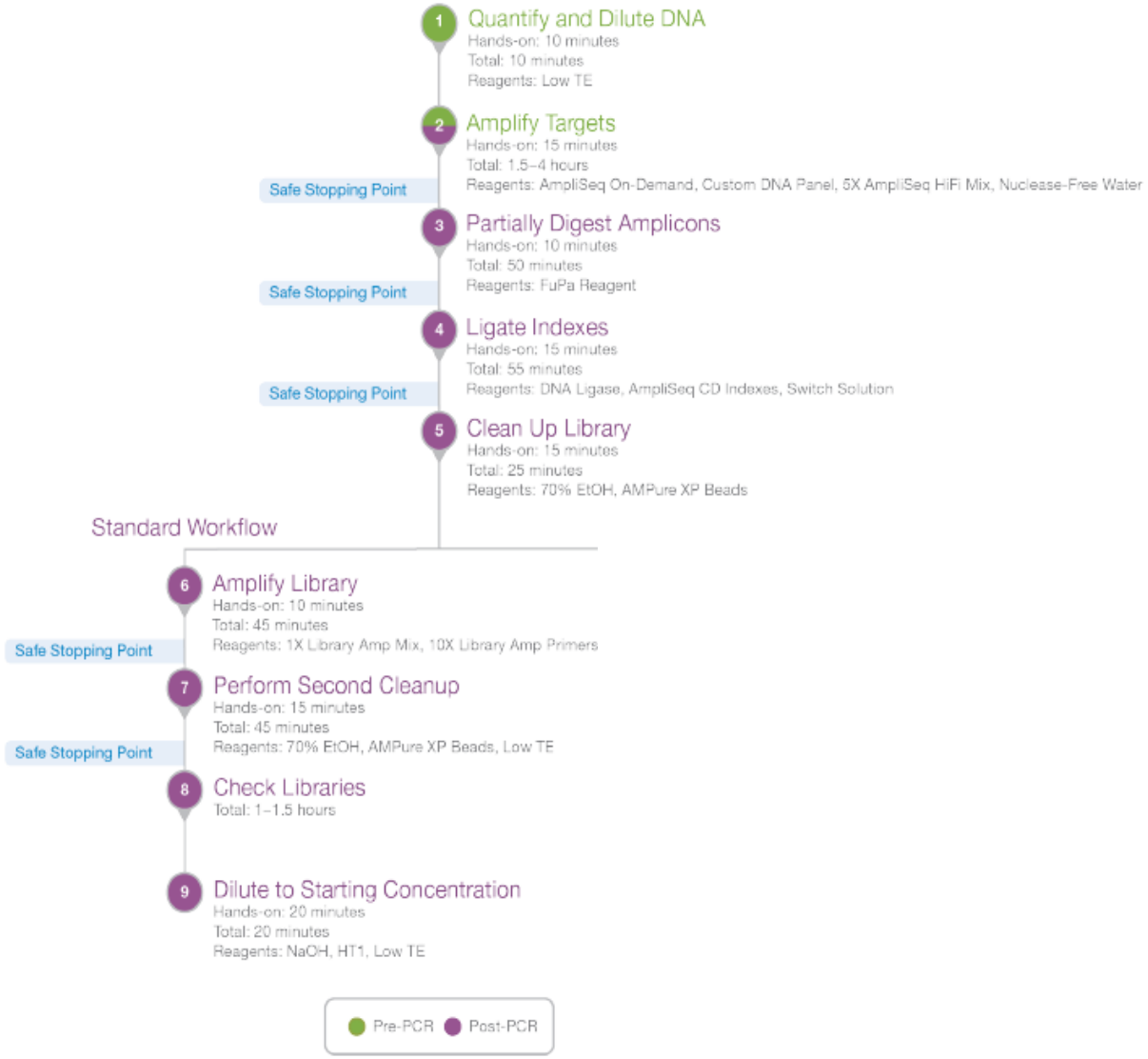

Figure 1. **Overview of procedures AmpliSeq library preparation. From 'AmpliSeq for Illumina On-Demand, Custom, and Community Panels – Reference guide.**

A. Sample preparation

This section quantifies and prepares the DNA extracted from DBS for library preparation.

1. Isolate DNA from Dried blood spots (DBS) according to standardized protocols (*e.g.* DNA extractions using the Qiagen 96 DNA blood kit.)

   Note: DNA extracted from whole blood or white blood cell depleted red blood cells can also be used as

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input material. However, take note of the DNA concentrations as described in step 3.

2. Quantify 3-10 µL DNA of (a subset of) samples using Qubit® dsDNA HS Assay according to manufacturer's protocol.
3. Recommended input concentration for the library preparation is 10 ng of high quality DNA per pool (the kit supports 1-100 ng DNA input. Please note however that due to the nature of our samples, we have a mixture of human and parasite DNA).

   Dilute samples with too high DNA concentration (>100ng) in Low TE (supplied with Ampliseq Library PLUS kit) to an input concentration of ~1-10 ng/µL . (*Note: In our procedures, mean DNA concentration after DNA extraction from DBS was 6.1±0.3 ng/µL and we used 7.5 µL undiluted sample (~23ng total input per pool) in the library preparation reactions. It is important not to exceed the 100ng DNA input as this will negatively affect the quality of the sequencing result. For DBS samples, in our experience, the DNA concentration was always below the upper limit. However, in the case of high parasite density whole blood samples, we have had to dilute the DNA. After testing the DNA concentration of a few samples with varying parasite densities at the start of a study we do not routinely check the concentration of every sample to save time and costs).*

   Important to consider is that we have a mixture of human and parasite DNA. It is important to quantify your parasite DNA in advance with a qPCR. From our validation procedure we recommend including samples with P. falciparum or P. vivax parasite densities ≥5 (Pv) or ≥10 (Pf) parasites/µl as determined by VarATS or PvMTCOX1 qPCR. If you do not include quantification in your PCR procedures, the threshold cycle (Ct value) in the qPCR is a good indication (e.g. a Ct-value of ≤34 cycles is generally a good indication to achieve AmpliSeq success). This limit depends also on the amount of blood spotted on filter paper and the amount of filter paper (e.g. 3 punches of DBS), and elution volume, which can impact the amount of template DNA in your sample.

4. Prepare a 96-well layout with the sample IDs (see excel template "Template_AmpliSeq.xlsx")

   Note: We usually do the library preparation for 96 samples at once, so we use one 96 sample Ampliseq Library PLUS kit per time. As this kit is the bulk of the costs per sample, we then sequence this one plate in one run for deep sequencing. You can also sequence multiple plates in one run, up to 384 samples. We always keep left over reagents from a library prep, and if you pipette carefully, you can do more than 96 samples from one 96 samples kit. Therefore we usually combine 1,5 plate (96 + 48 libraries) in one MiSeq run (v3 2x300bp), but then we first do the library prep for 96 samples and then separately 48 samples and combine them in the final pooling step.
5. Add 7.5 µL of (diluted) DNA for each sample in the corresponding well of your layout.
6. **SAFE STOPPING POINT:** Store the 96well plate with prepared samples at 4°C overnight or -20°C for longer periods if not immediately commencing with the library preparation procedures.

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B. Amplify DNA Targets

This section uses PCR to amplify the (overlapping) target regions of the DNA samples in two reactions with two different primer pools.

1. Thaw the following reagents:
   a) 96w plate with 7.5 µL of DNA prepared in previous section - *thaw on ice if frozen*
   b) 5X Ampliseq HiFi Mix (red cap; Ampliseq Library PLUS kit) - *thaw on ice and invert to mix*
   c) 1 aliquot of 2X Ampliseq Custom DNA Pool 1 (red cap, Ampliseq Custom DNA panel) - *thaw at room temperature (RT), vortex to mix*
   d) 1 aliquot of 2X Ampliseq Custom DNA Pool 2 (blue cap, Ampliseq Custom DNA panel) - *thaw at RT, vortex to mix*
2. Briefly centrifuge the 96w plate and prepared tubes to collect all liquid at the bottom of the wells.
3. Remove the lids/seal from the 96w plate with DNA.
4. To each well with sample (V=7.5 µL), add 5 µL 5X Ampliseq HiFi Mix using a Multipette and 0.5mL Combitip.
5. Centrifuge the plate briefly to collect all liquid at the bottom of the well.
6. Gently mix the DNA-HiFi mixture with a multichannel pipette and transfer 5 µL to the corresponding column of a new PCR plate (labelled pool 1), and 5 µL to a second new PCR plate (labelled pool 2).
7. To the 1st new plate (Pool 1), add 5 µL 2X Ampliseq Custom DNA Pool 1 (red cap) to each well using a Multipette and 0.5mL Combitip.
8. To the 2nd new plate (Pool 2), add 5 µL 2X Ampliseq Custom DNA Pool 2 (blue cap) to each well using a Multipette and 0.5mL Combitip.
9. Seal both plates with an adhesive seal or lids, and briefly centrifuge to collect all liquid at the bottom of the well. Check for air bubbles, remove by tapping/flicking the side of the well with your fingers, and centrifuge again. Do not vortex at this stage.
10. Place the 96w plate in the thermocycler, set the volume to 10 µL (if applicable) and run the AMP_DNA program as in Table 1 (with heated lid ON at 105°C):

Table 1. PCR cycling conditions AMP_DNA

Cycles	Temperature	Time
1X	99°C	2 min
21X	99°C 60°C	15 sec 8 min
Hold	10°C	up to 24 hrs

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11. **SAFE STOPPING POINT:** If you are stopping, leave the plate on the thermal cycler at 10°C for up to 24 hours. For longer durations, store at -25°C to -15°C.

C. Partially Digest Amplicons

This section uses FuPa Reagent to digest primer dimers and partially digest amplicons.

1. From this section forward, work in a clean area that you can clean to denature DNA. Use the dedicated library preparation room at ITM.
2. Thaw the following reagents:
    1. 96w plate with amplified Pool 1 prepared in previous section - *thaw on ice and vortex*
    2. 96w plate with amplified Pool 2 prepared in previous section - *thaw on ice and vortex*
    3. FuPa Reagent (brown cap; Ampliseq Library PLUS kit) - *thaw on ice*
2. If continuing with the next section (D) immediately after this section:
    1. Switch Solution (yellow cap; Ampliseq Library PLUS kit) - *thaw at RT*
3. Briefly centrifuge the 96w PCR plates with amplified Pool 1 and Pool 2 and prepared tubes to collect all liquid at the bottom of the wells.
4. Remove the seals from the 96w plates with amplified Pool 1 and Pool2.
5. For each sample, use a multichannel pipette to combine the 10 µL reaction from amplified Pool 2 in the corresponding well of amplified Pool 1. This will result in a total volume per sample of 20 µL.
6. Aliquot 30 µL of FuPa reagent in each well of a clean 8-well PCR strip. From here, using a multichannel pipette, transfer 2 µL FuPa reagent to each well of the combined Pool 1+ 2 product and mix. Discard the tips before continuing with the next column. (*Note: The reagent is very viscous and due to the low volume it is very difficult to do this with a multipette and combitip. So use a multichannel pipette with 10 µL tips for more accurate pipetting*).
7. Seal the plate with an adhesive seal, vortex briefly and briefly centrifuge to collect all liquid at the bottom of the well.
8. Place the 96w plate in the thermocycler, set the volume to 22 µL (if applicable) and run the FUPA program as in Table 2 (with heated lid ON at 105°C):

Table 2. PCR cycling conditions FUPA

Cycles	Temperature	Time
1	50°C	10 min
1	55°C	10 min
1	62°C	20 min
Hold	10°C	Up to 1 hr

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9. **SAFE STOPPING POINT:** If you are stopping, leave the plate on the thermal cycler at 10°C **for up to 1 hour**. For longer durations, store at -25°C to -15°C.

D. Ligate Indexes

This section ligates Index 1 (i7) and Index 2 (i5) adapters to the fragments of each sample. The indexes are premixed in a single-use plate to ensure unique combinations. (Note: there is enough volume to use an index plate twice, so if you work very clean, you can seal the plate after the first use, store it at -20°C and use it again for another run). Each library must have a unique index combination for dual-index sequencing. When more than 96 samples are being included in the same sequencing run, make sure to use different index sets (four sets are available from Illumina with different combinations: Set A, Set B, set C and/or Set D, allowing multiplexing of max. 384 libraries in one MiSeq run). For more information see the Illumina Index Adapter Pooling Guide.

To avoid library prep failure, do not combine the reagents for this section together outside the wells with the digested amplicons.

1. Thaw the following reagents:
    a) Switch Solution (yellow cap; Ampliseq Library PLUS kit) - *thaw at RT, vortex to mix*
    b) Ampliseq CD Index set - *thaw at RT, vortex to mix, write down in your lab book which set you are using (A, B, C, or D)*
    c) DNA Ligase (blue cap; Ampliseq Library PLUS kit) - *thaw on ice*
2. If continuing with the next section (E) immediately after this section:
    a) Equilibrate AMPure XP beads to room temperature (at least 30 min). Vortex vigorously to resuspend.
3. Briefly centrifuge the 96w plate with partially digested amplicons, Index plate and the prepared tubes of reagents to collect all liquid at the bottom of the wells.
4. Remove the seals from the 96w plate with partially digested amplicons and from the index plate.
5. Add (**in order listed!**) to each well of the 96w plate with partially digested amplicons:
    a) 4 µL Switch Solution (yellow cap) using a Multipette and 0.2mL Combitip (Multipette set to 48 steps of 4 µL; so you need to aspirate and dispense 2 times).
    (*Alternatively use a 8-well strip with 50 µL Switch Solution aliquots and multichannel to pipette 4 µL Switch Solution into each well of the 96w plate.*)
    b) 2 µL of the Ampliseq CD Index to the corresponding well of the 96w plate with partially digested amplicons + Switch Solution using a multichannel pipette and 10 µL tips. (*Use clean tips for each index well.)*
    c) Aliquot 30 µL of DNA Ligase reagent (blue cap) in each well of a clean 8-well PCR strip. From here, using a multichannel pipette transfer 2 µL DNA Ligase reagent to each well of the 96w plate with partially digested amplicons + Switch Solution + index.

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6. Seal the plate with an adhesive seal, vortex briefly and briefly centrifuge to collect all liquid at the bottom of the well.
7. Place the 96w plate in the thermocycler, set the volume to 30 µL (if applicable) and run the LIGATE program as in Table 3 (with heated lid ON at 105°C):

Table 3. PCR cycling conditions LIGATE

Cycles	Temperature	Time
1	22°C	30 min
1	68°C	5 min
1	72°C	5 min
Hold	10°C	up to 24 hrs

8. If the index plate contains unused indexes, seal the plate and return to storage (-25°C to -15°C). *(Note: there is enough volume to use an index plate twice, so if you work very clean, you can seal the plate after the first use, store it at -20°C and use it again for another run).*
9. **SAFE STOPPING POINT:** If you are stopping, leave the plate on the thermal cycler at 10°C for up to **24 hours**. For longer durations, store at -25°C to -15°C.

E. Clean Up Library

This section uses Agencourt AMPure XP beads to clean up the library. The library will be bound to the beads, which are carried over to the next section.

1. Prepare the following reagents:
   a) Equilibrate AMPure XP beads to room temperature (at least 30 min). Vortex vigorously to resuspend.
   b) **Freshly prepare** 50 mL 70% ethanol (EtOH) solution. (mix 35 mL 100% EtOH + 15 mL PCR grade H_2O)
2. For the next section (F) that should immediately be continued after this section, prepare:
   a) 4 tubes of 1X Lib Amp Mix (black cap; Ampliseq Library PLUS kit) - *thaw on ice and invert to mix*
   b) 2 tubes of 10X Library Amp Primers (pink cap; Ampliseq Library PLUS kit) - *thaw at RT and vortex to mix*
3. Briefly centrifuge the 96w library plate (with amplicons and index) and the prepared tubes of reagents to collect all liquid at the bottom of the wells.
4. Remove the seals from the 96w library plate.
5. Add 30 µL AMPure XP beads (vortex thoroughly before pipetting) to each well with library in the 96w plate using a multipette and 2.5 mL or 5 mL combitips.
6. Seal the plate with an adhesive seal and vortex briefly. Inspect each well to ensure the mixture is homogenous, then centrifuge briefly to remove air bubbles. Do not spin too fast to prevent pelleting the

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beads at the bottom of the wells (low speed ~500-1000rpm).

7. Incubate the plate at RT for 5 min.
8. Place the plate on a magnetic stand and remove the seal, wait till the mixture is clear (at least 2 min).
9. While on the magnetic stand, the library is bound to the beads:
    a) Use a multichannel pipette (200 or 300 µL tips) to remove and discard the entire supernatant from each well.
    b) Wash 2X:
        i. Add 150 µL freshly prepared 70% EtOH to each well using a multipette and 0.5 mL Combitips.
        ii. Incubate at RT until the solution is clear (> 30 sec).
        iii. Without disturbing the beads, remove and discard supernatant.
10. Seal the plate with an adhesive seal and centrifuge briefly (low speed ~500-1000 rpm).
11. Place the plate on a magnetic stand (make sure to place in the same orientation as in step 8 & 9 to keep the beads on the same side of the well), remove the seal, and wait for AMPure XP beads to bind until mixture is clear (~30 sec).
12. Remove any residual EtOH as follows:
    a) Use a 10 µL multichannel pipette to remove as much residual EtOH from each well as you can.
    b) Air-dry the 96w plate on the magnetic stand without seal for at least 10 min.
    c) Inspect the wells to make sure the residual EtOH has evaporated. If it remains in some wells, try to remove with 10 µL pipette and continue to air-dry until the EtOH is no longer visible. *(Note: Overdried or cracked beads do not negatively affect performance of the assay. However, residual EtOH causes library preparation failing in the next section by inhibiting amplification. So be rigorous in removing remaining EtOH.*)

F. Amplify Library

This section uses PCR to amplify the libraries to ensure sufficient quantity for sequencing on Illumina systems. The amplification reactions contains the beads, which are carried over from the previous section. The libraries are amplified using universal primers targeting the adapters.

1. In the previous section you should have already prepared the following reagents:
    a) 4 tubes of 1X Lib Amp Mix (black cap; Ampliseq Library PLUS kit) - *thaw on ice and invert to mix*
    b) 2 tubes of 10X Library Amp Primers (pink cap; Ampliseq Library PLUS kit) - *thaw at RT and vortex to mix*
2. If continuing with the next section (G) immediately after this section:
    a) Equilibrate AMPure XP beads to room temperature (at least 30 min). Vortex vigorously to resuspend.

3. Prepare the amplification master mix in a 15 mL falcon tube (for 96 reactions) by combining the reagents as

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in Table 4.

Table 4. Amplification master mix recipe

Reagent	Volume (µL) for 1 library	Volume (µL) for 96 libraries (make for 4 extra to have sufficient)	Volume (µL) for X libraries
1X Lib Amp Mix (black cap)	45	4500	
10X Library Amp Primers (pink cap)	5	500	
Total Volume (µL)	**50**	**5000**	

4. Vortex the master mix briefly and centrifuge
5. Remove the 96w library plate (previous section) from the magnet.
6. Add 50 µL amplification master mix to each well of the beads with library using the multipette and 5 mL combitip.
7. Seal the plate with an adhesive seal, vortex briefly to resuspend the beads and briefly centrifuge to collect all liquid at the bottom of the well.
8. Place the 96w plate in the thermocycler, set the volume to 50 µL (if applicable) and run the AMP_7 program as in Table 5 (with heated lid ON at 105^{o}C):

Table 5. PCR cycling conditions AMP_7

Cycles	Temperature	Time
1	98^{o}C	2 min
7	98^{o}C 64^{o}C	15 sec 1 min
Hold	10^{o}C	up to 24 hrs

9. **SAFE STOPPING POINT:** If you are stopping, leave the plate on the thermal cycler at 10^{o}C for up to **24 hours**. For longer durations, store at -25^{o}C to -15^{o}C.

G. Second Cleanup

This section performs second cleanup with AMPure XP beads for 2 rounds of purification.

First round - High molecular-weight DNA is captured by the beads and discarded. The library and primers are retained in the supernatant and transferred to a fresh plate for the second round of purification.

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<u>Second round</u> - Libraries in the saved supernatant are captured by the beads while primers remain in the supernatant. The bead pellet is saved, and libraries are subsequently eluted from the beads.

1. Prepare the following reagents:
    a) Equilibrate AMPure XP beads to room temperature (at least 30 min). Vortex vigorously to resuspend.
    b) Low TE (bottle; Ampliseq Library PLUS kit) – *thaw at RT for 45min, vortex to mix. Can be stored at RT or 4°C.*
    c) Freshly prepare 50 mL 70% ethanol (EtOH) solution. (mix 35 mL 100% EtOH + 15 mL PCR grade H_2O)
2. Briefly centrifuge the 96w library plate to collect all liquid at the bottom of the wells.
3. <u>First round:</u> Add 25 µL AMPure XP beads (vortex thoroughly before pipetting) to each well with ~50 µL library in the 96w plate using a multipette and 2.5 mL combitips. (*Note: this step adds beads to the beads already in the reaction).*
4. Seal the plate with an adhesive seal and vortex briefly, then centrifuge briefly (low speed ~500-1000 rpm). The beads do not need to be fully resuspended.
5. Incubate at RT for 5 min.
6. Place the plate on a magnetic stand and remove the seal, wait till the mixture is clear (at least 5 min).
7. Transfer the <u>entire supernatant</u> (~75 µL) to a new plate. Small amounts of bead carryover do not affect performance.

THE <u>SUPERNATANT</u> CONTAINS THE DESIRED AMPLICON LIBRARY!

8. <u>Second round:</u> Add 60 µL AMPure XP beads to each well with the transferred supernatant in the new 96w plate using a multipette and 5 mL combitips.
9. Seal the plate with an adhesive seal and vortex briefly, then centrifuge briefly (low speed ~500-1000 rpm).
10. Incubate at RT for 5 min.
11. Place the plate on a magnetic stand and remove the seal, wait till the mixture is clear (at least 5 min).
12. While on the magnetic stand, perform the following steps. **This time the library is bound to the beads.**
    a) Use a multichannel pipette (200 or 300 µL tips) to remove and discard the entire supernatant from each well.
    b) Wash 2X:
        i. Add 150 µL freshly prepared 70% EtOH to each well using a multipette and 0.5 mL Combitips.
        ii. Incubate at RT until the solution is clear (> 30 sec).
        iii. Without disturbing the beads, remove and discard supernatant.
13. Use a 10 µL multichannel pipette to remove as much residual EtOH from each well as you can.
14. Air-dry the 96w plate on the magnetic stand without seal for at least 5 min.

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15. Remove the plate from the magnet.
16. Add 30 µL Low TE to each well.
17. Seal the plate with an adhesive seal and vortex vigorously, then centrifuge briefly (low speed ~500-1000 rpm). (*note: libraries are bound to the beads and released into the TE buffer, therefore it is important that all beads get in resuspension. Here, libraries contain small fragments that are more resistant to shear stress and vortex shedding.*)
18. To ensure the beads are well resuspended, if necessary, you can mix by pipetting.
19. Place the plate on a magnetic stand and remove the seal, wait till the mixture is clear (at least 5 min).
20. Transfer 27 µL of the supernatant (containing the libraries) to a new 96w plate (while on the magnetic stand). *Note: do not take more than 27 µL as you will risk bead carryover.*
21. **SAFE STOPPING POINT:** If you are stopping, store at -25°C to -15°C (up to 30 days). *Note: according to the Illumina guidelines, there is no specific limit to the storage duration. We recommend to sequence them within a month, although we have successfully sequenced libraries that have been stored for longer periods. In any case avoid frequent freeze-thawing.).*

H. Quantify libraries

Qubit DNA concentration measurement

Use the Qubit® dsDNA HS Assay Kits (Invitrogen, Thermo Fischer Scientific) to determine the concentration of double stranded DNA in the libraries following the manufacturers procedures.

1. Set up the required number of 0.5-mL tubes for standards and samples. The Qubit® dsDNA HS Assay requires 2 standards.
2. Prepare the Qubit® working solution by diluting the Qubit® dsDNA HS Reagent 1:200 in Qubit® dsDNA HS Buffer. Use a clean plastic tube each time you prepare Qubit® working solution. For 96 samples, prepare 20mL working solution by mixing (*Note: Qubit ® dsDNA HS Reagent is photoreactive. Therefore cover the tube with tinfoil to reduce exposure to light*.)
    a. 19.9 mL Qubit® dsDNA HS Buffer
    b. 100 µL Qubit® dsDNA HS Reagent
3. Add 190 µL of Qubit working solution to each of the tubes used for standards.
4. Add 10 µL of each Qubit® standard to the appropriate tube, then mix by vortexing 2–3 seconds. Be careful not to create bubbles as these might get in the light path during the measurement.
5. Add 197 µL of Qubit working solution to each of the tubes used for the libraries.
6. Add 3 µL of each sample library to the appropriate tube, then mix by vortexing 2–3 seconds. Be careful not to create bubbles. (*Note: if you suspect the library concentration is very low, you can use higher volume (5-20 µL) of library in the qubit reaction. If this is the case, adjust also the volume of Qubit working solution in step 5 to make sure the final volume after adding the library is 200 µL. Take care not to use*

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too much library as you will need sufficient volume (up to 6 µL) to make the pool in the next section. If the library concentration is too high (i.e. beyond the linear range of the Qubit kit) after the first measurement, dilute the library (e.g. 1:2 or 1:4) and measure again to get an accurate concentration.)

7. Allow all tubes to incubate at room temperature for 2 minutes in order for Qubit® HS Reagent dye to bind dsDNA. (*Note: you can add the libraries to the working solution in batches of 16-24, then incubate and measure. Keep the unused tubes in the dark in the meantime, for example by covering with aluminum foil).*
8. On the Home screen of the Qubit® Flex Fluorometer, press DNA, then select dsDNA High Sensitivity as the assay type. The Standards screen is displayed.
9. On the Standards screen, press Yes to read the standards.
10. Insert the tube containing Standard #1 into the sample chamber, close the lid, then press Read. When the reading is complete (~3 seconds), remove Standard #1.
11. Insert the tube containing Standard #2 into the sample chamber, close the lid, then press Read. When the reading is complete, remove Standard #2. When the calibration is complete, the instrument displays the Sample screen.
12. In the Sample volume screen, select the sample volume and units for the Qubit™ quantitation assays:

a. Press the + or – buttons on the wheel to select the sample volume added to the assay tube (3 µL).

b. For the Qubit™ quantitation assays, select the units for the output sample concentration from the dropdown menu (ng/µL)

13. Insert a sample tubes into the sample chamber, close the lid, and then press Read tube. The reading takes approximately 3 seconds for the quantitation assays and approximately 5 seconds for the quality assays.

14. The Results screen displays the results of the sample run. If the results are within the assay's range, the concentration values are displayed. The top value (in large font) is the concentration of the original sample. The bottom value is the dilution concentration (the concentration of the sample in the tube inserted into the Qubit™ 4 fluorometer).

13. Repeat steps 5-12 until all samples have been read.

I. DILUTE AND POOL LIBRARIES

1. Thaw frozen Low TE buffer (AmpliSeq library prep kit) at RT.
2. Using the library concentrations determined with the Qubit kit (previous section), determine the molarity of the library.
    1. For Qubit measurements, we use the following formula: $(c * 10^6) / (660 * \text{library size})$, where c is the concentration (ng/µL) as measured with the Qubit.

    Note: we determined the mean size of the library of PV Ampliseq Vietnam with the Tapestation, and it was 475 bp. For other libraries, you can determine the mean size with the tapestation, or

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alternatively use the size from Pv Ampliseq (475 bp) or 350 bp as the default for Ampliseq.

2. You can calculate how to make the dilutions by entering the sample IDs in column C and Qubit measurements in column F in the template 'Template_Ampliseq_Qubit_pooling_v1.0_041021.xlsx', adjust where necessary (6 µL undiluted if concentration >2nM or adjust volumes so final volume of library +TE does not exceed 200 µL). In columns R -AD (row 29 and lower) you will find the final pipetting layouts for the libraries and TE.

3. Dilute each library to 2nM using Low TE in a 96w plate as indicated in the template. If the concentration (molarity) of the library (undiluted) is below 2 nM, then add 6 µL of the undiluted library to the final '2nM' plate.

   Note: Take care not to start with too low volume of library (at least 3 µL) for the dilution, as this will increase the inaccuracy of the final concentration. Also take care to keep the final volume of your dilution below 200 µL otherwise the well of your dilution plate will overflow. If needed, dilute in a separate Eppendorf tube for larger volumes, then transfer 50 - 150 µL of the diluted library to the appropriate well in the dilution plate.

   Mix libraries diluted in TE by pipetting 10X or using a vortex (cover plate with a seal), then spin the plate to collect the diluted libraries at the bottom of the well.

4. Make a pool with equal volumes of all 2 nM libraries:
   1. Using a multichannel pipette to combine 5 µL from each well from the rows of the 96w plate into one 8-well strip. (*i.e.* make a pool from each row). Mix by pipetting 10X.
   2. Combine the entire volume of the row pools from the 8-well strip into one 1.5 mL low bind tube.

Note: This example for the pooling is for 96 samples. When sequencing more than 96 samples in one run, pool all 2nM libraries of all samples to be included in the run into one final pool at equal volumes. When running more than 96 samples, take care to combine libraries prepared with different index sets, otherwise you will not be able to demultiplex the sequences from the different plates.

5. Preferably proceed to sequencing the diluted library pool soon after the dilution. If not possible, store diluted library at -20^{o}C up to one week.

J. PREPARING FILES FOR SEQUENCING ON MISEQ

1. Using the Illumina Experiment Manager software, create a Sample Plate:
   1. From the main screen, select Create Sample Plate.
   2. Select AmpliSeq CD Indexes Plate A (or B or C or D, depending on the index kit that you used during the library prep), and then select Next.
   3. In the Unique Plate Name field, enter a unique name for the sample plate. (do not use special characters and spaces in sample IDs and plate names). Index Reads should be '2 (Dual)' by default.

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Select Next.

4. Select the Table or Plate tab, depending on your preferred view.
5. Enter a unique 'Sample ID' for each well (for example by copy pasting from an excel layout).
6. Setting the indexes (in the Table tab)
    1. When using the default layout from the 96w index plates, you can autopopulate the indexes: select 'Apply Default Index Layout' button at the bottom left.
7. When you are using a different layout than the standard index plate layout:
    1. Select a well in the Index Well field.
    2. In the Index1 and Index2 fields, select the index adapter being used for each Index Read.
8. Check your layout; valid entries for all samples will have turned white instead of brown/grey. If everything is valid, select 'Finish', and then save the sample plate file in a desired location.

2. Using the Illumina Experiment Manager software, create a Sample Sheet:
    1. From the main screen, select Create Sample Sheet.
    2. Select MiSeq, and then select Next.
    3. Select the appropriate application (Other->FASTQ Only, to only generate fastq files for subsequent analysis) and then select Next. (Alternatively variants can be analyzed directly using the PCR Amplicon application and the manifest file in the basespace cloud system or local run manager).
    4. In the Reagent Kit Barcode field, enter the reagent kit ID from the label of box 1 or box 2 of the SBS kit that starts with 'RGT' and followed by 8 digits located underneath the barcode. (if unknown at this stage, you can correct this later)
    5. Select the appropriate Library Prep Workflow (AmpliSeq Library PLUS for Illumina)
    6. Select the appropriate Index Adapter (Ampliseq CD Indexes plate A, B, C or D, or 384 when combining more than 96 samples)
    7. Index Reads should be '2 (Dual)' by default.
    8. Enter the Experiment Name, Investigator Name, Description, and Date. (for sequencing at UA enter your email address in the 'Investigator Name' field so you will receive an automatic data download link after sequencing).
    9. Enter the expected date of sequencing
    10. Select the Paired End Read Type.
    11. In the Cycles Read fields, enter one more than the number of cycles. (301 for the v3 600 cycle kit) for both read 1 and for read 2
    12. In the workflow specific settings, select 'Use Adapter Trimming' (default)
    13. Select Next to continue to Select Samples for a MiSeq Sample Sheet.
    14. Select samples by selecting Select Plate, and then navigate to the sample plate prepared in step 1.

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15. Choose wells to include in the sequencing run. (Select all)
16. Select Add Selected Samples.

    Note: Make sure all the libraries included in the pool are in the sample sheet with corresponding indexes. So if you are running more than 96 samples in a run, add all plates to the one sample sheet.
17. Select Finish, and then save the sample sheet file (*.csv) in the desired location. Review the sample sheet in excel (there should be no spaces or special characters in the sample IDs).

K. WASHING THE SEQUENCER

1. A day before your scheduled sequencing, you need to wash the MiSeq system
2. Prepare 500mL incorporation buffer with 0.5% Tween-20
3. Fill the tubes of the washing cassette with the incorporation buffer with tween
4. Follow the instructions for washing on the MiSeq system,
    1. Make sure a flow cell is placed in the system.
    2. Enter the filled washing cassette and bottle of prepared incorporation buffer with 0.5% Tween 20
    3. Refill the washing cassette tubes with the buffer from the bottle when indicated by the machine (2x), continue washing
    4. Keep the washing cassette, bottle and flow cell in place until you start the run the next day.

L. INSTRUCTIONS FOR FINAL PREPARATION FOR SEQUENCING

1. Prepare a fresh dilution of 0.2N NaOH,
    1. Combine the reagents in an Eppendorf tube:
        1. 800 µL laboratory grade water
        2. 200 µL 1.0 N NaOH
    2. Mix the tube by inverting several times.
    3. Use within 12h
2. Prepare HT1
    1. Thaw the HT1 buffer (Miseq reagent kit v3, Illumina) at RT
    2. Store at 2-8^{o}C until use when not used immediately when thawed.
3. Denature libraries
    1. Combine 5 µL of library pool with 5 µL 0.2N NaOH
    2. Vortex briefly, then centrifuge briefly
    3. Incubate at room temperature for 5 min
    4. Add 5 µL 200 mM Tris-HCl, pH 7.0
    5. Add 985 µL pre-chilled HT1 buffer to the tube of denatured pool. The result is a 10 pM denatured

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library. Vortex and centrifuge briefly

6. Place the 10 pM libraries with final volume 1 mL on ice until you are ready to proceed to final dilution.

4. Dilute library pool to final loading concentration
    1. Dilute with pre-chilled HT1 buffer until the final loading concentration at a final volume of 600 µL.:
        1. Take 420 µL of 10 pM library
        2. Add 180 µL of pre-chilled HT1 buffer
        3. 7 pM library with final volume 600 µL for Qubit quantified libraries
        4. If you are stopping, seal the tube and store at -25°C to -15°C.
5. Spike library pool with 1-5% PhiX spike-in to include quality controls (5% for Pf AmpliSeq libraries as GC content and therefore library diversity is lower, or 1% for Pv AmpliSeq libraries).
    1. Prepare the stock of PhiX
        1. Use the following instructions to denature and dilute the 10 nM PhiX library to the same loading concentration (7 pM) as the Amplicon library. The final library mixture must contain at least 1% PhiX.
            a) Combine the following volumes to dilute the PhiX library to 4 nM:
                i. 10 nM PhiX library (2 µl)
                ii. 10 mM Tris pH 8.5 0.1% Tween-20 (3 µl)
            b) Combine the following volumes of 4 nM PhiX and 0.2 N NaOH in a microcentrifuge tube:
                i. 4 nM PhiX library (5 µl)
                ii. 0.2 N NaOH (5 µl)
                iii. Vortex briefly to mix the 2 nM PhiX library solution.
                iv. Incubate for 5 minutes at room temperature to denature the PhiX library into single strands.
            c) Add the following volumes of pre-chilled HT1 to the tube containing denatured PhiX library to result in a 20 pM PhiX library:
                i. Denatured PhiX library (10 µl)
                ii. Pre-chilled HT1 (990 µl)
            d) Dilute the denatured 20 pM PhiX library to the same loading concentration as the Amplicon library as follows:
                i. Take 70 µL of 20 pM library
                ii. Add 130 µL of pre-chilled HT1 buffer
    2. Mixing PhiX with the AmpliSeq library
        1. For 5% Phi-X (*P. falciparum* libraries or low diversity Pv libraries)
            a) Take 570 µL of 7 pM AmpliSeq library

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b) Add 30 µL PhiX (for 5%)

2. For 1% Phi-X (*P. vivax* or mixed libraries; libraries with expected higher ACGT diversity)
   a) Take 594 µL of 7 pM AmpliSeq library
   b) Add 6 µL PhiX

6. You obtained a 7pM library pool with 1-5% PhiX spike-in for loading onto the reagent cartridge and the MiSeq according to the directions of the manufacturer and Reagent. Keep on ice until loading
   1. Optional: to improve the cluster density
      a) Using a heat block, incubate the combined library and PhiX control tube at 96°C for 2 minutes.
      b) After the incubation, invert the tube 1–2 times to mix and immediately place in the icewater bath.
      c) Keep the tube in the ice-water bath for 5 minutes until loading.
      NOTE: Perform the heat denaturation step immediately before loading the library into the MiSeq reagent cartridge to ensure efficient template loading on the MiSeq flow cell.
7. Preparing the MiSeq system
   1. Load the library in the cartridge
   2. Correctly insert the flow cell in the MiSeq sequencer
   3. Correctly insert the cartridge in the MiSeq sequencer.
   4. Using the sample sheet prepared before and following the steps in the local run manager, start the MiSeq run. It will take approx.. 56 hous to complete.

5 Attachments and forms for completion

- Template_Ampliseq_v1.0_041021.xlsx
- Template_Ampliseq_Qubit_pooling_v1.0_041021.xlsx
- IAAQ198716_241_manifest_Pv_Ampliseq_Vietnam.txt
- IAAQ200463_241_manifest_Pf_Ampliseq_Vietnam.txt

6 Approval and distribution

Approval and distribution	
	Name and function
Initiated by:	Eline Kattenberg Post Doc/Scientific expert Malariology

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Approved by:	Anna Rosanas-Urgell, Unit Head Malariology
Manual distribution:	No manual distribution.

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7 Appendices

APPENDIX 1. PF Ampliseq Peru Custom DNA panel oligo sequences for design IAAQ179763_241

Amplicon_ID	Amplicon_name	POOL	ULSO Sequence	DLSO Sequence
AMPL3594143	CytB_1	1	CCACTCCATAATTCTCTTAAAATGT	AGGAATACGTCTAGGCATTACATTA
AMPL3594144	CytB_2	2	AGGATCACTCACAGTATATCCTCCA	ATGCATATGAAACATCTGGTGTATA
AMPL3594145	CytB_3	1	GGTACAATTTGAGATGGAGTAACAT	TACTGCTACTGGAATAGAGGATAAC
AMPL3593186	CytB_4	2	CATAATAAAGCATAGAATGCACACA	ACGATAGCATTATCAGGATGTGATA
AMPL3593414	CytB_5	1	ATACTCAGAAATGTCATCTTATCAC	AGGAACAGAATAATCTCTAGCACCA
AMPL3593090	cpmp_1	1	TATATAATCCATAAATTTTAATGAC	CTGAAATGACCAAATAATTTTATGA
AMPL3592418	cpmp_2	2	AGGAAAGTATTAATGATTGATTTTT	TCTTTTAGAATACGTGCTTTATAAA
AMPL3594108	ubp1_1	1	TTGCTTAATAAAATCGAATCTAGAA	GGTATATTTGGGATAAGGCGTTCGT
AMPL3594109	ubp1_2	2	TAATTATCATATGAGATAATATCTC	CATAATTCTTAATATTAGGAGTGTC
AMPL3594110	ubp1_3	1	CATGTTTATGTTACCTTTTCTGTTG	TTTCTTCGTATTAGATAAGCTGAAC
AMPL3594111	ubp1_4	2	CGTTGTGCGTATTCTTTTTATTTTT	GTCTTTCTTCTTTTTCATATGAGAT
AMPL3594112	ubp1_5	1	ATAATTAACGTTGTGCCTATTTTCT	ATTAATACTATTATTAATACTATCG
AMPL3594113	ubp1_6	2	GATACATTATTTTCCTTAGCAAAAT	CGTTTCTTTTATTTTTAAAAACATC
AMPL3594114	ubp1_7	1	TAATGGATAATTCTTTATTTACATT	GTTAATGCTTCTTGATTACTAAACA
AMPL3594116	ubp1_8	2	ATCATCTTCAATAGATTTCATTCCT	CATTATCGTTAATGGATAATTCTTT
AMPL3594117	ubp1_9	1	TGTCATTTCTTCCATATCATCATTA	TGTTCATCCATATGATAGCTCAACA
AMPL3594118	ubp1_10	2	ATGAATAGATTCATCCATTATATTT	TACAATTTTTGATAAATCACTTTTG
AMPL3594120	ubp1_11	1	TATTTTGTTTGTTGGAAATATATGT	TTGTTGTTTTTATGAATAGATTCAT
AMPL3594121	ubp1_12	2	CTGTTCACTTTGGTTATATATATTA	GTTATTATTACTGTTCATATTATTA
AMPL3594081	ubp1_13	1	TTTTTCATGGTCACTAGGTGAATAT	ATGTAAGAGATGTTTTGAATTTGTT
AMPL3594082	ubp1_14	2	ATTGTTTTCATCATACATAGCACTT	TTCTGCGATTTGTTTATGTAGATGT
AMPL3594122	ubp1_15	1	ATCCATATTTGTCGTTTTCATTTTT	ACTCTCATGATTATTAAGATGATTG
AMPL3594123	ubp1_16	2	TCCTTCTATTAAGGAATAAAAATAT	TTTCTTTATTTCTTCAAGATTTTGT
AMPL3594124	ubp1_17	1	TGTGTAGGAAGACCAATCCTGAATA	TGTCCTTCTATTAAGGAATAAAAAT
AMPL3594125	ubp1_18	2	ATTTTTATAGGTACGGTTCACGTCT	TGTTTTGATCTTCTTCCGAATCAGT
AMPL3594126	ubp1_19	1	TTTATGATTTAATTCTTCTTCTTTT	TCCTTTATTCATATTTATATCATCA
AMPL3594127	ubp1_20	2	TATTATTTTCTTCTATCAAAACACT	AATTTTTGACATGTGAACATTTTCA
AMPL3594128	ubp1_21	1	CACCACCATTATTAATATTATTATT	CCATAGCTTCATTATTTTCTTTATA
AMPL3594129	ubp1_22	2	GATGAATAAAATAAAATTTTCCTCA	TGTCATCACTATTATAACGATTTAT
AMPL3594131	ubp1_23	1	TTGGTTTCCTTCATTTAAATAATTT	TTTCATTAAACAAGTATACTAAATC
AMPL3594132	ubp1_24	2	GTGAGTTGTTACTGTGTTTCTCAAA	TTCTGCCATGACACTTTGATCAGCA
AMPL3594090	ubp1_25	1	TGAACGTTTAGGTTTCGATGAAGGT	ACGTGTTTTTATGGATTCCTTTTAA
AMPL3594133	ubp1_26	2	ATACACATAATATTCCATATAGATA	ATATGGAAATAACTAAACTTCTAAG
AMPL3594135	ubp1_27	1	GATATTCATTTTGATCTTCATGTTT	CCCAAAATAATATACACATAATATT
AMPL3594092	ubp1_28	2	TCGATGTAATAAATGTAGGTAAATA	TCTTGTTTATTATTTATGGATGAAT
AMPL3594093	ubp1_29	1	TTTTCTTGACGATTTCTCCATAAGG	GCCAAAGATATATTCGACATGCTGG
AMPL3594094	ubp1_30	2	CCTAGCCTTTTGTGATTTAGAAAAT	GGAGAGTTGTAATTATGACGTGTGT
AMPL3594136	ubp1_31	1	ACAAAATTTATTATTATGTATATTA	ATTGTTGTAAACATGATTTAGCATT
AMPL3594137	ubp1_32	2	TATTACAATTCAAACTTTGAAAACT	AATTTTCAGCATATGTACGTTCATT
AMPL3594138	ubp1_33	1	CTTCATCGTTTATAACATATGATGA	CTTGTTCCTCTTTACATAAAAGTAA
AMPL3594139	ubp1_34	2	ATGTAAATTTGTTATAAAATCTTTT	TTTGGATGGAATATATTATTTCCTA

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AMPL3594140	ubp1_35	1	GTACATATACATAATATTTTTGTCT	GTATTTTTACTATTGGATATATTAC
AMPL3594141	ubp1_36	2	GTCCTAAGCTTCCGATTATACTTGT	AGAAGATTCGGAAGATGATAAGAAA
AMPL3594100	ubp1_37	1	TTTGATCGGATATTCTATTTTGCGT	ACGATGAAAATTATTTATGGTCGAC
AMPL3593352	ubp1_38	2	CATACGATTCACATGATTTACACTA	ATATGCATACAAGGAATTTCTTCTG
AMPL3594101	ubp1_39	1	AACTCCTCCCATACGTATATCCTCA	TATTATTACGTTGATCATGTTGGTC
AMPL3594102	ubp1_40	2	TCGTATTCTCTTGATGCATTTGACT	TTGGGACTCACACGGTTTGCATGAT
AMPL3594103	ubp1_41	1	AAAACTTCTGTCACATCTTGTTGAT	TCCTACAGGTGGATGTGGATAATTT
AMPL3594105	ubp1_42	2	TAAGAATTAATATCAAGTGACAAGG	TTTGAAATGAAAAGACATTTTTGAC
AMPL3594106	ubp1_43	1	GAGTTAATTTTAACGTGCGTCTTGA	TTTCATTCCACTTTAAGGCATTTCT
AMPL3592674	ubp1_44	2	GTATTATTGCTCCATATAATTTGTA	TCGTTTGAGCTAAAGGACCAATTAT
AMPL3593039	Pf3D7_01_205066	1	GAGGTTGATTTAGATGAGTTTTGTT	ACCTGTATTAGTTCGTTGGTTATGT
AMPL3593040	Pf3D7_01_339436	2	TTTTTACTTTTCTTCATATCCGATT	CCATTTTCAATTCATTTGCTACATA
AMPL3594050	mrp1_1	1	AAATTCGGAGTCTTCTACTTCTATA	GTAATACGCATACCAAATATATTGG
AMPL3594051	mrp1_2	2	AACCCACTGAATACTTTGAAATCTT	AATTTAGATGCATAATATGGCACAT
AMPL3594052	mrp1_3	1	AGAGGAGGATGCATTCTTACCAATA	ACAGGAATCTTTTGACCTTCTAAAA
AMPL3594053	mrp1_4	2	AAGCAATGGACAACCATATTGCAAT	TCTGCTTATCTCATCAATTTCTGTT
AMPL3594054	mrp1_5	1	ATTCCCAATTAAACATTTTTATCAA	TGGACCCAATCTTTATATGAAACAC
AMPL3594067	mrp1_6	2	TAATATTTACTATACCTTCCATAAC	TTAATACATGATGCATGTTATCAAT
AMPL3594057	mrp1_7	1	CATCTACGTTCTTAAGTAAACCAGA	AGTTTGGAAAATTTGCTACATTCGA
AMPL3593290	mrp1_8	2	TTACTTTTATGTTCCTGGAAACATA	ATGTGATGTACCATCATCATGAGAA
AMPL3594069	mrp1_9	1	CTAGCTAAACATATTCTTACTTTTT	CCTATAATTATTGCTAATGAATTCC
AMPL3594070	mrp1_10	2	TATTTCATTAGGTTGTATAAGCTTT	AATTATGATCATCATTAATATATTT
AMPL3593213	mrp1_11	1	ATCCAACGTACTTTTATTCATTGAG	TGTACATAATTTGTGCATATGAATA
AMPL3594071	mrp1_12	2	CTTATATATCATTTTATTACTATGT	ACAATTATCTTTAAAACTTATATTG
AMPL3594060	mrp1_13	1	TCAAGCGTATATTCATTTCCTAACG	TTCCACTTCATCAAACAATTTTATT
AMPL3594061	mrp1_14	2	CTGTTGAAAATACCATAAATACGTT	GGACTATCATCTGTAGAATTAGGCC
AMPL3594072	mrp1_15	1	GTAATATTGTGTCTGAATGTTCTTT	GGAACCCTTAAAACTGGATGAGTTA
AMPL3594073	mrp1_16	2	AAGGATGATAAGATACAACGAAAAA	AAATAATACTCATCATAGTTAAAAA
AMPL3594074	mrp1_17	1	GATGCCCAAATATTTATAAGCCATT	ATTCTCTTTAAAAATCCATAATCAA
AMPL3594075	mrp1_18	2	CATAGAAGCATTTTCTTTATTAGAA	CTAATTCGAAAATTGTTTATATAAT
AMPL3594065	mrp1_19	1	TGATTTTCCTACTATCCCAATTTTT	TTCTTCTAATCTTTGAACACAGCAC
AMPL3594076	mrp1_20	2	CCATTCAATTTTAGAGCATGAACAA	TTTTTAATGATGGTTCTTCATCTAT
AMPL3594077	mrp1_21	1	ATGACTTTGCTTTACCAATTAAAAA	GTGAAATTATTATATGGATCAATAA
AMPL3594078	mrp1_22	2	TTTATTCATGTAATAATATACCGAT	CGTCATGAACAGAATTGTTTAAATT
AMPL3593042	Pf3D7_02_519457	2	AACCTCATGAAATAATAATCTCTGA	TCATATTTTATATTATTATGTGCTC
AMPL3593041	Pf3D7_02_694307	1	ATTTAGCATATCCTTTTCTTCTTGT	GTTAATTCTATTTAATTCTTCAACT
AMPL3593043	Pf3D7_03_361199	2	ATTTTATTTTTTGAAGGTGGTGGCT	GATTGTTATCTTTTGAGAAGCTATC
AMPL3593044	Pf3D7_03_849476	1	AAACGGTTTATATTACCTTCAAATT	TGGACGATTTTAGTAGTGAGGATAA
AMPL3593091	poly_alpha	2	ACATATTGTTATTTTGATTGTATTG	ATGAAGAAAATGTACATGAGATTTT
AMPL3592369	Pf3D7_04_691961	1	TTATGACCCTACTAATTCGGTTGCT	ACCCTTCTTTGGTTCCAAAATTATG
AMPL3593996	dhfr_1	2	TTCCTAGACCTCTAAATGTGTAGTT	CTATTTGGGAATACAAAAATGGCTA
AMPL3593997	dhfr_2	1	TTTACATTATCCACAGTTTCTTTGT	CCCTCATTTTTGCTTTCAACCTTAC
AMPL3593998	dhfr_3	2	TCTTGATAAACAACGGAACCTCCTA	TTGATTCATTCACATATGTTGTAAC
AMPL3594005	dhfr_4	1	ATCTTTGTCATCATTCTTTAAAGGC	GTAATTTAATTTCCCAAGTAAAACT
AMPL3594006	dhfr_5	2	TCCGAATTTACTTAAAACACCTACT	TTTTTCTTCTCCTTTTATACAATTT
AMPL3594003	dhfr_6	1	CCTAAATCGTTAACTTCTCTATGAA	CGTTCGATCACTTTGTTTATTTCCA

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AMPL3593191	dhfr_7	2	AGGTAATGCCATTTGGTCAAGATCT	TCTAAAAATTCCCTAGTACCATTAG
AMPL3594004	dhfr_8	1	GGATAGGGTATTCTGTTAAGTTGAA	TGCACACAAAAGAATTCTTCTACTT
AMPL3593194	dhfr_9	2	AGGTAATTTTGTCATCATTTGTTCA	TAAACATGTGCATTTCCTAAAACGT
AMPL3593045	Pf3D7_04_770292	1	ATCGGGTTCATTTCTCCCTTTTCTT	CAAAAGTCGTATACATTTACATAAT
AMPL3593047	Pf3D7_05_921893	2	TTCTATGTTTGAAAAATTAGTTTGT	TATCATCTAATGAATATCCTTTACG
AMPL3593994	mdr1_1	1	ACAGCACATACAAATGATATAAATA	AAATGAAATAAGCTATGTACACATA
AMPL3593995	mdr1_2	2	ATTCCTGAACTCACTTGTTCTAAAT	TGTTGTGCAGGTAAACATTTAAACG
AMPL3593978	mdr1_3	1	CTCCACAATAACTTGCAACAGTTCT	TTTCGTACCAATTCCTGAACTCACT
AMPL3593135	mdr1_4	2	AGGCACCATTAAAATCATTATTGGG	AAGCCTCTTCTATAATGGACATGGT
AMPL3593979	mdr1_5	1	AATGCATATGTTTTCCCTTCTTTTA	TAATTCTTGTACCATACCAAAAACC
AMPL3593981	mdr1_6	2	ACATCAACAACATCAGAATCTTTAA	TGGTTGATTTCCCACAACCTGATTC
AMPL3593982	mdr1_7	1	ATGGATATTCTTTGTTTTTGTCCAC	ACTCCAATTTTTGATCTCCACCATT
AMPL3593983	mdr1_8	2	GTTCAATAATATAGCTACCCTCATT	GATGCATTGGAACCTACTAAGGTAT
AMPL3593984	mdr1_9	1	ATTATCATTTCCATTATTTGAAGAT	TGGCATATCTTATAGTACTTAATCT
AMPL3593986	mdr1_10	2	CATAGTCTTTTCGACTTTTTCTCCT	TGGAACTTTCTCTTCTTTTTCATTT
AMPL3593987	mdr1_11	1	GAAAGAGCATTATGAAATGAGAGAA	ACGGGATATAATCCTCCAGCTACTA
AMPL3593988	mdr1_12	2	CTTACAGCAAATACACGCATATTAA	CTATTAATATGTGCAGATAAAACAC
AMPL3593989	mdr1_13	1	GATCCAAACCAATAGGCAAAACTAT	AAGTTAATACAGCTGCAACAATTGG
AMPL3593990	mdr1_14	2	ATCATCTCTTACATCAATATTTGAT	CCCATAAAGCTGCATTTACAATAAT
AMPL3593153	mdr1_15	1	CATAAAAGTTGATTTTCCACTACCT	AAATGATAATTTTGCATTTTCTGAA
AMPL3593991	mdr1_16	2	TTGCATCTTCTCTTCCAAATTTGAT	TCTCCAACGATTGCTGTAGTTTTTT
AMPL3593992	mdr1_17	1	CTATAGCAGCAAACTTACTAACACG	TGCAGATCCAGATTGGTTTGAAAAT
AMPL3593157	mdr1_18	2	GATCATATAAATGCATAAATATAAA	TCGTTTTATAGATGCAATTCTGTGG
AMPL3593046	Pf3D7_05_1188394	1	TGAAGGCAAAATTATGAACGTAACC	AGGACCTGATGGATTCTTTAGATTC
AMPL3593093	TA81	2	AATTTGAATCATGTGTATCACAATG	CATCCTTTTTGTCCTTTTCCTCACC
AMPL3593048	Pf3D7_06_148827	1	ATTCCTTTAATGGTTCCTGGTCGAA	ACCAAACGTTATAGAAATTGCAAAA
AMPL3593049	Pf3D7_06_636044	2	AGATTCGGTTGTTGTTAAAATAAAG	AATATGCAAAATGCTATTTTATTAA
AMPL3593958	crt_1	1	GGATACTTACTTCCTTCTTGTACTA	TGTCATATATGTGGAAGACAATGAA
AMPL3593095	crt_2	2	AGCACATTTACCAAGACAAGAACCT	TCTCTATAACGCTCGTCATTTTTGC
AMPL3593959	crt_3	1	TAATGTTTTATATTGGTAGGTGGAA	AGCCATCTGTTAAGGTCGACAAGGG
AMPL3593960	crt_4	2	GCATCTAACATGGATATAGCAAAAA	AAGTTGTGAGTTTCGGATGTTACAA
AMPL3593961	crt_5	1	GATTGGATATTTCCAGTAGTTCTTG	TTCGGTGTCGTTCCTAAAAAGGTCA
AMPL3593972	crt_6	2	ATTTTCTTCTTGTGTTTCAAAAGAT	TGTATAAGTGATATCTAAAAAGGAG
AMPL3593973	crt_7	1	TTAATCTTAAAATGTCAATCTTATA	TTGTTACAACAATAATAACTGCTCC
AMPL3593974	crt_8	2	GGGTGTATACAGGTAATATAAGACA	CTATTTCCCTTGTCATGTTTGAAAA
AMPL3593964	crt_9	1	AAATCCTATTTTACCTCTACGACTG	ATTGGAAAAAGGATACCATAGCCTA
AMPL3593965	crt_10	2	GTCACAATCATCACATAACTTAGCC	CCAAGAATAAACATGCGAAACCATT
AMPL3593966	crt_11	1	CATCCTTTTTATTCTTACATAGCTG	ACAATTCTGAAGAGGAAACAAAACA
AMPL3593967	crt_12	2	GAATTTAAAGTAATAAGCAATTGCT	AAAGAAGGAAAACAATGCGAAGGTT
AMPL3593968	crt_13	1	ACTTACCAAAGTTACGAAATCTAAT	TATATGTCATGGTAGAAAATTTGTC
AMPL3593969	crt_14	2	CAAATAGGTAGCCAAACTGTAAAAA	GATACGTTGTACCATCATAAACATT
AMPL3593970	crt_15	1	TGAATCGACGTTGGTTAATTCTCCT	TATGAACGAACAAGCCATTTGATAT
AMPL3593107	crt_16	2	CCTTATAAAGTGTAATGCGATAGCA	CGGAATCTTCATTTTCTTCATTTCT
AMPL3593050	Pf3D7_07_455494	1	TTGATTGTAGGCGAATTAAACAATT	TGGCTAAAGTGGCTAGCTATAACAA
AMPL3592804	Pf3D7_07_782111	2	ATTGAAAGAGATACAAAAGATGCAT	AAAGCCTTTGTGAACCCACCATCAG
AMPL3592805	Pf3D7_08_501042	1	GTGGAAAAACAGCTATAGCTATTGC	GTCTTTGAAGGAGAAGTAGTACAAA

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AMPL3594007	dhps_1	2	AGTTTCTAGAATCAACACAGCGTTT	ACTAATTTAAAAAGTTTGGCGCAAA
AMPL3594008	dhps_2	1	GCAACTTTCCTTTTTATCTAATACA	TGTTCCTAAGTTTAATACGGCAATA
AMPL3594016	dhps_3	2	TCTTCTAAATTTTGCATCAATTCGT	GAACGGTTTCATACAAGTAGGACGT
AMPL3594017	dhps_4	1	TATAACTACCAACATACTAAGAGGA	ACATCATATATACGACAATCCTTGT
AMPL3594018	dhps_5	2	AATCACAATCAATATCATTATTATT	AGTTTTAACTACAACTGTCAAATTA
AMPL3594019	dhps_6	1	TATCATATCATTTAAGCATAAAAGT	AAGATTTATATCTTTATCCATATTT
AMPL3594011	dhps_7	2	CCTATATCTATAACACTAGCACCTT	GTGTGTTGTATACACATGAGGAATG
AMPL3593182	dhps_7	1	ATTTCCTCTTTTATGCATTAGAACT	TCAAACATTCTTTGAACAGCACGTT
AMPL3593183	dhps_8	2	AATTGTGTGATTTGTCCACAATATT	TGTGGATTTCCTCTTTTATGCATTA
AMPL3594014	dhps_9	1	AGTTGATCCTTGTCTTTCCTCATGT	TACAACATTTTGATCATTCATGCAA
AMPL3593051	Pf3D7_08_803172	2	AGTCCATTATGAAACAATCCAGTAC	ACAAATATTGGCACTGCATCATTTT
AMPL3593062	hrp2_1	1	CCACGAAGCCGCCACACATTGCCTA	TTGTAATTTATGGGATAGCGATTTT
AMPL3593063	hrp2_2	2	GCTCATCATGCAGCCGATGCTCATC	GCCTACGCCATTAAATTTATTTAAT
AMPL3592823	hrp2_3	1	CATCACGCTCATCATGCAGCCGATG	CCGATGCTCATCATGCAGCCGATGC
AMPL3593064	hrp2_4	2	TAAGAGATTATTACACGAAACTCAA	CCGATGCCCATCATGCTCACCATGC
AMPL3593061	hrp2_5	1	AATAAAGTATTATCCGCTGCCGTTT	TGATGCCCATCATGCTCATCATGTA
AMPL3592820	hrp2_6	2	TTCATGTATTTATGTATGCAGAACT	TCCGTACTTTTGTTAGATAACGTAA
AMPL3593053	Pf3D7_09_231065	1	CGTTATATTTTAGAAATTTTAAAGA	CGACATTAGATATATATTTTGAAAA
AMPL3593052	Pf3D7_09_1005351	2	TTAGTTTAGTATTTGCAGATAATTG	CTATTACATAATACATTTGATGTCT
AMPL3593054	Pf3D7_10_341106	1	GGATTATATAAAAAGTTCTCAAAAC	GCAGTATTTACATATTCCATACATT
AMPL3592810	Pf3D7_10_1172712	2	GTAAAGGAGAATGCTGCAGATTGTG	ATGTGAGAATTTGCCGGATCGATTA
AMPL3593092	ARAII	1	TGTAGTACTTTCATTTAATATTTTT	CTTGTTGATTATTATTTAAATAACT
AMPL3592811	Pf3D7_11_874948	2	GATGTTCACTTCTAAATCATTTTCA	TCGTCCACTCCATTTTCTTCATTAT
AMPL3593078	ama1_1	1	TCTAAAACAAAACATGCTGTTTCTT	GAGGAAAAGCAAAACCTCCATCTTT
AMPL3593079	ama1_2	2	AAGCACTCAATTCAAAAACTAATTT	ATATCTAGGACCATTATTTTCTTGA
AMPL3593080	ama1_3	1	TAGTAGCAATGTATGATGAATTGTT	TGGTATATCTTCACAATTTCCATCG
AMPL3593087	ama1_4	2	ATTATTTGATGTTACTTCTGCCCTT	TGAATTGTTAATTAAACATGTTGGT
AMPL3593089	ama1_5	1	TGGTGTTGTATGTGATGCTCTTTTT	ACAACTTCATTATTTGATGTTACTT
AMPL3593055	Pf3D7_11_1505533	2	TTATTACCACCAGGGAAAAGATTCA	TAAAACATTCACACCTTGGTATCGT
AMPL3594038	ap2-mu_1	1	AGTTCTTTTGGTTGTGTCTCGATAA	AAGGGTCTTTTACATTTGACAGTCT
AMPL3594039	ap2-mu_2	2	GATATCCATAATCTATTATTTCATC	CAGAAGTTGCCCGTTAATAAAAAAT
AMPL3593197	ap2-mu_3	1	ATTACTTGTCCTATTATGTATATGT	CTTGTTAATACGGTTATAACTATTT
AMPL3594040	ap2-mu_4	2	ATATGAGCATATATTAAATTATTAC	CCTATTATGTATATGTGGATCATGT
AMPL3594041	ap2-mu_5	1	AATATTCTTTAATAAATTAATTTTA	TACCTGTTATATAATTAAAATGATT
AMPL3594042	ap2-mu_6	2	CAAATGTACCATCTGGTGGTGTGAA	TAATTCACATAAAGGCATTCCGGAG
AMPL3594043	ap2-mu_7	1	TTCAGTTTTGCCTATGGATTTATAT	TATTATTTTCATATTTGGATAAGGT
AMPL3594044	ap2-mu_8	2	ATACATGCCGCTTGAGGTAAACATA	CATTTTCTGAGAATTTATAGATTGG
AMPL3593262	ap2-mu_9	1	TTGTTTGAAGTAACACCCGATTGAA	GCTCAATGTTATGGGCATTTTATAT
AMPL3593056	Pf3D7_12_1127001	2	TCCTCACCATTGTTATGTTTATCCT	ACCTCTTCCTTTTTCACTTTCCAAA
AMPL3593057	Pf3D7_12_1552084	1	GCCACTGTTACATTTTTCGTATTAT	TTCTCCTCCCTCCTGTATTTCTTGT
AMPL3593108	PK2	2	AAGAACCTGAAGTGAAAATAATAGT	CATGCATTTCAGTCTGAGGAATTAT
AMPL3594045	coronin_1	1	TCGGTTGCTCTCGAGCAAATCCTCA	TTATTAACAATTAACAGGTGTTACA
AMPL3594046	coronin_2	2	TTCTCACTTGATTTTCTAATCTGAT	AGGTTATTTGACGGATCAGCTAAAA
AMPL3593199	coronin_3	1	CATGACGTATCTCCCATATTCTTAT	CCTTCAACTTGCCATGGTACCTATA
AMPL3593200	coronin_4	2	TGTAAAGAACTTAATTTCTTTGGCA	ACATGAAGCTAATATCTCACTATAA
AMPL3593201	coronin_5	1	ATAAAGGTGAAGCAGCATTATCTAA	AAGGCTTTCTTCTCATTTTCTATAT

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AMPL3593202	coronin_6	2	ACTTTACGTATGGAACCTTGTGAAT	ACCACCAAATCCATCAATCCATATA
AMPL3593203	coronin_7	1	TTAAATCCTTTATAGACACCCTTTT	CGACAATTACCATCACCTTTACCTA
AMPL3594047	coronin_8	2	AAATAAAAATTTGGGTGCTTCATTT	ATACCATCAATCCATTTGTTTGTAC
AMPL3592534	coronin_9	1	TCATTTGTTCCATTAACTATGAGAT	TTCTTTACATTCTTGTGGTTCAAAA
AMPL3594049	coronin_10	2	TTTCATAATACCGTTGCTGTACTTT	ACGTTGTCTTTCAAATGACATATTT
AMPL3592539	coronin_11	1	CACTTGGAAGGTACTATTTATTTTT	ATGTCTAGTATATTATCTAATACAT
AMPL3592815	Pf3D7_13_1595988	2	AGAATGAATTGGGAATAAGCAATGA	AAAGGAAACAAGGATCATGAACATT
AMPL3593126	K13_1	1	CAGATACAAATGAATGGCAGCTTGG	ACACATTACTTGATTGTTTATGATT
AMPL3593127	K13_2	2	GGCAATTTCTAAATGGTGTACCAGA	TAGTTCCCAGATTTGGTCACTCCGT
AMPL3593128	K13_3	1	AAGCATATGATCATCGTATGAAAGC	ATTTTGGAGCTGCCACATTGTCAGA
AMPL3593129	K13_4	2	TATGATCGTTTAAGAGATGTATGGT	TAGAGGTGGCACCTTTGAATACCCC
AMPL3593948	K13_5	1	GTTGAAAGAAGCAGAATTTTATGGT	ACCTAGAAGAAATAATTGTGGTGTT
AMPL3593952	K13_6	2	GTGGAGCTATTTTTGAAACATCTAG	ACCATTCCCATTAGTATTTTGTATA
AMPL3593953	K13_7	1	AAAGAAATTAGATATTGATATATCT	CACAACAAAAAGATTCATTTATAGA
AMPL3593954	K13_8	2	GAATTAAGTGATGCTAGTGATTTTG	AAGAAAAAGAAGAACATAGGAAACG
AMPL3593082	K13_9	1	CAAATAATATAACTAATAATCTTAT	GGTGATTTAAGAATTACATTTATTA
AMPL3593955	K13_10	2	TAGTTTCCTTTTAAATAATAGTAGT	TGAATTCTCCATCAATTATGAATAC
AMPL3593956	K13_11	1	GCGGAAGTAGTAGCGAGAATGATTC	AGATAGCCTATTAGAATCCATTGAT
AMPL3593957	K13_12	2	TAAAAATATATAGATATATGTGAAG	TGAATCTAACTAGTGATAAAAATGA
AMPL3593058	Pf3D7_13_1827569	1	GTACGTTCTGTTCTTGTGTTATTTA	AAGACTGTGCGGTTCTCATCAAAAC
AMPL3594026	exonuclease_1	2	GATATATAATTTCTACTACATTTTC	AACATGATAGGAACACATTTATTAG
AMPL3594027	exonuclease_2	1	TTGTTTCTTTCTTAAAGACGGACTA	CGTGTAGATATATAATTTCTACTAC
AMPL3594028	exonuclease_3	2	AGGTGTGAAAATATTCATGTTGACA	TATATCATCATTAAACAGGCTAAAT
AMPL3592420	exonuclease_3	1	TGTATTTTTCAACTGCTTATTTACT	TGAAGCGAATTGAATTGCTGTAGTA
AMPL3594029	exonuclease_4	2	TTAAGATCATTTTCATACTTGTTCA	TAATAAGAAATAATTAAATGTACCG
AMPL3592435	exonuclease_5	1	TATCGTTATCGTCATCGTAATCCTT	TTCTTTGCTGCTAAATGACTCCATT
AMPL3594030	exonuclease_6	2	ATTCGATATCTATACCTATATAATA	TTGATCTTTTCAAAATGTTAACATT
AMPL3594031	exonuclease_7	1	AGACATTATTTTAATATCCGAAGGG	CTTTTCTAAGTGTTTCATTAATATA
AMPL3593255	exonuclease_8	2	TCTATTCAATGTTTCAAAATATAAA	CAATTTATATATAAACGGATTTTCT
AMPL3594032	exonuclease_9	1	TTAAAACATATGAATCAATACATGC	CTTATAAGAAGGTGTTCCTTCCTCT
AMPL3594033	exonuclease_10	2	AGATACACCCTTATTGAAGGGATTA	TGTTCTTGGTTAAGTGGTCTTATAT
AMPL3593068	hrp3_1	1	TTTTGATGATTCTCACCATGACGAT	TCCATGTAAATATAGAATGATGAAT
AMPL3593069	hrp3_2	2	ATGCTCACCATGCAGCTAATGCTCA	TGGAGCACACCACGACGATGCCCAC
AMPL3593070	hrp3_3	1	AAGGACTTAATTCAAATAAGAGATT	CATGCAGCTAATGCTCATCATGCAG
AMPL3593071	hrp3_4	2	TAAAATATTATCCGCTGCCGTTTTT	GTCAAGCACATGCAGGTGATGCCCA
AMPL3593072	hrp3_5	1	GTATTCTATATTTTATAGATACCAT	TTTGTTAGATAACGTAAGTATTTTA
AMPL3592866	plasmepsin2_1	2	TTTGTTCTTTGAATTGTCAATGTTT	GTGGATTCTTATTAGTTTTATGTGT
AMPL3593125	plasmepsin2_2	1	ATTCTATCATGTGCATTTTCAACTT	TGTTGAATTGCTTTTGATAAAGCCA
AMPL3593110	plasmepsin2_3	2	AAATTAGCAGATCCTGTATCAAGAA	ACCACACATTACACTACAAAAGAGA
AMPL3593111	plasmepsin2_4	1	TTTAGTTAAACATCCTGCAGTTGTA	TTATCTCCAACTTCTGCATCACCAT
AMPL3593113	plasmepsin2_5	2	TAATTTGCTGTTGTTACAAAGAGTT	TCAACAACAATTGGATCTACTGAAC
AMPL3593114	plasmepsin2_6	1	TCCTTTGGTTTCCAAATTTTCGTTT	ATGGGACTTTGATAACATCTAAATT
AMPL3593059	Pf3D7_14_832594	2	AGAGTTGAAGAAAAGAAATCTTCCA	AGCAGATATGTGAAAGTGTCTTTCA
AMPL3592386	Pf3D7_14_1381943	1	TAGGATTAGGAGAAGGGAAAGGTAT	ACGAAGAAGCTATTGAAGCATCGTA
AMPL3594146	23SrRNA_1	1	CTATTAAAGCGATACGTGAGCTGGG	TGTTATATTTGCTAAAGTAGCTTAA
AMPL3594147	23SrRNA_2	2	ATATTTATGAGATAGTTTGACTGGG	CGTGAGACAGTTCGGTCCATATCTA

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AMPL3594148	23SrRNA_3	1	ATTATCTGTGAAGATACAGATTTCT	CTATATATAAACGGAGGAGTACAAT
AMPL3594149	23SrRNA_4	2	GATACTTTTTAGTTGAAAATAAAAA	AGAAAGACCCTATGAAGCTTTACTA
AMPL3594150	23SrRNA_5	1	ATAATTTAAGGTTTCCTATTTATAA	TGTTTAACAAAAACACAAATCTTTG
AMPL3594151	23SrRNA_6	2	ATTTAGAAGCAGTTATCTTTTAAAG	AGGGTTAGTCGAATCTTAAAATGAG
AMPL3594152	23SrRNA_7	1	TTAGTGGTGAAATGCCAATCGAATT	CGTAAAAGCTCATTAATTTAATAAT
AMPL3594153	23SrRNA_8	2	AAGAATTAGCAAGTTATAATAAATA	GGTTCTCTTTGAAATATATGTAAGT
AMPL3594154	23SrRNA_9	1	TAAAGGAATAAAAAGTAATAACGAT	AGGTTAAATATATTTAAATAATGAA
AMPL3594155	23SrRNA_10	2	TTTCGCTTATAATTATATAAATTTA	CGGCGAGCGAATTGAAAAAAAATAA

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APPENDIX 2. PV Ampliseq Vietnam Custom DNA panel oligo sequences for design IAAQ198716_241

Amplicon_ID	Amplicon_name	POOL	ULSO Sequence	DLSO Sequence
AMPL4340125	PvP01_01_v1_121166	Pool=1	GTTCCTCAGACTCTCCATATTGTCC	GTATTCTCATCCCAGATACGTGCAC
AMPL4340077	PvP01_01_v1_164620	Pool=2	AATTTGAACGGTAAGACGTTTTTAG	CATTTTGGCGAACGAGGTAGAGAAC
AMPL4340273	pvcrt_o_1	Pool=1	ATGGGGACGTCCTCTTGTATTTCGC	TAACGTGATGCAGATAACGTGACGC
AMPL4340265	pvcrt_o_2	Pool=2	GGCGACCAAACATAAAGTACAAGGC	CCTCACGTAAAGGGTAAAACACCCC
AMPL4340289	pvcrt_o_3	Pool=1	ATTGAACTCCGAAGTTTCGGTGTCT	GTTCCCAATCTTCTTCAGAGTCCTC
AMPL4340245	pvcrt_o_4	Pool=2	CCTGTATCGCAAAATCAAAAAGCAG	ATAGAAGGAGGTACTCCCGATGGAT
AMPL4340269	pvcrt_o_5	Pool=1	CCAAATCCTACAATCAGCGAGGCAA	TATCGGAATGCTCAGCTGCATGACG
AMPL4340285	pvcrt_o_6	Pool=2	CAGGCGCAGGATGTTTATTTTGTAC	CGTAATTGAACAGGTGGTATCTGCG
AMPL4340253	pvcrt_o_7	Pool=1	AAAGTTGGTGACCCATGTAGCTAAG	CGATTTCTCTGGTCATGTTGGAGAA
AMPL4340303	pvcrt_o_8	Pool=2	GCCTTACCCATGCTCCTTCGCAATC	GACATGGAGATTTGGGAAAGCACAA
AMPL4340302	pvcrt_o_9	Pool=1	AATGTTGGGGAAGCGTCTGCAGGGT	GAAGCAAAGCAGCCGTGGGGGGAGG
AMPL4340275	pvcrt_o_10	Pool=2	GGTGTAGGTCATGGTTGAGAATTTC	CATTCAGTTAAAGCAGCTGCGGTTT
AMPL4340283	pvcrt_o_11	Pool=1	CATATTTGGCTCCCCCTTACCAAAG	ACAGGTAGTCCTCAAAAGACACACA
AMPL4340282	pvcrt_o_12	Pool=2	CTTACTCTCAAGAATTATGTTTCCT	CCCTACCGCAAGGAACTTAAAGTAG
AMPL4340263	pvcrt_o_13	Pool=1	CACTCATCCAGAGAGCAAATCTTCT	GATCCGAAGAGGTAGCCAAACTGAC
AMPL4339537	PvP01_01_v1_671781	Pool=2	ATCCCATATGCAATACGGAACTCCA	AGATAATATTTGTGGCGACACGCAT
AMPL4339900	pvmrp1_1	Pool=1	GTACTTGTCTATAGTTCGTCTTTTC	TGTGCCTGTATATACCACGTTCGAC
AMPL4339546	pvmrp1_2	Pool=2	GACATTATCACCGTTTTGCCGCAGT	AATAGTGTGGACTCGAATTTGAATA
AMPL4339695	pvmrp1_3	Pool=1	CGGTATTGTAGACCCACCAGCCATA	TCACAACTGGAACGTCAGAACGTTT
AMPL4339793	pvmrp1_4	Pool=2	TTTCAACAAAATGGGAAACCTGTAC	TGTTTATCTCGAGAACGTATTCGTC
AMPL4339697	pvmrp1_5	Pool=1	AAATTTTCCAGAGGGTGTAAAGAGG	ATTACTTTTTCCTCAAGACTTGGGG
AMPL4339789	pvmrp1_6	Pool=2	TATATGGCACGGTAATTTCAGCAGT	AACATATATAGCAACACCATATCGG
AMPL4339520	pvmrp1_7	Pool=1	CGCAAATGTTTCTCCTGCTAAGGAT	CAGATGTGCTGAAGAGCATTTTGAG
AMPL4340029	pvmrp1_8	Pool=2	CCCGAGAAATGTGGAAGCCAAATAA	AGTTGGAGGCGTTTTAATACTGTAC
AMPL4339526	pvmrp1_9	Pool=1	AGTTTTGTTGTGTCTATGAATGAAA	GCGTAAACCCTTTTTGGAAAATGAC
AMPL4339871	pvmrp1_10	Pool=2	TGCATAAATTGAGCTCTAACGGTGA	CCTTTTTGAGAATATCCAGTACAAA
AMPL4339679	pvmrp1_11	Pool=1	GGAGACATTCAGTTGATCCACGGTT	GTTTTGCCAACAAAAATAGTCGAAC
AMPL4339885	pvmrp1_12	Pool=2	AGTGTGTTTCCAGACAAGAGTTGAC	AGAACAGTTGGTTGTCCATAGGAAA
AMPL4339557	pvmrp1_13	Pool=1	GAAGGCACAGTGAATATTGCGCGTA	GCAGTAGTAGTAGCATACACGAGAA
AMPL4339904	pvmrp1_14	Pool=2	TGCTGTTTTGCAAAGTGCGACTTTA	GGAGAATGTTTCGAAAAAGAAGGAG
AMPL4339606	pvmrp1_15	Pool=1	TTTACTTGAGGATGGGTTCTAATGC	CTCAGCTGACATAGTTGAAGTGTTG
AMPL4340142	pvmrp1_16	Pool=2	AAGAATCTTTGAATACGCCATTAGG	GAGCATCACTGTCTGTTGTATTGTA
AMPL4339985	pvmrp1_17	Pool=1	TGCTGTTGGAGGATCTATAGACAAA	TGGAAAGAAAAAGCTGTAACAGTGT
AMPL4339639	pvmrp1_18	Pool=2	TGTGACACATTATGCATCTGAATTG	TTTGGATTGTACATCGTTGGTTTAT
AMPL4340041	pvmrp1_19	Pool=1	AAATTAACCTTACACAAACATTTAT	TCAAAAGACATAAAGGCAAAGAAGG
AMPL4339989	PvP01_02_v1_198112	Pool=2	GCTAGCACTCATTGGTCTGCATCTG	GTTTTTGATGCGCTAGCCATGGCCT
AMPL4339801	PvP01_02_v1_373744	Pool=1	GACGATGTCGAACAGTCGGTTCTCC	GGTACGCGGCCAACAGTATACCCAA
AMPL4339759	PvP01_02_v1_594798	Pool=2	ACAACGTGAAGGAGAAAATTCGAGT	CGAAGAAATCACAGAGACGTACTTC
AMPL4339542	PvP01_03_v1_127847	Pool=1	CCCTCTGCAGTAGGAACTTCTCGAA	GCTATCCATAAAACGCCCTTCTTTT
AMPL4347647	DPAP3	Pool=2	GCAATAAACAGCTGGTCCTTTGCGA	GAAAATCCTCCACCCATGATGAACA
AMPL4339674	PvP01_03_v1_334738	Pool=1	GTAGGTGTGCTTCCTTTACTCTGAT	GGTAAACATGTGTCAACAGTTCATC
AMPL4339916	pvdmt2_1	Pool=1	TTAATACCTGGTTTACGAGGTCCAG	CGATCACCGGTAGGCAAATGCTCCT
AMPL4340057	pvdmt2_2	Pool=2	CCCATTAAACACACGATGTTCTGTC	AAAGATCTTCATCCATTTGCACTCA

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AMPL4339751	pvdmt2_3	Pool=1	GAAAAATAATGGCGACTTTGAGTCC	GCTCACGATGATTAAAATGACTCCA
AMPL4339638	pvdmt2_4	Pool=2	ACAAATCACCTGAACAGGTCATAAA	TGAGTGATCCGCTAATCTTCATGAT
AMPL4339800	PvP01_03_v1_782122	Pool=2	ATGCGATGGTATCACCCCAGGACGA	CTGAGGAGCCTCAAAGAAAACCAAT
AMPL4340043	PvP01_04_v1_421012	Pool=1	AGTCCTCCATAACGGTGAACTCGTT	AGGTCCCAAGTTGTAGTCATCTGTG
AMPL4340010	PvP01_04_v1_514934	Pool=2	GCTTCTTCTCCTTCACGGAGTTCAC	CTGAATTATGTTTACCACGATGGTG
AMPL4339667	PvP01_04_v1_885624	Pool=1	CTCCTTTCTTTGTAGCAATTTTTGA	TCTTCGCATGGGAGTAAAGAGGGGG
AMPL4339502	PvP01_05_v1_192482	Pool=2	CCTTCTGATGTTTGGATGGGTGGTC	GGTACTATATGGGGAGCTTTCCAGT
AMPL4339643	PvP01_05_v1_452277	Pool=1	AACAACGTTGCTAAATTGTAATTCG	GAAGAAGCATGAAATAAACGCAGCT
AMPL4347655	PVP01_0516600	Pool=2	CTTGTTCAAATTTTCATCCCCTTGG	TGTTGATCGTTTCCTCGTCAATTTT
AMPL4339850	PvP01_05_v1_701523	Pool=1	CGCAAACTGGGCGTTTCCGTAAAAG	AGTTGGTTAGGAGAGATGCATAAAC
AMPL4339583	pvdhfr_1	Pool=2	GGTACCTCTCCCTCTTCCACTTTAG	TATAGCTCCACTGGGTGTGATGGTG
AMPL4339531	pvdhfr_2	Pool=1	CCCCCAATGATGAAGCATTTGTAGT	CCTGAAGTACTTCATATCGACGGAG
AMPL4339951	pvdhfr_3	Pool=2	CCTTGCTGTTGTACACCTCACTGAC	GAAAGCACGACGTTGATTCTGTTTG
AMPL4340056	pvdhfr_4	Pool=1	TTGTTAAAGCTGAAGTACACGAGGT	CGTTGATCCTCGTGAAGTAGATCTG
AMPL4339608	pvdhfr_5	Pool=2	CATGATGATGTCGTATATGATGCCT	CTTGCTGTAAACCAAAAAGTCCAGA
AMPL4339573	pvdhfr_6	Pool=1	GTGTATTCAGCACCGAAGTGTCTCC	GTGCTGCTTAATCTTCAGGCTGTTG
AMPL4339870	pvdhfr_7	Pool=2	AATCATGTGTGTGAATATGGAATAC	GGAATAATTTCCTGTTGTCGAGGAA
AMPL4340044	pvdhfr_8	Pool=1	CGCTAGCTAGCTATAAAAGTATTTT	CCAAGACCCAAGTCACAAGACCTCT
AMPL4347626	PvP01_05_v1_1079460_1079461	Pool=2	GGGAATTGTCTTAAAGCTCCCTCTT	GCAATAACACTTCGCTAGCTAGCTA
AMPL4347636	PVP01_0530500	Pool=1	AAATTGCCATAAAATGAACCCCACT	AATTACCCGGCAACACCAACTTCGT
AMPL4339715	PvP01_06_v1_45794	Pool=2	AATCCCCTACTCCAAACGGGTCGAT	TAAGTCATCTCCCAAGTCACCTTTA
AMPL4339861	PvP01_06_v1_278171	Pool=1	AGAAGATATACCCCACCTTCCTCAA	GATTACATCATTTCGATGGAGCTCA
AMPL4347653	CLAMP	Pool=2	CTCCTACTGCTTCTACATCTTTATG	GGATTAATCATAATGGGTTCCCTGG
AMPL4340157	PvP01_06_v1_944771	Pool=1	TACACGCCCTTTTCACACAAATTAA	GTATTACCTGCACGTGTATGCATTT
AMPL4347648	SEC27	Pool=2	AACAATGGATTTTATGTGCAGGTGA	ACCTTAACAGGTCATACAAAAGGGG
AMPL4347649	PvP01_07_v1_595235_595236	Pool=1	GGATATCCATACAGCGACATATGTG	GTCAAGGTGAATCCCACCAAAGTTA
AMPL4339613	PvP01_07_v1_754506	Pool=2	TCCCCTTCTTGCTTCGAACAAAGCG	AAGAGGGTCCACTCACAACTGATAT
AMPL4339654	PvP01_07_v1_1020470	Pool=1	TTTACAGACTGCTCTACTTTCTGGT	GAAAAATTGCGACTTGATAGGGGTC
AMPL4340063	PvP01_07_v1_1211093	Pool=2	TGATGCTGATGTATATGTATTTGAG	TCTTCATAGATTTCCATCAACGAGT
AMPL4338615	PvP01_08_v1_45083	Pool=1	CATAAATTTATATCGCACAATGCGT	GGTACATTATTTTCCAGTTTGTATG
AMPL4339749	PvP01_08_v1_53327	Pool=2	CAATAACTGAACACGCAAAAGAGTG	ATTTGGTATGTGGTGAAAGAAGCAA
AMPL4347630	PVP01_0809900	Pool=1	AAAGGAGATCAGCCTGATTGACAAC	GATGACCTCCACTTTGTGAATTGCG
AMPL4347642	PvP01_08_v1_879061_879062	Pool=2	CTCCTACACCCCTACACAAACATTC	CAGTTGGAGAGGCATATACAGACAG
AMPL4347632	PVP01_0833200	Pool=1	CTCTTCTGTTTTTATGTTTCTCCCT	TGACTTGCCCGGAGTGAAATTCAAG
AMPL4340083	PvP01_08_v1_1591244	Pool=2	GCAAACGAGAAGATAGACCCTTTTG	CCCTTCTACGCATATGTATCAGTTT
AMPL4347645	SNF2L	Pool=1	GCGGAGAAGAGAACTATGGAAATTG	TTCCTCGATTTAGGAGAAAGAAAAA
AMPL4347646	PVP01_0908400	Pool=2	GAGAAAAAGGAAAAACTTCAATCCG	ACGAGAAAAGAAAACGAAATTGAAA
AMPL4340060	PvP01_09_v1_539410	Pool=1	TCCAAGCCCGTGGAGTCGAAATATG	AAACATTTCGTCCTCATGACGATTA
AMPL4340172	PvP01_09_v1_1070402	Pool=2	ACTTCGCTTCTAAGATAATACTGCT	CTATACGCGCTGGGGGAATTATTCT
AMPL4347633	PVP01_0924700	Pool=1	AGCCACTCGCTGTTATCCTCCTTCG	CTGTTTGACATACGGGTTCCTCGGA
AMPL4339754	pvama1_1	Pool=1	GTTAAGAAGCTAACAGCGGAATTCT	ACTTAAGAGAAAGGCAGCGATTTGG
AMPL4339671	pvama1_2	Pool=2	CGGACCCATATTTTCCTGCGCTGAT	ATTCTGTACTTTGCATTTTCCACTT
AMPL4339631	pvama1_3	Pool=1	CGTCATTTCTTCTTCATACTGAGTT	GTCGTATACAGCTGGGTGTCTGTAG
AMPL4339839	pvama1_4	Pool=2	TGTTCCTCGATTGTTTCCTAATTTC	CGCTTCGAAAACGATTCGGTTGCAT
AMPL4340166	pvama1_5	Pool=1	CTTCTTCTTGAAGTAGGCCATAGAG	CGTCTTTATATATGCTGCAGGGGAA
AMPL4339902	pvama1_6	Pool=2	GCCAACGTGGCTTCGTGAATTCGTT	TAGCATCTGCTTGTTCGATTTTTCC

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AMPL4339757	PvP01_09_v1_1838632	Pool=2	AGGAGATCTACTACTACTGCGTCAA	TGAGAAACAACTCGGTGAGCTATTA
AMPL4347637	IMC1b	Pool=1	TAAAGTGATAGAAGTCCCCGAATTG	AAATGGCGACATCATAAGAAATAGC
AMPL4339987	PvP01_10_v1_351755	Pool=2	GTAGTGTGTCCTACCATTAAACTCG	ATGAACCGGTTCAGCACTATGTCCC
AMPL4339696	pvmdr1_1	Pool=1	GAGAGAGCCAAAGATTTTGTTGTTA	TATGTACGTACGTGCCTCTCCAATC
AMPL4340114	pvmdr1_2	Pool=2	GAACAGTGGAAAGATACTGCTCGAC	ATTCGGAGAAGCTCATTGAGAAGAC
AMPL4339905	pvmdr1_3	Pool=1	ACAAAGATTTGACCTTCTCCTGTGA	GTTAGCCAAGAACCCATGCTCTTTA
AMPL4339611	pvmdr1_4	Pool=2	TAACAGTTTTGCCTACTGGTTTGGT	CTATTGTTGGCGAAACGGGTAGTGG
AMPL4339779	pvmdr1_5	Pool=1	TTCATTTTTATGAGAGTGTTTGCCA	AAGAGGTACAATACAAGTGGATGAC
AMPL4340162	pvmdr1_6	Pool=2	CGATTGCCATGTTCATTTCTGAGAC	GCCAACAAGGATGTAGAGAAGAAGC
AMPL4339645	pvmdr1_7	Pool=1	AAAATGAGTGACGCCAAAGCAAGTA	GAGAGAAAGTAGAGAAGACCATGAA
AMPL4339566	pvmdr1_8	Pool=2	AGAAGAATGAGAAGCATGATAAGCA	AGGAAGGTTAGCCTTTTTGAGAAAC
AMPL4340137	pvmdr1_9	Pool=1	ACGCTGGTGGGTTCTAATGCATCTA	AAAATAGCAGCGCGAACCAAAAAAT
AMPL4339809	pvmdr1_10	Pool=2	TGTACAGCCTGAAAGATTTAGAAGC	TGATTCTCGATGAAGCCACCTCATC
AMPL4339874	pvmdr1_11	Pool=1	CAGTTTAAGAATGTGCGTTTTCACT	ACGAAGATGGTTTTTCTTCTCAAAG
AMPL4339788	pvmdr1_12	Pool=2	CACATTGGTATGATTAACGGGTTCA	AAGGATGTAGAAATTTACAAGGACC
AMPL4339936	pvmdr1_13	Pool=1	ACGCAAGTGCATTTTTGGGTCTATA	TGGTTTTTGGTACGGAACGAGAATC
AMPL4339506	pvmdr1_14	Pool=2	TGCCCTTCTTCGTATCCGTTTTTGG	TTTAAGAACGCTAGACTCACCCTCT
AMPL4339560	pvmdr1_15	Pool=1	GCCCTCCCTTACCGCCTTTTATGCC	TTTCGCTAGTCCTCATCGGAATATT
AMPL4347652	PvP01_10_v1_483567_483568	Pool=2	TATCGCATTTTTGTGTGCATATGGA	TGAGAACAGAACGCTTTTAAAGTCG
AMPL4339685	PvP01_10_v1_523718	Pool=1	TGCCCCCTACCTTGCGATAACAATT	TCGTTCATAAGTATAAGCAAATGGA
AMPL4340168	pvp13k_1	Pool=2	TTGGCATATAAATACCTGCGCTACC	AATTTTCTCACGCGGAAAGCAGCTC
AMPL4339903	pvp13k_2	Pool=1	GTGCAGGCTACAGTGTCATCACGTA	AAAAGTTCCGGCTGGACTTAAACGA
AMPL4339627	pvp13k_3	Pool=2	AAAGGTACATTTACAAAGCGGGAGA	CTTGGACAATCTCATGGTTTCACGA
AMPL4339827	pvp13k_4	Pool=1	CTTCTGATTTTGAGCGGCACTACAG	AACATATGGAAGCGATACGGACTGG
AMPL4339661	pvp13k_5	Pool=2	AAGCAGAAGATTAAGAAAATACGAG	TCTACAATGGAAGGAAGGTGGAGAG
AMPL4340035	pvp13k_6	Pool=1	GGCGGACGCCTACTGCTTCCAGTAC	TCCTACCTGAACAGTCATACGTTTT
AMPL4339798	pvp13k_7	Pool=2	TCCGACAGCGAGGTCTACGACTTTG	GAGGACAGCAAAACGGTCAACTACA
AMPL4339811	pvp13k_8	Pool=1	TTCAGGAATCAGCTGCTGTACCTTA	GCGTAACTCCGTGTACTACCTGAAC
AMPL4339984	pvp13k_9	Pool=2	ATATTTGTTCCAACTGGTTCAGAGC	TCTTTTGCTACCGCCAGAACTACGG
AMPL4340126	pvp13k_10	Pool=1	CCAGCGATGGAGGAAATAAAAACGA	AATCACGAGCCGATTGACAGTCTCT
AMPL4339660	pvp13k_11	Pool=2	GGGCCTTCCTGAAAAGGGTGAAGCG	ACACACCAGTGATTAAGCTAAGTGA
AMPL4340000	pvp13k_12	Pool=1	GAAGAAATGAAGTGGGACGCGATGA	TATTCGAGCACATGAACCGGTACGC
AMPL4339783	pvp13k_13	Pool=2	TATGACCAGTCAGGTGAAACGATTG	ATCGGGTGGGAAGCGATCTCGGGGA
AMPL4340145	pvp13k_14	Pool=1	TTGATATGCCCCATAGAAGGAGGAC	CGGTACGAAGGGGAGTTGTTTTGCG
AMPL4339530	pvp13k_15	Pool=2	AAAAAGCTTTTTCATCTCGGGAGGA	GCATTGAACGTTACGTACGCTCGGT
AMPL4339705	pvp13k_16	Pool=1	GAAACAGAAAATCCGAGGCGATACG	CGTGATTTGTTGTGTTTGTACCGTT
AMPL4339686	pvp13k_17	Pool=2	CGCGGAAAAGTTGCGGTGATAGGAT	TCAGCTACCCTATTAGGCACTCCCA
AMPL4339785	pvp13k_18	Pool=1	AGGAGAAAATCCCGAGGGACGAATT	CGTTTTGTGAAAAGCCAGTGGGGGG
AMPL4339588	pvp13k_19	Pool=2	GAAGAAGAAGCACCTGATGAGCGTT	CGACTGTATGAACCGCTTTAACCAT
AMPL4339730	pvp13k_20	Pool=1	GGTGAGGAAGCTAACGGAGCTAACC	GTTGAATCGCAAAAGGAGAGAAGCT
AMPL4340091	pvp13k_21	Pool=2	AGGTGAGCAGTTACCAAAGGGTACA	AACGAAGCTGACTCCTCAAACGCCG
AMPL4347627	SET9	Pool=1	CTGTTCAAAAATATGCAGTACGTTG	CCATTCTTATGAGCGGAAAAACGAA
AMPL4339646	PvP01_10_v1_1385673	Pool=2	CCTAACTGCCTGTTTGTGCCTACAT	ACCGACTCGCCTTACATATAACTTC
AMPL4339786	ABCE1_1	Pool=1	CTTATGTAGGCTATCTTCGAGGTGT	GTTCAATTTGGCAGACAAGGAGGTA
AMPL4340040	ABCE1_2	Pool=2	AACTCATTTCCTCGGAAGAAGGATA	CGTTTTGACGATTGGGCAGTTTTTC
AMPL4339930	ABCE1_3	Pool=1	TACACATTTGTCGTCTGCCCTATGA	TTCAGCGCTGTGGATTTTCCTATTC

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AMPL4339514	ABCE1_4	Pool=2	TCATCTGTTACGTCCTGATCTGTAG	AGCGAATCTTTGTAACTCTCCTCCA
AMPL4339817	ABCE1_5	Pool=1	AGGGATCTGTGTATAGCCCCTTTAG	AGAGACTCCTCCCTTATTCGTAGGT
AMPL4339619	ABCE1_6	Pool=2	CCACGACGAACGCCGTTTTGTTAGT	AGACTTTCTACGTTATCCGGTTTGA
AMPL4339587	ABCE1_7	Pool=1	TACGGTTATGTACACACGTATGCAG	AAACGATGATTCTCTGCTCGGAGTC
AMPL4339539	ABCE1_8	Pool=2	AAGTGCTGCCAATTTGTTGTTTTCC	CGTACTTGTTTATCCTGGGGCGGTA
AMPL4340030	PvP01_11_v1_245834	Pool=1	CGGAGGGAAGATACCATAATTGAGA	AGAGGCTAATCAAATCGACTACATT
AMPL4347656	PVP01_1109600	Pool=2	AAGTGGAATGTCATAAGATGGCTCA	GGTAGATTACAAGTGGACCGATCCT
AMPL4347635	PVP01_1112200	Pool=1	TGTGCAAATTGCTCAGCTTTACAAC	ATGCTGCTTAAAAAGAGGGACGAGA
AMPL4340156	PvP01_11_v1_720439	Pool=2	CACCTCTCTAGAAAAATATGCACTC	AGGAGGTAGATACAGAAAAAGGGGA
AMPL4347643	PvP01_11_v1_1137409_1137410	Pool=1	TTTGTGAAAACGATCGCAGAATGAT	GAGTTAAAGATAACCGCGTGGGAAA
AMPL4339598	PvP01_11_v1_1145363	Pool=2	CGGTAGTTATCGGCAGCTATCGATG	CAGTTTAGCGATAAAAAGACATGTA
AMPL4347628	ALV7	Pool=1	AGGGATGGGTAGACCCAAACATTAC	TATGAAACGGTGATGAACTGAGCTG
AMPL4347625	PVP01_1133700	Pool=2	TTCCCCATTGTGGACCATCAAATTG	TCATTCGTGTTCCACTGGAAAATTT
AMPL4347644	PVP01_1144100	Pool=1	GACCCTTTTAATCTGCACAACACAT	CGATATGCCGTGCACCTGTAAAGAT
AMPL4339745	PvP01_12_v1_94291	Pool=2	TGGAGAATGAGGAAAGGGACACATA	CGCATGTTGTGATTTGTAATTTGTC
AMPL4339656	pvk13_1	Pool=1	TCCCAAGGTTTTCTTTCGACAAATT	GCTTTCATGCGTGAAGATTCATCTG
AMPL4339743	pvk13_2	Pool=2	ACTTGAGTCACTCAACTCCGTTTCG	ACGCTCAAATCGATCGATTCCAAGA
AMPL4339896	pvk13_3	Pool=1	CCGTTTGATATATCAATGTCCAGTT	TTATCGGGGTGGATGAATCCATGAA
AMPL4340099	pvk13_4	Pool=2	GTACCTCCCACTTAGCAACTTTTCT	CAGTTTCTGTTCCTCGATTGATTTT
AMPL4339964	pvk13_5	Pool=1	GAAATATGCCTTCTTCGTGGACATG	GTGTGCCTAGAAGTTTCGAATATGG
AMPL4339521	pvk13_6	Pool=2	AGGCTACACACATGGAGGAAGATCG	AATGTCTAACAGCTCCATGGAGTTC
AMPL4339804	pvk13_7	Pool=1	CCACCAGTGATGATGTACGAATCGG	GCGATTTCTACCCAAGCCTTCATCC
AMPL4339737	pvk13_8	Pool=2	GGGGAAACATATACCGTGGTAGTGG	ATCTTCTTCTCTGGAACTCCATTGA
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AMPL4347654	PVP01_1227900	Pool=2	TCTAAAGAAATCGGTGGCACAAACC	CTGCACATGTTTGGTCAATTCTAAT
AMPL4347651	PVP01_1235200	Pool=1	CACCCAAATGGAGACTCAAATGTTC	GCGATGCTGAACGTGTTGAAAATAA
AMPL4347641	PVP01_1236900	Pool=2	AAAGCAAAATGAAAAATGCCTCGTG	CGCAAAAATTGAACAAAGTCGTACG
AMPL4339578	PvP01_12_v1_1844936	Pool=1	CTTCAGAACCTTTATGTCGTTATCG	TAACTTTTCTGCACTTTTGGAGAGC
AMPL4347638	PVP01_1249000	Pool=2	CAACGGAGGTAGTGACGATATTAGT	GGATGATGAACAGTTGGGAGAATCT
AMPL4380317	pvmdr2_1	Pool=1	TAACTCTGCTTCACATCAAATTGGT	GCTCTTTCACGAATTATGAGTTCAC
AMPL4380308	pvmdr2_2	Pool=2	GCATAATAACTCCCCTCATGATTCC	GTCCACCACATGGTAGATGCTAATT
AMPL4380318	pvmdr2_3	Pool=1	TGTACGACTGGTTCCAATACAACGC	TATGATGGCCAATATCCCTGTGAAG
AMPL4380311	pvmdr2_4	Pool=2	TGTCCTCCAGGAAGCTTATGTTCGG	GAATCGTTGTTCATCGTGCTCGTGT
AMPL4380309	pvmdr2_5	Pool=1	CATATCCCTTTTCAACACCTCGTTG	TTATCCGGGCGGTAGCTCTTCTTCT
AMPL4380310	pvmdr2_6	Pool=2	AAAATGATGCAGGTAACAACTCCTT	TGATTACGCTGAATACTTTTGAGAG
AMPL4380322	pvmdr2_7	Pool=1	GCACCCCCAAACTGTTAAGGATCTT	GCACTCTCAGTACCTCTGTCTACAA
AMPL4380321	pvmdr2_8	Pool=2	CTGACTCCAAATTTCTTTTCATGTG	AGAGCACTACAGAATCTCCTAATTT
AMPL4380312	pvmdr2_9	Pool=1	GAGCAGTTTCGAGATGGTCGTTTTT	CTATCCGCTCCGTCATATACAATCA
AMPL4380327	pvmdr2_10	Pool=2	CCTTTGTCTCCAACGAGAGTATCCC	GCCATATGCATTGGTTGTGATGGGT
AMPL4380315	pvmdr2_11	Pool=1	TCTGGACTGCATATTCCACATCTCG	GACATAATAAAATCGTACAGTTGAG
AMPL4380324	pvmdr2_12	Pool=2	CACTGGTTTTACTGCCTCGGGCAAG	ATTCAATTTGAGCAGATGCTGATGG
AMPL4380313	pvmdr2_13	Pool=1	ATACAGTGTGCTGTAGTTCTCCTTA	TTCGCGGCTTCCTTCACAATGCTGT
AMPL4380325	pvmdr2_14	Pool=2	CGGTGTGGTTCACCTCGCTGTAGGA	AGACGCCGTTCACATTTTGGTTGCT
AMPL4380320	pvmdr2_15	Pool=1	CTAATCTCTCCCTCCACATGAGCTT	TACCACGCTCACTTTGTCTGCCACT
AMPL4380323	pvmdr2_16	Pool=2	TCTCCACGCATGTCAATTTCGTTGT	ATCAATTGCTCCCTCCACATGAGCA
AMPL4380316	pvmdr2_17	Pool=1	CTGCTGTAGTCTTGGTGGTCCAAAT	GACACATGATCACTTTCACCAATCG

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AMPL4380314	pvmdr2_18	Pool=2	GTTCGTTAGCCGTGGTAAGCTCGTT	ACTGAAGGTGTTCGCGTCATTATTA
AMPL4380326	pvmdr2_19	Pool=1	CACATCAATAGTCATCGTCGTCAGC	CGGATCGTTGACAACTTCCCTGTCG
AMPL4380319	pvmdr2_20	Pool=2	TTTCCTTCAATTCTGGGCATTCAAT	ATTGTAGTCGTAGCTGACGGAGGGT
AMPL4347634	PVP01_1301600	Pool=1	TGATGATTTTATTTTTGCTGACGCT	GGTAGTACAGCTCGTCCATGATTTC
AMPL4340078	PvP01_13_v1_162821	Pool=2	TTTTTCGGAGCTTGTTTACGTACGA	ATTGGGAAACAGCGTCCCTATTTTT
AMPL4340180	PvP01_13_v1_659592	Pool=1	GGCTAACTTCAAAGGGACGAAACTC	CAAATCGCGAAGTGGCCAATTGGGC
AMPL4339701	PvP01_13_v1_1770129	Pool=2	TCCCTTTTTGTTAGTGTCCTCCATG	ACCTTCTGCCTACTGAACTTCTTAT
AMPL4347650	RPT4	Pool=1	GAAATTCAAAGAACGCTCATGGAGT	AAGGCCGCTCGAAAGATTAATGAGG
AMPL4339821	PvP01_14_v1_743338	Pool=2	ACACGTGCGTCCGAGGTTAACTTAG	CGAGTATACGTTACAGTGGGTGCGC
AMPL4347640	PVP01_1427200	Pool=1	TTAAAGGAGTAGTGCTTAGTGTTGC	CAAAATACCACCACTTGGTGTTTAT
AMPL4347631	PVP01_1428700	Pool=2	CGCCTTTTCCTTAGCTTCCTTATCC	GTTTCTCTGGAATGATAAAGCAGGC
AMPL4347639	PvP01_14_v1_1258543_1258544	Pool=1	TGCCCCACGATATGCTATGTTTATG	TGGGAGCGAAAAATATAGGCACAAT
AMPL4347629	PvP01_14_v1_1266325_1266326	Pool=2	ATCCATCTGAATGCGTACGCAGAAA	GAATGTGTACCTGTGCAGAGGTAAA
AMPL4339663	pvdhps_1	Pool=1	ATCACAACTGTGGAGGTTCAAAATG	GGTAATCTCCTGGCAGTGCACGAAA
AMPL4339721	pvdhps_2	Pool=2	AAGCACGACCAGTCTATTAAGCTGT	GCTTTTGTACCAGAAAAATATTTGC
AMPL4339572	pvdhps_3	Pool=1	TAAGCATCGACACGGTCAATTATGA	TACGATGAGTACCCGCTGTTTCTTG
AMPL4339969	pvdhps_4	Pool=2	TGGCGGTTTATTTGTCGATCCTGTG	GAGTTGGTGGACATCCTAAACGATA
AMPL4340085	pvdhps_5	Pool=1	ATCATTCCAGAGTATAAGCACAGCA	GTCATGCCTGTTTTGAAGCTCTTTA
AMPL4339876	pvdhps_6	Pool=2	ATTGAGCAAATCATGAAAAGAAGGG	GCCATTCGCTCAACTTATAACAGTT
AMPL4339717	pvdhps_7	Pool=1	TCTTGGATAGGCGATTTGATCCCAA	TCAGGGAGAAATATTTCAAAATCGC
AMPL4339843	pvdhps_8	Pool=2	GTGCATACCATCCCCCAGTAGTAAA	ATTATTAGGGAAGTCAGCGTAGAGG
AMPL4340007	pvdhps_9	Pool=1	GAAGAACGCATATAAACAGAACAGC	GTAGACACATAGGTCCAAATGCCGC
AMPL4339775	PvP01_14_v1_1911110	Pool=2	TCCCGTGTGGACTTCACCTCTGATC	TAAGGCGGTTGGTATGGAAGCGCTG
AMPL4339602	pvmrp2_1	Pool=1	TACGGAACTACTTCGCGGACATCAC	TGTTTTAGAGTCCGCCCGAATCCGG
AMPL4340161	pvmrp2_2	Pool=2	ACAGAAGAAGAAGAGTGCATCTAGG	CTTCATTTACGTCGTGGCCAAGGGC
AMPL4339772	pvmrp2_3	Pool=1	TATCAAGACCATGAGTTTGCAGGAA	ATCTTCCTAAACAGACACACATACA
AMPL4340042	pvmrp2_4	Pool=2	ACTTCGAAAACGTGTTCGTGAGCTA	GACGACATTATGGAGGCCTTTAAAC
AMPL4339640	pvmrp2_5	Pool=1	GTTCATCATAAAAGCGCTGCTCTAT	ATAGACAAGTCGCGCAACCTTTATT
AMPL4339731	pvmrp2_6	Pool=2	TTCCCTCTACGTACAGCTGATTGTG	AAGGAAGTATCAAAGGAGGTGTCGA
AMPL4339813	pvmrp2_7	Pool=1	CTTTCTTTCGTTTCCTTTTCACCAT	TGGCTTCTACATCATTTACCCTTAT
AMPL4340160	pvmrp2_8	Pool=2	TCTGAAATATTGAAGAAGCAATTGG	GGTCTACGTATTCCCGATGATCATT
AMPL4340065	pvmrp2_9	Pool=1	ACAGGATGACAAAATAACTCTTCAC	TACTTTGTCCTTCTACCATGTGTGT
AMPL4340177	pvmrp2_10	Pool=2	CAAGAACGACCTCAAGTACCAGAAG	AAGCCCAGCTGAAGGATAACTATAT
AMPL4339891	pvmrp2_11	Pool=1	CAACCAGAACATCTGGCACAGCTTT	GAGCTGAAGAGCACCTACTCGTGCC
AMPL4339777	pvmrp2_12	Pool=2	GTGGAAGCAACAACGATGTGATTAT	CAGTACGACGTGCAGATCTACCGCC
AMPL4340079	pvmrp2_13	Pool=1	GAAGCTCTTCGTAAAAGGAGGAGAT	TCTTATTTGTACCTCCTGGATGACC
AMPL4339742	pvmrp2_14	Pool=2	AGAGGAAGGACCTAAGGTACGTGAA	CTGCACGACGTAGATAATTCGACCA
AMPL4339508	pvmrp2_15	Pool=1	GGCAGCTGCTACGTGAAAAGCTTCG	GGTTGTTCAAAACGGCTAGCTCCCT
AMPL4339729	pvmrp2_16	Pool=2	GGTAATTTTGAAGCTGAGCGGGTGT	TACTCTTTGGAAACAGATTCGACCC
AMPL4339513	pvmrp2_17	Pool=1	GGGGGCCCTCATCAAGTCGATTTTT	TGCTGAAGAACGTCAACCTGACGCT
AMPL4340141	pvmrp2_18	Pool=2	TCAATCATCACTCCTCTATTCGTTT	GCAGTAACAGGACCCACTACGGCGC
AMPL4339761	pvmrp2_19	Pool=1	AAGATAAAGCACCTCAAGTGTAGGG	TAACCTACTCGAGGGGACCATCAAC
AMPL4340031	pvmrp2_20	Pool=2	GGGAAATTGTCCAGAGGGAAGAATC	AGTAACATGCATCACATCCTTAAGG
AMPL4339935	pvmrp2_21	Pool=1	GCTATGCAGCTTCCCTTATCCTGAG	CGGAAGGAGACAAGGAAGAGAGCGA
AMPL4339706	pvmrp2_22	Pool=2	TATGTGATTCATACCCTCTTCCTCA	GAGATCACCACGATGTGCAGGTGGA
AMPL4340054	pvmrp2_23	Pool=1	ATAGAGGAAGATGCCGCGATAGAGT	GAATTGGCATTCGGCTTCATCCTAG

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AMPL4339868	pvmrp2_24	Pool=2	GCGTTACAGCGCTTCATCGCTACAG	CACAGAATAACCCAAGTGAACGACC
AMPL4340171	PvP01_14_v1_3004298	Pool=1	GAACCTGTAGAAGGTGAAGAAGTCG	CCAACAACATTCGTTGAAACTGTAG

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APPENDIX 3. PF Ampliseq Vietnam Custom DNA panel oligo sequences for design IAAQ200463_241

Amplicon_ID	amplicon_name	Pool	ULSO Sequence	DLSO Sequence
AMPL4380293	Pf3D7_01_v3_163145	Pool=1	CTTGATCAACAAATTTGAAGTGAGG	ATTCGGCTTGATGATCGGTAGTATA
AMPL4346863	ubp1_1	Pool=1	TTCGTATTAGATAAGCTGAACGAGT	TGTGGGTTGGTATTTATATGTTTAC
AMPL4347325	ubp1_2	Pool=2	GTCCATGTTTATGTTACCTTTTCTG	GTTTGTTGTGACTTTGTCGTTTTTA
AMPL4347242	ubp1_3	Pool=2	CATAATTAACGTTGTGCCTATTTTC	GTATCGGAGTCGTATGTTTCTAATG
AMPL4346955	ubp1_4	Pool=1	TACGGATGAGATACATTATTTTCCT	GGGATGAGTATCGAAAGAATTATGT
AMPL4346988	ubp1_5	Pool=1	TTGATAAATCACTTTTGGAATAGCT	CCTCTTTATTCTTTTCAATAATACG
AMPL4347261	ubp1_6	Pool=2	TCTTGTCATTTCTTCCATATCATCA	ACCACCTTTATTATCATCTTCAATA
AMPL4346935	ubp1_7	Pool=1	TGTTATCATATTTTTCTGCGATTTG	CCTTTATCATGTTGTATTATTTTGT
AMPL4347497	ubp1_8	Pool=2	TGACTTTTCATTGTTCTTTCCTTTT	ATGAAGAGACCAATTCTGTTCACTT
AMPL4347265	ubp1_9	Pool=1	CTTACAATTTCTTCTTCAGCACGTT	TTTTGTTTTTCATGGTCACTAGGTG
AMPL4347302	ubp1_10	Pool=2	CTGAATCGTTCATATAATCACTATT	CTGCTATTGTTTTCATCATACATAG
AMPL4347372	ubp1_11	Pool=2	ATTTTTATAGGTACGGTTCACGTCT	GTTTTGATCTTCTTCCGAATCAGTT
AMPL4347208	ubp1_12	Pool=1	TTTTGACATGTGAACATTTTCATTT	TTTTGTGTAGGAAGACCAATCCTGA
AMPL4347319	ubp1_13	Pool=2	AACACTCTTATAAAAATCCATAGCT	AATTGTTTGAAAAGAACTCTAGCCC
AMPL4347281	ubp1_14	Pool=1	AGATGAATAAAATAAAATTTTCCTC	TACGACGATTCTTATCACCACCATT
AMPL4346865	ubp1_15	Pool=2	TGATCAGCATACATATTGCTGTCCT	CATCGCTAGATGAATAAAATAAAAT
AMPL4347320	ubp1_16	Pool=1	TGTTATCATCATCTTTTTGGTTTCC	GGTACGTTTTTAAGAACCATTCAGC
AMPL4347001	ubp1_17	Pool=2	AGTGAGTTGTTACTGTGTTTCTCAA	TTTCTGCCATGACACTTTGATCAGC
AMPL4346796	ubp1_18	Pool=1	TAAATGAACGTTTAGGTTTCGATGA	GTGTTTTTATGGATTCCTTTTAAAC
AMPL4347240	ubp1_19	Pool=2	ACCAGCCAAAGATATATTCGACATG	ACATCATGGTGATATCCTGTTAGAA
AMPL4347034	ubp1_20	Pool=1	AGCAAGCGATCGATGTAATAAATGT	ATTCATTTTGATCTTCATGTTTGTC
AMPL4347102	ubp1_21	Pool=2	ATCTTTCTTCTTCGTCTTTTATTCT	TTTATATTTTTCCTCATAAACTCAC
AMPL4347187	ubp1_22	Pool=1	CCTAGCCTTTTGTGATTTAGAAAAT	GGAGAGTTGTAATTATGACGTGTGT
AMPL4346867	ubp1_23	Pool=2	CACCCGGAAGCATTTGATTAGAGGT	TGAAATTGTTGTAAACATGATTTAG
AMPL4346996	ubp1_24	Pool=1	CCCCATCTTTTCCGAAATAGAATGA	ACACCCGGAAGCATTTGATTAGAGG
AMPL4347470	ubp1_25	Pool=2	GTATGTTTTTCTTGTTCCTCTTTAC	TCATATTTTGATTTGATACACCCGG
AMPL4346970	ubp1_26	Pool=1	ATTCTCCATGTTTGTGTTCATGTTT	AACAAGACGTCCATTTTGATCAAAA
AMPL4346936	ubp1_27	Pool=2	CATCTTCATCGTTTATAACATATGA	CGTTCTATTACAATTCAAACTTTGA
AMPL4347473	ubp1_28	Pool=1	ATGATAAGAAAGGATCATATTTCAT	TGTTCATCATCTTCATCGTTTATAA
AMPL4347525	ubp1_29	Pool=2	AATCCTTATAATTTGGTTCATTTGG	CATCATCTAGGTTAGCAAAATGTAA
AMPL4347506	ubp1_30	Pool=1	AGAATCATCTTGTCCTAAGCTTCCG	GTCTTCATTGTAGTTAGAAGATTCG
AMPL4347178	ubp1_31	Pool=2	CCATTTGATCGGATATTCTATTTTG	ACGATGAAAATTATTTATGGTCGAC
AMPL4346920	ubp1_32	Pool=1	CATACGATTCACATGATTTACACTA	GATATGCATACAAGGAATTTCTTCT
AMPL4346973	ubp1_33	Pool=2	GGATGTGGATAATTTCTTTTACTCA	CGTTGATCATGTTGGTCTGAGCCGT
AMPL4347269	ubp1_34	Pool=1	GTACTATATAAAGCCTGTAATAAAC	ATATTATTGGGACTCACACGGTTTG
AMPL4346974	ubp1_35	Pool=2	AGGTAACATATTTAAAACTCTATCT	TTTCCTAAATTCATTAATCCTACAG
AMPL4347146	ubp1_36	Pool=1	TTTTCGTTCGTACTTATAGGCACAG	TCGTATTCTCTTGATGCATTTGACT
AMPL4347082	ubp1_37	Pool=2	GGTTAAGAATTAATATCAAGTGACA	ACTTCTGTCACATCTTGTTGATTTC
AMPL4347443	ubp1_38	Pool=1	AGTACAAATCTGGAGATATGGGTGC	CGTTTGAGCTAAAGGACCAATTATA
AMPL4380248	Pf3D7_01_v3_340448	Pool=2	GTGGTGGTGTTATTTGCACTTTTAT	TATGAACGTTCATCATTTTATCAAC
AMPL4347586	Pf3D7_01_v3_399716	Pool=1	ACCTTTTGAGCATTCAACAGATCGT	ACCATTCAAATCATATTCTTCATCC
AMPL4347487	pfmrp1_1	Pool=1	AATATGGCACATCGAAGTTCCGACA	TTTTCATGTAATACGCATACCAAAT
AMPL4347271	pfmrp1_2	Pool=2	CTTTCTTTTCACTTGCATCATTTGA	TGATATTCCAACATTTTCTTTATAT

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AMPL4347241	pfmrp1_3	Pool=1	AATACTTTGAAATCTTTTAAGAATG	TCTTCTAATTTAGATGCATAATATG
AMPL4347038	pfmrp1_4	Pool=2	TTATTCCTGATGAAGAGGAGGATGC	GGAATCTTTTGACCTTCTAAAATAC
AMPL4346851	pfmrp1_5	Pool=1	TTCCAACTGAATTGGACCCAATCTT	AGGAGGATGCATTCTTACCAATACT
AMPL4346766	pfmrp1_6	Pool=2	TGCATGTTATCAATTCTTTTATCTC	TGTTCACATTAGGTAAACTCCTATT
AMPL4347031	pfmrp1_7	Pool=1	TAACCACTTCAACTATATCAGAGGA	GGACAACCATATTGCAATTCCAACT
AMPL4347384	pfmrp1_8	Pool=2	TAACATTATTAACTAAGTTTGGAAA	GCAAATGATTCCCAATTAAACATTT
AMPL4346951	pfmrp1_9	Pool=1	TCAAATTATGTGATGTACCATCATC	TGGAAAATTTGCTACATTCGAAATT
AMPL4347121	pfmrp1_10	Pool=2	TGAATTCATTACTCATTGTGCTATT	TGTGATGTACCATCATCATGAGAAG
AMPL4347361	pfmrp1_11	Pool=1	TGCACTTTTTCCTGATCCAACATTT	GTATTATCATCTACGTTCTTAAGTA
AMPL4347398	pfmrp1_12	Pool=2	CAAATCATTCAATAATTCACTTTGT	TGATCCAACATTTCCTATAATTATT
AMPL4347368	pfmrp1_13	Pool=1	TAATTTGTGCATATGAATATAATGC	ATCTCCTAATATAGAATGGAAAAAT
AMPL4347223	pfmrp1_14	Pool=2	TAAACATTTTTGAAGGTAATTTTCA	ATTTCATATCTCCATGTTCTATGGT
AMPL4346944	pfmrp1_15	Pool=1	ATTTAAGTTTGAATAACCCCAGTGA	ACATTTTTGAAGGTAATTTTCATTG
AMPL4347253	pfmrp1_16	Pool=2	ACACTCTCCGTATTCCCTTTTACGA	AGAAAATTATCCAACGTACTTTTAT
AMPL4347330	pfmrp1_17	Pool=1	CGTATATTCATTTCCTAACGAAGAA	CCACTTCATCAAACAATTTTATTCT
AMPL4347048	pfmrp1_18	Pool=2	AACTTTTGACAAAAGGCATTGATGA	ACTATCAATTTCAAAGGAAACACTC
AMPL4347128	pfmrp1_19	Pool=1	ACTTGCTTTTGTAATATTGTGTCTG	TCAGAATTATTACTAGTATAGGTAT
AMPL4347225	pfmrp1_20	Pool=2	TAAAAATCCATAATCAAAAGCAGAT	GCTTTTGTAATATTGTGTCTGAATG
AMPL4347533	pfmrp1_21	Pool=1	TTGTGCTTCTTTACAACCTCTCGAA	ATTCTCTTTAAAAATCCATAATCAA
AMPL4346823	pfmrp1_22	Pool=2	TCCACTTGCATATAAATGAGGATGC	ACAACCTCTCGAAAATCTTTTGAAA
AMPL4346906	pfmrp1_23	Pool=1	ATAACACCTAGTCTAGCAGAAAACG	ACATGATAAATACAGCCTTTGTGCT
AMPL4347213	pfmrp1_24	Pool=2	CAAATTCTTCTAATCTTTGAACACA	TCCAAGGGTACTCAAAATTCGAACA
AMPL4346971	pfmrp1_25	Pool=1	CTTCATCTATGTATTTATATGTACC	CTTCTAATCTTTGAACACAGCACAT
AMPL4347220	pfmrp1_26	Pool=2	GTATAGTACTTTTTCCTGCGCCTGA	TTCATTTTCCTTATTCATAGAAGCA
AMPL4347442	pfmrp1_27	Pool=1	AAAGAAGATTGAGCTAAAATACCAA	TCCTGCGCCTGATTTTCCTACTATC
AMPL4347079	pfmrp1_28	Pool=2	TTGGTTTATTACTTTTGATGTTTGT	GTTCGAATGTCTCTTCCTTCTACTG
AMPL4346928	pfmrp1_29	Pool=1	GATGTGAAATAATTAGGACTGTATT	TTCAATTTTAGAGCATGAACAATTT
AMPL4347290	pfmrp1_30	Pool=2	GCATGGGTGTGTGTAAGTTTATTCA	AAAACTATTTAATTCGTCATGAACA
AMPL4380233	Pf3D7_02_v3_158568	Pool=2	TTATAATACGTTTGCAAATGTGAAT	TGATGTGAATGACAAATGTGTTGTT
AMPL4380250	Pf3D7_02_v3_587411	Pool=1	ATGAAGATTCCTATTCCGAAAACCT	AGGTAAACACATAAAAAGGGACACG
AMPL4380284	Pf3D7_02_v3_714480	Pool=2	GTTATACTTTATCAAAAGAGGAGTT	TGAATGTATGTTATAATGAAATGAA
AMPL4380210	Pf3D7_03_v3_241184	Pool=1	TACAGAAGAATAAAAATGAAGAAGC	ATGCAAAAGATGATACGTTTCTTTT
AMPL4380279	Pf3D7_03_v3_457954	Pool=2	ATACAATGCAGAACAACATGATAAT	TGTGATGATGCGGAAAGGAGAAATA
AMPL4346991	Pf3D7_03_v3_993530	Pool=1	AAGTTAAGAGAAAAGTTAGGTCTGA	GACGTAAATGATGTTGAAGCATGGA
AMPL4347198	Pf3D7_04_v3_184289	Pool=2	CAACAATATGTTCTCATCACCCCTA	CGGAAAGTATTCATGTTAGCACTCC
AMPL4380307	Pf3D7_04_v3_249888	Pool=1	TGTGTAGCATACATTTCTTCTTGGT	TGATCGATCCAAATTAATTATGTTT
AMPL4347430	pfdhfr_1	Pool=1	ATTCATTCACATATGTTGTAACTGC	AAGTTAAAATGAACTAGCTATTTGG
AMPL4346993	pfdhfr_2	Pool=2	AAGTAAAACTATTAGATCTTCAACT	CCTTTATTTCCTAGACCTCTAAATG
AMPL4347297	pfdhfr_3	Pool=1	GCTAACAGAAATAATTTGATACTCA	GTTCTTCCCATAACTACAACATTTT
AMPL4346939	pfdhfr_4	Pool=2	CTTCATCATCATCATCATTTTCATA	TTCTTGATAAACAACGGAACCTCCT
AMPL4346827	pfdhfr_5	Pool=1	CGAATTTACTTAAAACACCTACTCC	TGTATCTTTGTCATCATTCTTTAAA
AMPL4346921	pfdhfr_6	Pool=2	ATATTCAGCACCGAAATGTCTCCAT	TGGTATTCAGGATGATATTTATATT
AMPL4346898	pfdhfr_7	Pool=1	ACTTGTGCAATCATATGAGTAAAAA	AATAGGTCCTAAATCGTTAACTTCT
AMPL4347238	pfdhfr_8	Pool=2	CGTTCAGGTAATTTTGTCATCATTT	CCTAGCCCTAAATCACATGATCTTT
AMPL4380247	Pf3D7_04_v3_881569	Pool=2	AAATATTATATGCAACACCCACCAT	TGCTGTTTCCATAATAATGTACCTT
AMPL4347152	Pf3D7_04_v3_999012	Pool=1	GATAAGGATAAGATACTCCCACGTT	ATCTCCATAACTTTTCAAATTTTTC

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AMPL4346908	Pf3D7_05_v3_95628	Pool=2	GGTTGTAATAAAGTTCATAATGGAA	AATGGTGGGAAAGGAATACATAATT
AMPL4390064	Pf3D7_05_v3_578468	Pool=1	ATCAAAGAAATTACCATGGCAAGCG	AGATGGACAAGAAAATAACTTGGAT
AMPL4347481	mdt_CNV_1	Pool=1	ATGGCAACATTGCGATTTGAATAGT	CCTTTTCTAATAAGGTTGATGTTAC
AMPL4347141	mdt_CNV_2	Pool=2	TGTTTATATTTTTAACATGTCTGCC	AGAGGGAATTTATCAAATGAGCTTT
AMPL4347004	mdt_CNV_3	Pool=1	GATTCGCACACCATGATCTGAAAAG	AAATGGATCCCGTAAATTGTAAAAG
AMPL4346932	mdt_CNV_4	Pool=2	TCCTCTTGATCCTACAAAGTTTACC	GAAGCATTATACACATCCAGAAGGA
AMPL4347425	mdt_CNV_5	Pool=1	TGCATAAGTCATTAGATATGATGTG	AGAAACTACCGAATATAATACCCAT
AMPL4347316	mdt_CNV_6	Pool=2	AATAATCGAACCCAATTCTGATTCT	TATCTACAACCACAGGAGCAAAAGC
AMPL4347044	mdt_CNV_7	Pool=1	AACAACAAAACAAATAAAGGCACAT	CCACTCGTTTTGTCATTTGGCTAGT
AMPL4346877	mdt_CNV_8	Pool=2	AATCATATTGCATTGTATAGGTCAA	AGGAGCCTAAAACGAAGCATACATA
AMPL4346938	pfmdr1_1	Pool=1	GTAATGTTCCTCCTGATAATACAGC	GCTCTTTACCCATCTTTCAACACAA
AMPL4347391	pfmdr1_2	Pool=2	TCGTACCAATTCCTGAACTCACTTG	GTTGTGCAGGTAAACATTTAAACGG
AMPL4346871	pfmdr1_3	Pool=1	TCTTTTCTCCACAATAACTTGCAAC	AGGATTATTATCATGAAATTGTCCA
AMPL4347413	pfmdr1_4	Pool=2	ATTCGTTGCACTATTTATAATAATT	TTACATATGACACCACAAACATAAA
AMPL4346960	pfmdr1_5	Pool=1	CCACAAATGCATATGTTTTCCCTTC	CCATACCAAAAACCGAATGCATAAG
AMPL4347468	pfmdr1_6	Pool=2	TCTCCTTCGGTTGGATCATAAAGTC	ATGGATATAACTGAGGCACCATTAA
AMPL4347135	pfmdr1_7	Pool=1	TTGGACACATCAACAACATCAGAAT	TAGTATGGTTGATTTCCCACAACCT
AMPL4347251	pfmdr1_8	Pool=2	TCTTGCAATGGATATTCTTTGTTTT	ACAACTCCAATTTTTGATCTCCACC
AMPL4347456	pfmdr1_9	Pool=1	TTGTTCAATAATATAGCTACCCTCA	GGATGCATTGGAACCTACTAAGGTA
AMPL4347282	pfmdr1_10	Pool=2	TTATCTGCATCATTACCTGTATCTG	ATTGGCATATCTTATAGTACTTAAT
AMPL4346950	pfmdr1_11	Pool=1	AGCAAATACGGGATATAATCCTCCA	GCTACTTTTGTTATCCGATCCATTA
AMPL4346783	pfmdr1_12	Pool=2	TTTCATAGTCTTTTCGACTTTTTCT	AAATGATACGTAAATTGTTTGGTGC
AMPL4347154	pfmdr1_13	Pool=1	TAGCTCTTACAGCAAATACACGCAT	AATAGTTTTTGAGTGTTTCTGAAAT
AMPL4347172	pfmdr1_14	Pool=2	TAAGAAGGATCCAAACCAATAGGCA	GTTAATACAGCTGCAACAATTGGAC
AMPL4347248	pfmdr1_15	Pool=1	ATTCCACCATCATCTCTTACATCAA	CCATAAAGCTGCATTTACAATAATT
AMPL4346907	pfmdr1_16	Pool=2	CATAAAAGTTGATTTTCCACTACCT	AATTTTGCATTTTCTGAATCTCCTT
AMPL4347424	pfmdr1_17	Pool=1	TGCATCTTCTCTTCCAAATTTGATA	TTTCTCCAACGATTGCTGTAGTTTT
AMPL4347507	pfmdr1_18	Pool=2	CTCTGTTTTTGTCCACCTGATAAGC	GCAGATCCAGATTGGTTTGAAAATT
AMPL4347164	pfmdr1_19	Pool=1	CTGATAATAATTCATCGTGTGTTCC	TCTATAGCAGCAAACTTACTAACAC
AMPL4347246	pfmdr1_20	Pool=2	AACGGACAAGAGTTGATACTGTTCA	TGGAATCAAGTGATGATGTTGCTTC
AMPL4380297	Pf3D7_05_v3_1274281	Pool=2	ATGACAGTGTATATAACACAGACAA	ATGACGATCCAACAAATAAAGATCA
AMPL4347543	Pf3D7_06_v3_116977	Pool=1	ATAAGAATATTTACAGAGTATTTTC	TATTTGAAACATCTTTAAATTGGTT
AMPL4347088	Pf3D7_06_v3_302456	Pool=2	AAACGGATAGAATTCCTACCCCTGA	ATGTTAAAGCCATTAAATTCATTAC
AMPL4347339	Pf3D7_06_v3_825207	Pool=1	ATATGCATTTATTCACCTGGGCTCT	TAGTACACATTTCACAGATGGGCGT
AMPL4347513	pfcrt_1	Pool=1	CATTTTTGGATACTTACTTCCTTCT	TGACTGCGTGTATTTATTATTAACG
AMPL4347446	pfcrt_2	Pool=2	TTAAACACATGAGCACATTTACCAA	CGCTCGTCATTTTTGCTTGAATTTT
AMPL4346896	pfcrt_3	Pool=1	TAATGTTTTATATTGGTAGGTGGAA	TCTGTTAAGGTCGACAAGGGAAAAA
AMPL4347155	pfcrt_4	Pool=2	CTTAATTGAAGAACAAATGATTGGA	TCTTACTTTTGAATTTCCCTTTTTA
AMPL4347426	pfcrt_5	Pool=2	CAAGAAGTGAACAATTGGAAAAAGG	TCATGTTTGAAAAGCATACAGGCTA
AMPL4347277	pfcrt_6	Pool=1	CTTCCCAAGAATAAACATGCGAAAC	GGAAAAAGGATACCATAGCCTATAA
AMPL4347596	pfcrt_7	Pool=2	AGACCACAATTCTGAAGAGGAAACA	GGAAGGGTGTATACAGGTAATATAA
AMPL4347438	pfcrt_8	Pool=1	TATAAGCTTCTTACCCATGCTCCGT	CCTCTACGACTGTGTTTCTTCCCAA
AMPL4346979	pfcrt_9	Pool=2	TGTATCAACGTTTTTCATCCTTTTT	AACTTAGCCATACCAAGACCACAAT
AMPL4347420	pfcrt_10	Pool=1	ACATTCCCATATTTATTTCCTCTTG	AAGAAGGAAAACAATGCGAAGGTTT
AMPL4346961	pfcrt_11	Pool=2	GCTAAGAATTTAAAGTAATAAGCAA	ACATTCCCATATTTATTTCCTCTTG
AMPL4347233	pfcrt_12	Pool=1	CACACTTACCAAAGTTACGAAATCT	TGTCATGGTAGAAAATTTGTCGATA

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AMPL4346964	pfcrt_13	Pool=2	ATTTATGAACGAACAAGCCATTTGA	GATACGTTGTACCATCATAAACATT
AMPL4347264	pfcrt_14	Pool=1	CCTACACGGTAAATTATAGAACCAA	GAACAAGCCATTTGATATTACACAC
AMPL4347488	pfcrt_15	Pool=2	AATTGAATCGACGTTGGTTAATTCT	ATTATAGAACCAAATAGGTAGCCAA
AMPL4347472	Pf3D7_07_v3_451640	Pool=1	GATGGTTAGTGTAACGGATAAAGAC	AATCTTATGTTGATGAACAAGAATC
AMPL4346777	Pf3D7_07_v3_635254	Pool=2	AATGACTCTTATGCTATGCAAGATG	ACTCAACAAATGTTAAGGGTGTGAA
AMPL4347390	Pf3D7_07_v3_990172	Pool=1	CTTCTCACCACCACATGTATGTTCG	ATGAAAAGTAAGTTTTGTTTGATCT
AMPL4380294	Pf3D7_08_v3_393098	Pool=2	TTCCTGTTACTTATACGTTCATCCC	ACATGATACGATTAATTCGCTCAAG
AMPL4347375	pfdhps_1	Pool=1	CTAAATATTTTTCGACAAGGTGCAG	ACTAATTTAAAAAGTTTGGCGCAAA
AMPL4347156	pfdhps_2	Pool=2	CTTTCCTTTTTATCTAATACAATGT	ACAGCGTTTCTTCTATCATTTGTTC
AMPL4347037	pfdhps_3	Pool=1	TTTCCATTTTTCAAAAATGTTTCAT	TCATACAAGTAGGACGTATTAATAA
AMPL4346791	pfdhps_4	Pool=2	TTTCTTTCTCTTTTACATTTTCCCT	AGATTCTTCTAAATTTTGCATCAAT
AMPL4347601	pfdhps_5	Pool=1	TACTTTAGACATATTGTCATTTCCA	AACTACAACTGTCAAATTATAAAAG
AMPL4347216	pfdhps_6	Pool=2	TATTCGGGTATCATATCATTTAAGC	TCCATATTTACTTTAGACATATTGT
AMPL4347466	pfdhps_7	Pool=1	ACCTATATCTATAACACTAGCACCT	TTGTATACACATGAGGAATGGATAA
AMPL4346953	pfdhps_8	Pool=2	CTCTTTTATGCATTAGAACTACACT	CTTTGAACAGCACGTTTAGGTTCAA
AMPL4347169	pfdhps_9	Pool=1	AACATTTTGATCATTCATGCAATGG	TCTGGATTATTTGTACAAGCACTAA
AMPL4346837	pfdhps_10	Pool=2	AGTTGATCCTTGTCTTTCCTCATGT	TCAAATAGTATCCTATAACGAGGTA
AMPL4347144	pfdhps_11	Pool=1	GTTTAATCACATGTTTGCACTTTCC	ACATCCAATTGTGTGATTTGTCCAC
AMPL4380251	KIC7_1	Pool=1	CTGATTTTGCCCCTGTAAACGTTTC	TGCCTTATGTATGATATCATGTGTG
AMPL4380218	KIC7_2	Pool=2	AAATCATAATCAAAATCCATTGAAC	TCCACACCTAACAACCGAAAATCAT
AMPL4380224	KIC7_3	Pool=1	ATGAGTATGGTACCATATGACCCTT	CCTAAATCATAATCAAAATCCATTG
AMPL4380212	KIC7_4	Pool=2	TGAGCGAACATAATTATCATGATTT	GCTATGGATAATGCAAATTATTATA
AMPL4380243	KIC7_5	Pool=1	GATTCAGATGATGATTTTGATGACG	ATGAACTCACCAAGTAGTGATCTAG
AMPL4390050	KIC7_6	Pool=2	AATCGACGCTCATCAACTAGAAAAC	GATCCAAATACTCCTGGTATGATTG
AMPL4390057	KIC7_7	Pool=1	CTTTAGCTGTGGAGAAATTGTTTTT	AAGTAGTAACAGATAGTTCTGATTC
AMPL4390051	KIC7_8	Pool=2	TGCTTTAAAATTAATGTTTTGTTCT	AGAAGATTCGATAAGTTATTATGAT
AMPL4346844	Pf3D7_08_v3_702128	Pool=2	AATATTCAATACACGCCTTGACATC	TCTTTATTCCATGATCCTTGTTGAT
AMPL4347188	Pf3D7_08_v3_845342	Pool=1	TCTAAGGGAGGAACTCATCCAAACA	CAAAAGGCAGTAGAAAGAAATCCAA
AMPL4346885	Pf3D7_08_v3_1233717	Pool=2	CGCTATTCCATTCAAGGCAATATGT	TCATCTGTCGATATATCGCTCGTAT
AMPL4347184	pfhrp2_1	Pool=1	CTCATCATGCAGCCGATGCTCATCA	ACATTGCCTACGCCATTAAATTTAT
AMPL4347504	pfhrp2_2	Pool=2	ACTTGTGTAGCAAAAATGCAAAAGG	CGATGCCCATCATGCTCACCATGCA
AMPL4346914	pfhrp2_3	Pool=1	AATAAAGTATTATCCGCTGCCGTTT	TAGCCGATGCCCATCATGCTCATCA
AMPL4347028	pfhrp2_4	Pool=2	CTTCATGTATTTATGTATGCAGAAC	AGATAACGTAAGCATTTTAATTGCA
AMPL4390053	Pf3D7_09_v3_291373	Pool=1	CTTTTTGTTGAAAATTTGGATGGCT	TGAAGGTTGGATGGTGAATATCTAC
AMPL4346830	Pf3D7_09_v3_1110640	Pool=2	CCGTTCATGTTATTCACATCATTCA	CGAATTATTAGGATGAGCACCCATA
AMPL4347340	Pf3D7_09_v3_1137809	Pool=1	ATAAAAATGTAACCTCCAAGGTAGC	CGAACAAGAGGAAGAGGAATATGAA
AMPL4347182	Pf3D7_10_v3_157280	Pool=2	CATAAACTCTCAGCTGATCATATGT	ATTACTAAAGATGAATGCTCAAAGG
AMPL4380232	Pf3D7_10_v3_218859	Pool=1	AAAACATTTCGAGGGTTAATCGAGA	ATTGGCGCTATTCGTAAAAAGAGAC
AMPL4347576	Pf3D7_10_v3_377197	Pool=2	CCTCTAGTTCATCTACTTTAAATTC	GCGAAATGTGTCTTGATCTATGTCT
AMPL4380226	atg18_T281I	Pool=1	CCAGGATTATGGTTGTTTGTGTATG	GGGAAATAGCGAAACTAACATTTTC
AMPL4380282	Pf3D7_10_v3_768820	Pool=2	TTCATCAAGTATGAAAAGGGAAACG	AATTCTGAGTATCACATAACGATGA
AMPL4347539	EPS15_Formin2_1	Pool=1	AAAAGGGCATACCAAATAATCACGT	CGATCTTGAATCAGTAAAAGATGAG
AMPL4347134	EPS15_Formin2_2	Pool=2	AACATATTCTTCTTTTCAACTCATT	AGGGCATACCAAATAATCACGTAAT
AMPL4347307	EPS15_Formin2_3	Pool=1	AAAACAAAGAGCTCTCAAATTACAA	ACAAAATAATGAGAACAAAATTGTG
AMPL4347080	EPS15_Formin2_4	Pool=2	ATTATGATGAGTGTGAAGCGTCACC	GATTTCCATTTGAACGATAAGAAAG
AMPL4347439	EPS15_Formin2_5	Pool=1	TGGATACGATAAATTTCGTCAAGGA	ATAAAAAGAAGATGCACGGTAAGGG

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AMPL4346855	EPS15_Formin2_6	Pool=2	GGTAAAAAGGAATCCATTCATTTTG	TGGATAAGGATTTAAATTCAACAAA
AMPL4346899	EPS15_Formin2_7	Pool=1	AACTTTTCGACAGAATGCTGATGAG	CCAACTTTGAAGGGTATGACCAAAT
AMPL4346873	EPS15_Formin2_8	Pool=2	TACCCATGGAGTTGTTACAATCTGT	GTCCCTGGGGGATATTTTAAAATCA
AMPL4347445	EPS15_Formin2_9	Pool=1	ATATGGAAGGAAGTTTAAAATGGAA	TCCCTTCGGAAGGTAACAAAAATGT
AMPL4347176	EPS15_Formin2_10	Pool=2	TTATTTTAGAACCCGCTTGTTTACC	CGGTATGTGAGTTAATGCAAATATG
AMPL4346989	EPS15_Formin2_11	Pool=1	CGGGTCTGTCAATATCTGTGTTACA	AGAAATGATTTCCATTCGTAAGTTG
AMPL4347064	EPS15_Formin2_12	Pool=2	GCCTCTTCCTTTCTTCAGAATTCGG	TCAGAATGGTAACGTCATAAGTACA
AMPL4346954	EPS15_Formin2_13	Pool=1	CATGGGAACAATGAATAAAGCTTTT	TCCTTTCTTCAGAATTCGGGTCTGT
AMPL4346774	EPS15_Formin2_14	Pool=2	TATGTAGATCTAGAACATTTCTGTT	GAAAGGATCGTATTACCTTCAGAGG
AMPL4347259	Pf3D7_11_v3_787953	Pool=1	AAGTAACGAACAGGAGATAAATGGG	AAGAGGTAAATCCTTCAAATGTGAG
AMPL4347022	pfama1_D1_1	Pool=1	TCGACCCATAATCCGAATTTTGCAT	TTCCTGCATGTCTTGAACATAAAGT
AMPL4346761	pfama1_D1_2	Pool=2	CATATTGTTTAGGTTGATCCGAAGC	TCTAGGACCATTATTTTCTTGAGCT
AMPL4347478	pfama1_D2_1	Pool=1	GGGACAAAGCAGTAGTAGCAATGTA	GGTATATCTTCACAATTTCCATCGA
AMPL4347587	pfama1_D2_2	Pool=2	ATTATTTGATGTTACTTCTGCCCTT	AAACATGTTGGTTTGACATTAAAAA
AMPL4346949	pfama1_D2_3	Pool=1	AAATAGTTGCTAATACAGCGACAGC	TTAATTCGTTTTGATTCTCTTTCGA
AMPL4347326	pfama1_D2_4	Pool=2	GTATGGTTTTTCCATCAGAACTGGT	AGTTGGTTTATGTTCAGGAATATCT
AMPL4380270	Pf3D7_11_v3_1376357	Pool=2	TCTTAGCCTTTTCGATATTAGCGAT	ATTTTTCTATGGCTCAATTTGCAGC
AMPL4347270	Pf3D7_11_v3_1816380	Pool=1	GCATGAATGTGAAAATGATAAACGC	TCCAATAGACGACACATCATTGTTA
AMPL4380256	Pf3D7_12_v3_217436	Pool=2	ATAGTAGCAGTCCTTTCTTTGTTGT	CAAAAGATATCACGTAAGCTGAAAA
AMPL4346967	pfap2-mu_1	Pool=1	TTTGAATTGCTTCTTGTTAATACGG	AACAAATGACGCTAATCGTGTTAAC
AMPL4347151	pfap2-mu_2	Pool=1	AAATGTACCATCTGGTGGTGTGAAG	AAGGTTACCTTTCCATTTATATGAG
AMPL4346824	pfap2-mu_3	Pool=2	TGCCTATGGATTTATATTTAACTTG	TTTTCATATTTGGATAAGGTAACAC
AMPL4347276	pfap2-mu_4	Pool=1	TTATATACATGCCGCTTGAGGTAAA	ACTTGAACATTTTCTGAGAATTTAT
AMPL4346808	pfap2-mu_5	Pool=2	ACTTATTTGTTGTTCCTTGTTTGAA	GCTCAATGTTATGGGCATTTTATAT
AMPL4347115	Pf3D7_12_v3_741810	Pool=2	CACATATCCTTAGGGTCCCCCGTTA	AAATTGACGACATTTGTAGTAACAA
AMPL4347422	Pf3D7_12_v3_852775	Pool=1	TATGAAGTAATACATGTGCACGTCT	ATCTTTTCAATTTATAGTATTTACT
AMPL4347194	tetQ_CNV_1	Pool=1	CTGTAGCTAAATATGCATGTAATCA	CATGCTAACTTTCTTATGACTTTTT
AMPL4347202	tetQ_CNV_2	Pool=2	TATTTGAAAACAGTGTTACTGTCCA	TTTAATACAAACAGACGAAGCATAT
AMPL4347370	tetQ_CNV_3	Pool=1	ATAAAGGATCATCCTCATAAGCAAA	CTTAAAAATATTTGATAGTTCAACT
AMPL4347583	tetQ_CNV_4	Pool=2	AACCTGGATAAAGATAACAATTTGT	CCTGAACTACTTTGTGATAATGATG
AMPL4347475	tetQ_CNV_5	Pool=2	GATATCAAAACGAGTCCAGTTGAAA	CCACTTTTTATCATCAGAAGAAGGA
AMPL4347060	tetQ_CNV_6	Pool=1	ATGAAATACCAAATAAGCAATGGTT	TCCAGTTGAAATTATTCAGAAGGAA
AMPL4347407	tetQ_CNV_7	Pool=2	AGAAGGACGATGAAAAACCATCCCA	CATGTGCTATCGAACCAAAGGAATA
AMPL4346784	tetQ_CNV_8	Pool=1	ACGACAAATGTGCTAGATACTAACG	GCTCTTCATGAAGGAACATATTCAC
AMPL4347043	tetQ_CNV_9	Pool=2	ATATGATATAACGTACAACCATAAC	TTCTATGTGATATAATTTGTGAGAA
AMPL4346965	tetQ_CNV_10	Pool=1	AAAGACAGATGAACCATAATAAACA	GGAAACTAAGCAAAAACACCAAATT
AMPL4347530	tetQ_CNV_11	Pool=2	TATGGTGTACATATATTGTTAGATT	GGCAACAATTCAGACATGTATCATC
AMPL4346769	tetQ_CNV_12	Pool=1	TGCTATGATAAATCCTAAACCAGAT	ACATAATGAGAAGGGGATGGAGAAG
AMPL4346806	tetQ_CNV_13	Pool=2	ATTAATTATGGTCAAACCTTTATGT	GGAAGTGCTCTGCATTCGTATGGTG
AMPL4347042	tetQ_CNV_14	Pool=1	CCTGGACATATAGATTTTAGTAATG	CCCTTCTATGGTTTTATATTCTTAT
AMPL4347508	tetQ_CNV_15	Pool=2	GGGATTTTGGCACATATTGATGCAG	CTCTAAAGAAGGTGTACAAATTCAA
AMPL4347479	tetQ_CNV_16	Pool=1	TAATTTTTACACCCATGAGATAATG	TAAAAGTGCTTATTCATGTTTTGAA
AMPL4380269	Pf3D7_12_v3_1612066	Pool=2	GTTCTATGTATTCTCCTTGTGCTAA	CCAACCTTCTGATATGGGAGATGAA
AMPL4346929	pfcoronin_1	Pool=1	CAGCACTACAAGCTATACCACATGT	TCTTGATTAAAGGAACATTATACAT
AMPL4347343	pfcoronin_2	Pool=2	GGGTTAAATGACAAATCAAGGATGG	TTCGGTTGCTCTCGAGCAAATCCTC
AMPL4347249	pfcoronin_3	Pool=1	ACCACCGATATCCCATTGTAAAGAA	TACAGGGGGATTTCTCACTTGATTT

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AMPL4347055	pfcoronin_4	Pool=2	TACCTACGCTCTCATCATAATGTGG	AGGCTTTCTTCTCATTTTCTATATC
AMPL4346998	pfcoronin_5	Pool=1	AATTTCACATTTGTATACGTCACAC	ACCACCAAATCCATCAATCCATATA
AMPL4347594	pfcoronin_6	Pool=2	TCTTCGGTTAAATCCTTTATAGACA	CGACAATTACCATCACCTTTACCTA
AMPL4347224	pfcoronin_7	Pool=1	AACGTCCTCACAAGCAAATAAAAAT	GTTTGTACTACGTTCAGGATCTCTC
AMPL4347441	pfcoronin_8	Pool=2	CAGTTTCTTCGTATGGCTCATTTGT	ATCAGCTTCAATCGAAGATTTGGTT
AMPL4347166	pfcoronin_9	Pool=1	TCCCCCCTTTTCATAATACCGTTGC	GTTGTCTTTCAAATGACATATTTCA
AMPL4380286	Pf3D7_13_v3_173108	Pool=2	ACCATGAACGAAATCGACATGGTCC	GTGAAAATGCAAATATAAATGGTGG
AMPL4390055	Pf3D7_13_v3_736261	Pool=1	GAGGAAGAGGAGCAATCACTACAAT	GTTTATAACTATAGAATTCCCTCCT
AMPL4380304	Pf3D7_13_v3_1005251	Pool=2	TAGAACAAAAGAAATCAAACGAAGA	GGAAAAAGATACAAATATAACATAC
AMPL4347501	Pf3D7_13_v3_1603150	Pool=1	TGAGGAGGGATAAGACAAGTGAAAA	AGAACAAAGGGGGAATATGAGCTTT
AMPL4347215	KEL1_lineage1	Pool=2	AATGCGTCATGTAAAGAAGACAATT	AAAATCCTTAGATAAGACACCATCA
AMPL4347310	KEL1_lineage2	Pool=1	GATTGAATCGAATTTTTATTCTTAA	ACTACAGAATATCCAGATAATTCTT
AMPL4347016	KEL1_lineage5 + RAD5	Pool=2	TTAAATGGAAATAATCGTCTGCACA	CACTTTTAAATACCTTCTTCACGTC
AMPL4347356	pfk13_1	Pool=1	TACAGGAGGAGAAAATGGCGAAGTT	ACACATTACTTGATTGTTTATGATT
AMPL4347429	pfk13_2	Pool=2	GTCATTGGTGGAACTAATGGTGAGA	CAGATACAAATGAATGGCAGCTTGG
AMPL4347025	pfk13_3	Pool=1	AACTGAGGTGTATGATCGTTTAAGA	AGTTCAGGAGCAGCTTTTAATTACC
AMPL4347303	pfk13_4	Pool=2	GCCTTGTTGAAAGAAGCAGAATTTT	TTGGGGGATATGATGGCTCTTCTAT
AMPL4347362	pfk13_5	Pool=1	TTGGTGGAGCTATTTTTGAAACATC	GCGTATGTGTACACCTATGTCTACC
AMPL4346926	pfk13_6	Pool=2	ACAGAAATTACATGATGAAAGAAAG	GTGGAAGACATCATGTAACCAGAGA
AMPL4346793	pfk13_7	Pool=1	GAATTAAGTGATGCTAGTGATTTTG	AGGAAACGATTTGATGAAGAAAGAT
AMPL4347485	pfk13_8	Pool=2	TCTCCATCAATTATGAATACCAACA	AGACACAAATGAATTTTATTCGAGA
AMPL4346839	pfk13_9	Pool=1	AAGGAGAAAAAGTAAAAACAAAAGC	TGAGTGTATTAGATTCGAACTTTGA
AMPL4347503	KEL1_lineage3	Pool=2	TGAAGAACATGCACCTTACAGAAAT	ATTGGCTAGTTGCTGAAAATTCATT
AMPL4347447	KEL1_lineage4	Pool=1	TGTAATTCACTTAAAGATGTATTGG	GCAAATCGGATCCACAAAACAATTC
AMPL4346829	pfhrp3_1	Pool=1	CACGGATTTCATTTTAACCTTCACG	ACACCATTAAATCCATTTAATCGAA
AMPL4347562	pfhrp3_2	Pool=2	ACCATGCAGCTAATGCTCATCATGC	GTTTTGATGATTCTCACCATGACGA
AMPL4347049	pfhrp3_3	Pool=1	AAGGACTTAATTCAAATAAGAGATT	ACCATGCAGCTAATGCTCACCATGC
AMPL4346893	pfhrp3_4	Pool=2	TAAAATATTATCCGCTGCCGTTTTT	GATGCCCATCATGCACATCATGTAG
AMPL4347482	Pf3D7_14_v3_83126	Pool=2	TAATTGGTGCTAAAACTTAAATTGT	AGTTCTTTGTTAAAACTATAAGACA
AMPL4347101	plasmepsin2_CNV_1	Pool=1	CATGTGCATTTTCAACTTTAAATCC	TCTCTTACTGTAATATCCATTTGGT
AMPL4346848	plasmepsin2_CNV_2	Pool=2	TGGGACCCATAAATTAGCAGATCCT	ACCACACATTACACTACAAAAGAGA
AMPL4347192	plasmepsin2_CNV_3	Pool=1	TGTTGAAGCAGTATAAGTTGGTTCG	CCAACTTCTGCATCACCATAAAACA
AMPL4346849	plasmepsin2_CNV_4	Pool=2	GGTTTAATTTTTCGTAAGTTAGTGG	CCACTAACAGTTCCTGACACATAAT
AMPL4347570	plasmepsin2_CNV_5	Pool=1	AGCATACATAATCCTGGACCAACAT	CACCAATGGTTAAGAATCCTGTATG
AMPL4347380	plasmepsin2_CNV_6	Pool=2	TTTTCCTTTGGTTTCCAAATTTTCG	TTGGTAATTTGCTGTTGTTACAAAG
AMPL4347353	mdr2	Pool=1	GTATTCTAGTAAAAATTCGGGTGGT	AAAAATTAGAACAAAAGCAAATGAG
AMPL4347140	arps10	Pool=2	TTTACAACTGGAAGGTGAAAAACAT	ACCTCTTTCTTATTGTCTTTTGGGG
AMPL4380306	Pf3D7_14_v3_3002068	Pool=1	TTAGTGCTGTTGTAGGTATTGTTGT	GCTTATATGCATAAATGTAAGGCAA

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APPENDIX 4. PV Ampliseq Peru Custom DNA panel oligo sequences for design IAAQ212588_242

Amplicon_ID	Amplicon_name	POOL	ULSO Sequence	DLSO Sequence
AMPL4340273	pvcrt_o_1	Pool=1	ATGGGGACGTCCTCTTGTATTTCGC	TAACGTGATGCAGATAACGTGACGC
AMPL4340265	pvcrt_o_2	Pool=2	GGCGACCAAACATAAAGTACAAGGC	CCTCACGTAAAGGGTAAAACACCCC
AMPL4340289	pvcrt_o_3	Pool=1	ATTGAACTCCGAAGTTTCGGTGTCT	GTTCCCAATCTTCTTCAGAGTCCTC
AMPL4340245	pvcrt_o_4	Pool=2	CCTGTATCGCAAAATCAAAAAGCAG	ATAGAAGGAGGTACTCCCGATGGAT
AMPL4340269	pvcrt_o_5	Pool=1	CCAAATCCTACAATCAGCGAGGCAA	TATCGGAATGCTCAGCTGCATGACG
AMPL4340285	pvcrt_o_6	Pool=2	CAGGCGCAGGATGTTTATTTTGTAC	CGTAATTGAACAGGTGGTATCTGCG
AMPL4340253	pvcrt_o_7	Pool=1	AAAGTTGGTGACCCATGTAGCTAAG	CGATTTCTCTGGTCATGTTGGAGAA
AMPL4340303	pvcrt_o_8	Pool=2	GCCTTACCCATGCTCCTTCGCAATC	GACATGGAGATTTGGGAAAGCACAA
AMPL4340302	pvcrt_o_9	Pool=1	AATGTTGGGGAAGCGTCTGCAGGGT	GAAGCAAAGCAGCCGTGGGGGGAGG
AMPL4340275	pvcrt_o_10	Pool=2	GGTGTAGGTCATGGTTGAGAATTTC	CATTCAGTTAAAGCAGCTGCGGTTT
AMPL4340283	pvcrt_o_11	Pool=1	CATATTTGGCTCCCCCTTACCAAAG	ACAGGTAGTCCTCAAAAGACACACA
AMPL4340282	pvcrt_o_12	Pool=2	CTTACTCTCAAGAATTATGTTTCCT	CCCTACCGCAAGGAACTTAAAGTAG
AMPL4340263	pvcrt_o_13	Pool=1	CACTCATCCAGAGAGCAAATCTTCT	GATCCGAAGAGGTAGCCAAACTGAC
AMPL4591735	PvP01_01_v1_491892	Pool=2	GGCAAAGGAGACCTCCCAGAATATG	CCCTTCTGATGCAAACCTCTTTTTT
AMPL4591767	PvP01_01_v1_642154	Pool=1	CACGGGTGTCTTTCAAGACGACCAT	GTGCAGACGATTTAGCTGTTTGCAT
AMPL4591768	PvP01_01_v1_856459	Pool=2	CTCACACTATCAGCTTCAGCTGTGT	AGGATGTACAAATACGGGATGGCTA
AMPL4339900	pvmrp1_1	Pool=1	GTACTTGTCTATAGTTCGTCTTTTC	TGTGCCTGTATATACCACGTTCGAC
AMPL4339546	pvmrp1_2	Pool=2	GACATTATCACCGTTTTGCCGCAGT	AATAGTGTGGACTCGAATTTGAATA
AMPL4339695	pvmrp1_3	Pool=1	CGGTATTGTAGACCCACCAGCCATA	TCACAACTGGAACGTCAGAACGTTT
AMPL4339793	pvmrp1_4	Pool=2	TTTCAACAAAATGGGAAACCTGTAC	TGTTTATCTCGAGAACGTATTCGTC
AMPL4339697	pvmrp1_5	Pool=1	AAATTTTCCAGAGGGTGTAAAGAGG	ATTACTTTTTCCTCAAGACTTGGGG
AMPL4339789	pvmrp1_6	Pool=2	TATATGGCACGGTAATTTCAGCAGT	AACATATATAGCAACACCATATCGG
AMPL4339520	pvmrp1_7	Pool=1	CGCAAATGTTTCTCCTGCTAAGGAT	CAGATGTGCTGAAGAGCATTTTGAG
AMPL4340029	pvmrp1_8	Pool=2	CCCGAGAAATGTGGAAGCCAAATAA	AGTTGGAGGCGTTTTAATACTGTAC
AMPL4339526	pvmrp1_9	Pool=1	AGTTTTGTTGTGTCTATGAATGAAA	GCGTAAACCCTTTTTGGAAAATGAC
AMPL4339871	pvmrp1_10	Pool=2	TGCATAAATTGAGCTCTAACGGTGA	CCTTTTTGAGAATATCCAGTACAAA
AMPL4339679	pvmrp1_11	Pool=1	GGAGACATTCAGTTGATCCACGGTT	GTTTTGCCAACAAAAATAGTCGAAC
AMPL4339885	pvmrp1_12	Pool=2	AGTGTGTTTCCAGACAAGAGTTGAC	AGAACAGTTGGTTGTCCATAGGAAA
AMPL4339557	pvmrp1_13	Pool=1	GAAGGCACAGTGAATATTGCGCGTA	GCAGTAGTAGTAGCATACACGAGAA
AMPL4339904	pvmrp1_14	Pool=2	TGCTGTTTTGCAAAGTGCGACTTTA	GGAGAATGTTTCGAAAAAGAAGGAG
AMPL4339606	pvmrp1_15	Pool=1	TTTACTTGAGGATGGGTTCTAATGC	CTCAGCTGACATAGTTGAAGTGTTG
AMPL4340142	pvmrp1_16	Pool=2	AAGAATCTTTGAATACGCCATTAGG	GAGCATCACTGTCTGTTGTATTGTA
AMPL4339985	pvmrp1_17	Pool=1	TGCTGTTGGAGGATCTATAGACAAA	TGGAAAGAAAAAGCTGTAACAGTGT
AMPL4339639	pvmrp1_18	Pool=2	TGTGACACATTATGCATCTGAATTG	TTTGGATTGTACATCGTTGGTTTAT
AMPL4340041	pvmrp1_19	Pool=1	AAATTAACCTTACACAAACATTTAT	TCAAAAGACATAAAGGCAAAGAAGG
AMPL4591773	PvP01_02_v1_446232	Pool=2	CGTTGCATATTGATGTAGAGAGCTG	GGGAAGTGGTAGGACGCAAAAAAAA
AMPL4591753	PvP01_02_v1_560561	Pool=1	TGATTACGCATTTGTTTGTTTTGTG	TTCTAGTCAAAATGGGAAAGTCCCA
AMPL4591743	PvP01_03_v1_114702	Pool=2	TATGGGTTACTTTCAATTCGGAAAT	GGTCACTTCTACTACCACTGCTATA
AMPL4347647	DPAP3	Pool=1	GCAATAAACAGCTGGTCCTTTGCGA	GAAAATCCTCCACCCATGATGAACA
AMPL4339916	pvdmt2_1	Pool=1	TTAATACCTGGTTTACGAGGTCCAG	CGATCACCGGTAGGCAAATGCTCCT
AMPL4340057	pvdmt2_2	Pool=2	CCCATTAAACACACGATGTTCTGTC	AAAGATCTTCATCCATTTGCACTCA
AMPL4339751	pvdmt2_3	Pool=1	GAAAAATAATGGCGACTTTGAGTCC	GCTCACGATGATTAAAATGACTCCA
AMPL4339638	pvdmt2_4	Pool=2	ACAAATCACCTGAACAGGTCATAAA	TGAGTGATCCGCTAATCTTCATGAT
AMPL4591766	PvP01_03_v1_556656	Pool=2	CGTTCTGCACGTTCAGGTAGACTAG	CGTCTTACTGAGGAATTATTTCGTT
AMPL4591751	PvP01_04_v1_268128	Pool=1	CTGTTATAACGGTAGCTCTCTAACT	TCCTTTTCGCCACTTCACATTGATA
AMPL4591764	PvP01_04_v1_310483	Pool=2	AACTTGGCAAACTTGACAAACATGA	CCGTTTATGTATACATGTGCGTGTT
AMPL4591770	PvP01_04_v1_760567	Pool=1	CCGCCGCTTAAACCGCCGCTTGAAT	CTGCACATAAAGCGAGTTCGAAAAA
AMPL4591736	PvP01_05_v1_348599	Pool=2	TTTTTATTTGCGTTCTCATTTTGGC	CGTCTAGGGGTGTTAATTAAGTATC
AMPL4591748	PvP01_05_v1_526292	Pool=1	AAGCACGCATGTATGTACACACGTA	AACGCGAAAATGTGAAGAAAAAGGA
AMPL4347655	PVP01_0516600	Pool=2	CTTGTTCAAATTTTCATCCCCTTGG	TGTTGATCGTTTCCTCGTCAATTTT
AMPL4339583	pvdhfr_1	Pool=1	GGTACCTCTCCCTCTTCCACTTTAG	TATAGCTCCACTGGGTGTGATGGTG
AMPL4339531	pvdhfr_2	Pool=2	CCCCCAATGATGAAGCATTTGTAGT	CCTGAAGTACTTCATATCGACGGAG
AMPL4339951	pvdhfr_3	Pool=1	CCTTGCTGTTGTACACCTCACTGAC	GAAAGCACGACGTTGATTCTGTTTG

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AMPL4340056	pvdhfr_4	Pool=2	TTGTTAAAGCTGAAGTACACGAGGT	CGTTGATCCTCGTGAAGTAGATCTG
AMPL4339608	pvdhfr_5	Pool=1	CATGATGATGTCGTATATGATGCCT	CTTGCTGTAAACCAAAAAGTCCAGA
AMPL4339573	pvdhfr_6	Pool=2	GTGTATTCAGCACCGAAGTGTCTCC	GTGCTGCTTAATCTTCAGGCTGTTG
AMPL4339870	pvdhfr_7	Pool=1	AATCATGTGTGTGAATATGGAATAC	GGAATAATTTCCTGTTGTCGAGGAA
AMPL4340044	pvdhfr_8	Pool=2	CGCTAGCTAGCTATAAAAGTATTTT	CCAAGACCCAAGTCACAAGACCTCT
AMPL4347626	PvP01_05_v1_1079460_1079461	Pool=1	GGGAATTGTCTTAAAGCTCCCTCTT	GCAATAACACTTCGCTAGCTAGCTA
AMPL4347636	PVP01_0530500	Pool=2	AAATTGCCATAAAATGAACCCCACT	AATTACCCGGCAACACCAACTTCGT
AMPL4591749	PvP01_05_v1_1389200	Pool=1	CTTTTCGGTAACGTTCCTTCAATTC	GGCAATAAATGCGGTAAATTGGTAC
AMPL4591761	PvP01_06_v1_448117	Pool=2	AGCTGGTGTAGTTCGGGTAGTCCTG	CAGCACTCCTCAAATGGGACCACGA
AMPL4591772	PvP01_06_v1_590839	Pool=1	CTTTTCTGAAGATCGAAAGCACAGA	TGAGTACGTTTGGTGGAGCTGGCTT
AMPL4347653	CLAMP	Pool=2	CTCCTACTGCTTCTACATCTTTATG	GGATTAATCATAATGGGTTCCCTGG
AMPL4591737	PvP01_06_v1_828443	Pool=1	TAATTACCACACAAGCGGAAATAGA	AACAAAATGGAGCAACCAAATGGAG
AMPL4591755	PvP01_07_v1_96155	Pool=2	TCGCAAAATATATTCATAGCAACCG	CCCTATCTCTTGTACAGTTCGTTTA
AMPL4347648	SEC27	Pool=1	AACAATGGATTTTATGTGCAGGTGA	ACCTTAACAGGTCATACAAAAGGGG
AMPL4591744	PvP01_07_v1_273907	Pool=2	CGCTTGGCATGATGTAGCGGATGTG	GGAGTAAACTGTAGGCACATAATTG
AMPL4347649	PvP01_07_v1_595235_595236	Pool=1	GGATATCCATACAGCGACATATGTG	GTCAAGGTGAATCCCACCAAAGTTA
AMPL4591738	PvP01_07_v1_959564	Pool=2	CCATTTGATTGCCTCCCCCATCTTC	ACGAACTGCTGAAGTGGATGGGGGA
AMPL4591760	PvP01_07_v1_1420306	Pool=1	ACGTCCTGCTCGAAAAGGTACTTCT	ATTGGACCTTCCAAAAATGCATGCA
AMPL4591774	PvP01_08_v1_203155	Pool=2	GAGGAGAGTTGGGAAGAACATAGGG	TGGTGGCATAATGATGCAGGAACAG
AMPL4347630	PVP01_0809900	Pool=1	AAAGGAGATCAGCCTGATTGACAAC	GATGACCTCCACTTTGTGAATTGCG
AMPL4347642	PvP01_08_v1_879061_879062	Pool=2	CTCCTACACCCCTACACAAACATTC	CAGTTGGAGAGGCATATACAGACAG
AMPL4591762	PvP01_08_v1_1062973	Pool=1	ATAATGAAATTCCCCCAATGTTACG	AGAAGTAAAACGGCACACGTGGCTA
AMPL4347632	PVP01_0833200	Pool=2	CTCTTCTGTTTTTATGTTTCTCCCT	TGACTTGCCCGGAGTGAAATTCAAG
AMPL4591775	PvP01_08_v1_1584557	Pool=1	GGAAATCTTACGAGCGGCTTACCAA	ATTTTTAAACGCAATTCCAAAACGA
AMPL4591747	PvP01_09_v1_295024	Pool=2	AGCACTTCATGCGAGTGGACGAATC	CGATGCAGGCGGTCAGATATTATCG
AMPL4347645	SNF2L	Pool=1	GCGGAGAAGAGAACTATGGAAATTG	TTCCTCGATTTAGGAGAAAGAAAAA
AMPL4347646	PVP01_0908400	Pool=2	GAGAAAAAGGAAAAACTTCAATCCG	ACGAGAAAAGAAAACGAAATTGAAA
AMPL4591754	PvP01_09_v1_776023	Pool=1	TTTAGCGATTCTGGTCAGTTAACCG	GAACCGCTCAGCAAGAAGAACCTAC
AMPL4591739	PvP01_09_v1_811181	Pool=2	TCTGCGTAGTTGCTTAGTTTGAACC	TGTGCATGCAATTTGCTTCATTCAG
AMPL4347633	PVP01_0924700	Pool=1	AGCCACTCGCTGTTATCCTCCTTCG	CTGTTTGACATACGGGTTCCTCGGA
AMPL4339754	pvama1_1	Pool=1	GTTAAGAAGCTAACAGCGGAATTCT	ACTTAAGAGAAAGGCAGCGATTTGG
AMPL4339671	pvama1_2	Pool=2	CGGACCCATATTTTCCTGCGCTGAT	ATTCTGTACTTTGCATTTTCCACTT
AMPL4339631	pvama1_3	Pool=1	CGTCATTTCTTCTTCATACTGAGTT	GTCGTATACAGCTGGGTGTCTGTAG
AMPL4339839	pvama1_4	Pool=2	TGTTCCTCGATTGTTTCCTAATTTC	CGCTTCGAAAACGATTCGGTTGCAT
AMPL4340166	pvama1_5	Pool=1	CTTCTTCTTGAAGTAGGCCATAGAG	CGTCTTTATATATGCTGCAGGGGAA
AMPL4339902	pvama1_6	Pool=2	GCCAACGTGGCTTCGTGAATTCGTT	TAGCATCTGCTTGTTCGATTTTTCC
AMPL4347637	IMC1b	Pool=2	TAAAGTGATAGAAGTCCCCGAATTG	AAATGGCGACATCATAAGAAATAGC
AMPL4591741	PvP01_10_v1_183419	Pool=1	AAAAAAGACCCCTCAGAAGTGAGTC	TCAGAGTGTGGACCCGTTTTTTCGA
AMPL4339696	pvmdr1_1	Pool=2	GAGAGAGCCAAAGATTTTGTTGTTA	TATGTACGTACGTGCCTCTCCAATC
AMPL4340114	pvmdr1_2	Pool=1	GAACAGTGGAAAGATACTGCTCGAC	ATTCGGAGAAGCTCATTGAGAAGAC
AMPL4339905	pvmdr1_3	Pool=2	ACAAAGATTTGACCTTCTCCTGTGA	GTTAGCCAAGAACCCATGCTCTTTA
AMPL4339611	pvmdr1_4	Pool=1	TAACAGTTTTGCCTACTGGTTTGGT	CTATTGTTGGCGAAACGGGTAGTGG
AMPL4339779	pvmdr1_5	Pool=2	TTCATTTTTATGAGAGTGTTTGCCA	AAGAGGTACAATACAAGTGGATGAC
AMPL4340162	pvmdr1_6	Pool=1	CGATTGCCATGTTCATTTCTGAGAC	GCCAACAAGGATGTAGAGAAGAAGC
AMPL4339645	pvmdr1_7	Pool=2	AAAATGAGTGACGCCAAAGCAAGTA	GAGAGAAAGTAGAGAAGACCATGAA
AMPL4339566	pvmdr1_8	Pool=1	AGAAGAATGAGAAGCATGATAAGCA	AGGAAGGTTAGCCTTTTTGAGAAAC
AMPL4340137	pvmdr1_9	Pool=2	ACGCTGGTGGGTTCTAATGCATCTA	AAAATAGCAGCGCGAACCAAAAAAT
AMPL4339809	pvmdr1_10	Pool=1	TGTACAGCCTGAAAGATTTAGAAGC	TGATTCTCGATGAAGCCACCTCATC
AMPL4339874	pvmdr1_11	Pool=2	CAGTTTAAGAATGTGCGTTTTCACT	ACGAAGATGGTTTTTCTTCTCAAAG
AMPL4339788	pvmdr1_12	Pool=1	CACATTGGTATGATTAACGGGTTCA	AAGGATGTAGAAATTTACAAGGACC
AMPL4339936	pvmdr1_13	Pool=2	ACGCAAGTGCATTTTTGGGTCTATA	TGGTTTTTGGTACGGAACGAGAATC
AMPL4339506	pvmdr1_14	Pool=1	TGCCCTTCTTCGTATCCGTTTTTGG	TTTAAGAACGCTAGACTCACCCTCT
AMPL4339560	pvmdr1_15	Pool=2	GCCCTCCCTTACCGCCTTTTATGCC	TTTCGCTAGTCCTCATCGGAATATT
AMPL4347652	PvP01_10_v1_483567_483568	Pool=1	TATCGCATTTTTGTGTGCATATGGA	TGAGAACAGAACGCTTTTAAAGTCG
AMPL4591769	PvP01_10_v1_569233	Pool=2	ATCTACGCATGTAAGTGGAAGAAGG	AAACGGTTACATTTGGACGTTCAAA
AMPL4340168	pvp13k_1	Pool=1	TTGGCATATAAATACCTGCGCTACC	AATTTTCTCACGCGGAAAGCAGCTC

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AMPL4339903	pvp13k_2	Pool=2	GTGCAGGCTACAGTGTCATCACGTA	AAAAGTTCCGGCTGGACTTAAACGA
AMPL4339627	pvp13k_3	Pool=1	AAAGGTACATTTACAAAGCGGGAGA	CTTGGACAATCTCATGGTTTCACGA
AMPL4339827	pvp13k_4	Pool=2	CTTCTGATTTTGAGCGGCACTACAG	AACATATGGAAGCGATACGGACTGG
AMPL4339661	pvp13k_5	Pool=1	AAGCAGAAGATTAAGAAAATACGAG	TCTACAATGGAAGGAAGGTGGAGAG
AMPL4340035	pvp13k_6	Pool=2	GGCGGACGCCTACTGCTTCCAGTAC	TCCTACCTGAACAGTCATACGTTTT
AMPL4339798	pvp13k_7	Pool=1	TCCGACAGCGAGGTCTACGACTTTG	GAGGACAGCAAAACGGTCAACTACA
AMPL4339811	pvp13k_8	Pool=2	TTCAGGAATCAGCTGCTGTACCTTA	GCGTAACTCCGTGTACTACCTGAAC
AMPL4339984	pvp13k_9	Pool=1	ATATTTGTTCCAACTGGTTCAGAGC	TCTTTTGCTACCGCCAGAACTACGG
AMPL4340126	pvp13k_10	Pool=2	CCAGCGATGGAGGAAATAAAAACGA	AATCACGAGCCGATTGACAGTCTCT
AMPL4339660	pvp13k_11	Pool=1	GGGCCTTCCTGAAAAGGGTGAAGCG	ACACACCAGTGATTAAGCTAAGTGA
AMPL4340000	pvp13k_12	Pool=2	GAAGAAATGAAGTGGGACGCGATGA	TATTCGAGCACATGAACCGGTACGC
AMPL4339783	pvp13k_13	Pool=1	TATGACCAGTCAGGTGAAACGATTG	ATCGGGTGGGAAGCGATCTCGGGGA
AMPL4340145	pvp13k_14	Pool=2	TTGATATGCCCCATAGAAGGAGGAC	CGGTACGAAGGGGAGTTGTTTTGCG
AMPL4339530	pvp13k_15	Pool=1	AAAAAGCTTTTTCATCTCGGGAGGA	GCATTGAACGTTACGTACGCTCGGT
AMPL4339705	pvp13k_16	Pool=2	GAAACAGAAAATCCGAGGCGATACG	CGTGATTTGTTGTGTTTGTACCGTT
AMPL4339686	pvp13k_17	Pool=1	CGCGGAAAAGTTGCGGTGATAGGAT	TCAGCTACCCTATTAGGCACTCCCA
AMPL4339785	pvp13k_18	Pool=2	AGGAGAAAATCCCGAGGGACGAATT	CGTTTTGTGAAAAGCCAGTGGGGGG
AMPL4339588	pvp13k_19	Pool=1	GAAGAAGAAGCACCTGATGAGCGTT	CGACTGTATGAACCGCTTTAACCAT
AMPL4339730	pvp13k_20	Pool=2	GGTGAGGAAGCTAACGGAGCTAACC	GTTGAATCGCAAAAGGAGAGAAGCT
AMPL4340091	pvp13k_21	Pool=1	AGGTGAGCAGTTACCAAAGGGTACA	AACGAAGCTGACTCCTCAAACGCCG
AMPL4347627	SET9	Pool=2	CTGTTCAAAAATATGCAGTACGTTG	CCATTCTTATGAGCGGAAAAACGAA
AMPL4591750	PvP01_10_v1_1409490	Pool=1	GTTGACAAGAATGAGGAGGAGCAGA	GACAGCGAAATTCTGGACACACCAA
AMPL4339786	ABCE1_1	Pool=1	CTTATGTAGGCTATCTTCGAGGTGT	GTTCAATTTGGCAGACAAGGAGGTA
AMPL4340040	ABCE1_2	Pool=2	AACTCATTTCCTCGGAAGAAGGATA	CGTTTTGACGATTGGGCAGTTTTTC
AMPL4339930	ABCE1_3	Pool=1	TACACATTTGTCGTCTGCCCTATGA	TTCAGCGCTGTGGATTTTCCTATTC
AMPL4339514	ABCE1_4	Pool=2	TCATCTGTTACGTCCTGATCTGTAG	AGCGAATCTTTGTAACTCTCCTCCA
AMPL4339817	ABCE1_5	Pool=1	AGGGATCTGTGTATAGCCCCTTTAG	AGAGACTCCTCCCTTATTCGTAGGT
AMPL4339619	ABCE1_6	Pool=2	CCACGACGAACGCCGTTTTGTTAGT	AGACTTTCTACGTTATCCGGTTTGA
AMPL4339587	ABCE1_7	Pool=1	TACGGTTATGTACACACGTATGCAG	AAACGATGATTCTCTGCTCGGAGTC
AMPL4339539	ABCE1_8	Pool=2	AAGTGCTGCCAATTTGTTGTTTTCC	CGTACTTGTTTATCCTGGGGCGGTA
AMPL4591756	PvP01_11_v1_251753	Pool=2	TATAGTGTACTGTACGCAGAAGGGT	AAGCGAAAGTATGACCTTTGCGTGA
AMPL4591765	PvP01_11_v1_326984	Pool=1	ACTCCAGTGAGCCACTCCAGTGAAC	CTCGGAGTTATGCATCAAATAGCCG
AMPL4347656	PVP01_1109600	Pool=2	AAGTGGAATGTCATAAGATGGCTCA	GGTAGATTACAAGTGGACCGATCCT
AMPL4347635	PVP01_1112200	Pool=1	TGTGCAAATTGCTCAGCTTTACAAC	ATGCTGCTTAAAAAGAGGGACGAGA
AMPL4347643	PvP01_11_v1_1137409_1137410	Pool=2	TTTGTGAAAACGATCGCAGAATGAT	GAGTTAAAGATAACCGCGTGGGAAA
AMPL4347628	ALV7	Pool=1	AGGGATGGGTAGACCCAAACATTAC	TATGAAACGGTGATGAACTGAGCTG
AMPL4347625	PVP01_1133700	Pool=2	TTCCCCATTGTGGACCATCAAATTG	TCATTCGTGTTCCACTGGAAAATTT
AMPL4347644	PVP01_1144100	Pool=1	GACCCTTTTAATCTGCACAACACAT	CGATATGCCGTGCACCTGTAAAGAT
AMPL4591759	PvP01_11_v1_1898201	Pool=2	TGTTCTCTCCATTTGGCAATTTTCG	CCCATCCTACTCACCACTTTGCACA
AMPL4591758	PvP01_12_v1_381435	Pool=1	TGCAGTTGTGATGTTCCTAATGACA	AAGTTTGTTTGTACGCATGCGAAAA
AMPL4339656	pvk13_1	Pool=1	TCCCAAGGTTTTCTTTCGACAAATT	GCTTTCATGCGTGAAGATTCATCTG
AMPL4339743	pvk13_2	Pool=2	ACTTGAGTCACTCAACTCCGTTTCG	ACGCTCAAATCGATCGATTCCAAGA
AMPL4339896	pvk13_3	Pool=1	CCGTTTGATATATCAATGTCCAGTT	TTATCGGGGTGGATGAATCCATGAA
AMPL4340099	pvk13_4	Pool=2	GTACCTCCCACTTAGCAACTTTTCT	CAGTTTCTGTTCCTCGATTGATTTT
AMPL4339964	pvk13_5	Pool=1	GAAATATGCCTTCTTCGTGGACATG	GTGTGCCTAGAAGTTTCGAATATGG
AMPL4339521	pvk13_6	Pool=2	AGGCTACACACATGGAGGAAGATCG	AATGTCTAACAGCTCCATGGAGTTC
AMPL4339804	pvk13_7	Pool=1	CCACCAGTGATGATGTACGAATCGG	GCGATTTCTACCCAAGCCTTCATCC
AMPL4339737	pvk13_8	Pool=2	GGGGAAACATATACCGTGGTAGTGG	ATCTTCTTCTCTGGAACTCCATTGA
AMPL4591740	PvP01_12_v1_976909	Pool=2	TGCGTCGTCCCATGCGAGCATAAAG	AATCCTGAAGCTGTGCAACCTGCGG
AMPL4347654	PVP01_1227900	Pool=1	TCTAAAGAAATCGGTGGCACAAACC	CTGCACATGTTTGGTCAATTCTAAT
AMPL4347651	PVP01_1235200	Pool=2	CACCCAAATGGAGACTCAAATGTTC	GCGATGCTGAACGTGTTGAAAATAA
AMPL4591757	PvP01_12_v1_1431548	Pool=1	GGACGGTATACAAACGAATGTACTT	GCAAATTTGACTGAAATCATTCTGT
AMPL4347641	PVP01_1236900	Pool=2	AAAGCAAAATGAAAAATGCCTCGTG	CGCAAAAATTGAACAAAGTCGTACG
AMPL4347638	PVP01_1249000	Pool=1	CAACGGAGGTAGTGACGATATTAGT	GGATGATGAACAGTTGGGAGAATCT
AMPL4380317	pvmdr2_1	Pool=1	TAACTCTGCTTCACATCAAATTGGT	GCTCTTTCACGAATTATGAGTTCAC
AMPL4380308	pvmdr2_2	Pool=2	GCATAATAACTCCCCTCATGATTCC	GTCCACCACATGGTAGATGCTAATT

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AMPL4380318	pvmdr2_3	Pool=1	TGTACGACTGGTTCCAATACAACGC	TATGATGGCCAATATCCCTGTGAAG
AMPL4380311	pvmdr2_4	Pool=2	TGTCCTCCAGGAAGCTTATGTTCGG	GAATCGTTGTTCATCGTGCTCGTGT
AMPL4380309	pvmdr2_5	Pool=1	CATATCCCTTTTCAACACCTCGTTG	TTATCCGGGCGGTAGCTCTTCTTCT
AMPL4380310	pvmdr2_6	Pool=2	AAAATGATGCAGGTAACAACTCCTT	TGATTACGCTGAATACTTTTGAGAG
AMPL4380322	pvmdr2_7	Pool=1	GCACCCCCAAACTGTTAAGGATCTT	GCACTCTCAGTACCTCTGTCTACAA
AMPL4380321	pvmdr2_8	Pool=2	CTGACTCCAAATTTCTTTTCATGTG	AGAGCACTACAGAATCTCCTAATTT
AMPL4380312	pvmdr2_9	Pool=1	GAGCAGTTTCGAGATGGTCGTTTTT	CTATCCGCTCCGTCATATACAATCA
AMPL4380327	pvmdr2_10	Pool=2	CCTTTGTCTCCAACGAGAGTATCCC	GCCATATGCATTGGTTGTGATGGGT
AMPL4380315	pvmdr2_11	Pool=1	TCTGGACTGCATATTCCACATCTCG	GACATAATAAAATCGTACAGTTGAG
AMPL4380324	pvmdr2_12	Pool=2	CACTGGTTTTACTGCCTCGGGCAAG	ATTCAATTTGAGCAGATGCTGATGG
AMPL4380313	pvmdr2_13	Pool=1	ATACAGTGTGCTGTAGTTCTCCTTA	TTCGCGGCTTCCTTCACAATGCTGT
AMPL4380325	pvmdr2_14	Pool=2	CGGTGTGGTTCACCTCGCTGTAGGA	AGACGCCGTTCACATTTTGGTTGCT
AMPL4380320	pvmdr2_15	Pool=1	CTAATCTCTCCCTCCACATGAGCTT	TACCACGCTCACTTTGTCTGCCACT
AMPL4380323	pvmdr2_16	Pool=2	TCTCCACGCATGTCAATTTCGTTGT	ATCAATTGCTCCCTCCACATGAGCA
AMPL4380316	pvmdr2_17	Pool=1	CTGCTGTAGTCTTGGTGGTCCAAAT	GACACATGATCACTTTCACCAATCG
AMPL4380314	pvmdr2_18	Pool=2	GTTCGTTAGCCGTGGTAAGCTCGTT	ACTGAAGGTGTTCGCGTCATTATTA
AMPL4380326	pvmdr2_19	Pool=1	CACATCAATAGTCATCGTCGTCAGC	CGGATCGTTGACAACTTCCCTGTCG
AMPL4380319	pvmdr2_20	Pool=2	TTTCCTTCAATTCTGGGCATTCAAT	ATTGTAGTCGTAGCTGACGGAGGGT
AMPL4591742	PvP01_13_v1_32509	Pool=2	AAGAATGATGTGCACATGCATGCAA	AGCAGCAAAATAACAGAACAGCTGA
AMPL4347634	PVP01_1301600	Pool=1	TGATGATTTTATTTTTGCTGACGCT	GGTAGTACAGCTCGTCCATGATTTC
AMPL4591746	PvP01_13_v1_1351644	Pool=2	ACCCGTTCATGTCGGATGTAAAAAT	GCAGATGATCAAAATGGATTGCTTC
AMPL4591763	PvP01_13_v1_1736418	Pool=1	AAGGGGTAAAGAGTCAGCGGCTAAG	TGGGACGCGTTAACATAATCTGCCA
AMPL4347650	RPT4	Pool=2	GAAATTCAAAGAACGCTCATGGAGT	AAGGCCGCTCGAAAGATTAATGAGG
AMPL4591771	PvP01_14_v1_816546	Pool=1	GCATACGTTTTCATGACCCCTGTCG	AACGACGCGCATATAATTGATAAAA
AMPL4347640	PVP01_1427200	Pool=2	TTAAAGGAGTAGTGCTTAGTGTTGC	CAAAATACCACCACTTGGTGTTTAT
AMPL4347631	PVP01_1428700	Pool=1	CGCCTTTTCCTTAGCTTCCTTATCC	GTTTCTCTGGAATGATAAAGCAGGC
AMPL4347639	PvP01_14_v1_1258543_1258544	Pool=2	TGCCCCACGATATGCTATGTTTATG	TGGGAGCGAAAAATATAGGCACAAT
AMPL4347629	PvP01_14_v1_1266325_1266326	Pool=1	ATCCATCTGAATGCGTACGCAGAAA	GAATGTGTACCTGTGCAGAGGTAAA
AMPL4339663	pvdhps_1	Pool=2	ATCACAACTGTGGAGGTTCAAAATG	GGTAATCTCCTGGCAGTGCACGAAA
AMPL4339721	pvdhps_2	Pool=1	AAGCACGACCAGTCTATTAAGCTGT	GCTTTTGTACCAGAAAAATATTTGC
AMPL4339572	pvdhps_3	Pool=2	TAAGCATCGACACGGTCAATTATGA	TACGATGAGTACCCGCTGTTTCTTG
AMPL4339969	pvdhps_4	Pool=1	TGGCGGTTTATTTGTCGATCCTGTG	GAGTTGGTGGACATCCTAAACGATA
AMPL4340085	pvdhps_5	Pool=2	ATCATTCCAGAGTATAAGCACAGCA	GTCATGCCTGTTTTGAAGCTCTTTA
AMPL4339876	pvdhps_6	Pool=1	ATTGAGCAAATCATGAAAAGAAGGG	GCCATTCGCTCAACTTATAACAGTT
AMPL4339717	pvdhps_7	Pool=2	TCTTGGATAGGCGATTTGATCCCAA	TCAGGGAGAAATATTTCAAAATCGC
AMPL4339843	pvdhps_8	Pool=1	GTGCATACCATCCCCCAGTAGTAAA	ATTATTAGGGAAGTCAGCGTAGAGG
AMPL4340007	pvdhps_9	Pool=2	GAAGAACGCATATAAACAGAACAGC	GTAGACACATAGGTCCAAATGCCGC
AMPL4591752	PvP01_14_v1_1385718	Pool=1	GTTTGCGAAGGCTGTATTCGCAATT	TGAGTTCCCACTTCGCATATCCTCT
AMPL4339602	pvmrp2_1	Pool=1	TACGGAACTACTTCGCGGACATCAC	TGTTTTAGAGTCCGCCCGAATCCGG
AMPL4340161	pvmrp2_2	Pool=2	ACAGAAGAAGAAGAGTGCATCTAGG	CTTCATTTACGTCGTGGCCAAGGGC
AMPL4339772	pvmrp2_3	Pool=1	TATCAAGACCATGAGTTTGCAGGAA	ATCTTCCTAAACAGACACACATACA
AMPL4340042	pvmrp2_4	Pool=2	ACTTCGAAAACGTGTTCGTGAGCTA	GACGACATTATGGAGGCCTTTAAAC
AMPL4339640	pvmrp2_5	Pool=1	GTTCATCATAAAAGCGCTGCTCTAT	ATAGACAAGTCGCGCAACCTTTATT
AMPL4339731	pvmrp2_6	Pool=2	TTCCCTCTACGTACAGCTGATTGTG	AAGGAAGTATCAAAGGAGGTGTCGA
AMPL4339813	pvmrp2_7	Pool=1	CTTTCTTTCGTTTCCTTTTCACCAT	TGGCTTCTACATCATTTACCCTTAT
AMPL4340160	pvmrp2_8	Pool=2	TCTGAAATATTGAAGAAGCAATTGG	GGTCTACGTATTCCCGATGATCATT
AMPL4340065	pvmrp2_9	Pool=1	ACAGGATGACAAAATAACTCTTCAC	TACTTTGTCCTTCTACCATGTGTGT
AMPL4340177	pvmrp2_10	Pool=2	CAAGAACGACCTCAAGTACCAGAAG	AAGCCCAGCTGAAGGATAACTATAT
AMPL4339891	pvmrp2_11	Pool=1	CAACCAGAACATCTGGCACAGCTTT	GAGCTGAAGAGCACCTACTCGTGCC
AMPL4339777	pvmrp2_12	Pool=2	GTGGAAGCAACAACGATGTGATTAT	CAGTACGACGTGCAGATCTACCGCC
AMPL4340079	pvmrp2_13	Pool=1	GAAGCTCTTCGTAAAAGGAGGAGAT	TCTTATTTGTACCTCCTGGATGACC
AMPL4339742	pvmrp2_14	Pool=2	AGAGGAAGGACCTAAGGTACGTGAA	CTGCACGACGTAGATAATTCGACCA
AMPL4339508	pvmrp2_15	Pool=1	GGCAGCTGCTACGTGAAAAGCTTCG	GGTTGTTCAAAACGGCTAGCTCCCT
AMPL4339729	pvmrp2_16	Pool=2	GGTAATTTTGAAGCTGAGCGGGTGT	TACTCTTTGGAAACAGATTCGACCC
AMPL4339513	pvmrp2_17	Pool=1	GGGGGCCCTCATCAAGTCGATTTTT	TGCTGAAGAACGTCAACCTGACGCT
AMPL4340141	pvmrp2_18	Pool=2	TCAATCATCACTCCTCTATTCGTTT	GCAGTAACAGGACCCACTACGGCGC

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Nationalestraat 155 | 2000 Antwerpen | Belgium | Tel: +32 (0)3 247 66 66 | Fax: +32 (0)3 216 14 31 | E-mail: info@itg.be | Website: www.itg.be

AMPL4339761	pvmrp2_19	Pool=1	AAGATAAAGCACCTCAAGTGTAGGG	TAACCTACTCGAGGGGACCATCAAC
AMPL4340031	pvmrp2_20	Pool=2	GGGAAATTGTCCAGAGGGAAGAATC	AGTAACATGCATCACATCCTTAAGG
AMPL4339935	pvmrp2_21	Pool=1	GCTATGCAGCTTCCCTTATCCTGAG	CGGAAGGAGACAAGGAAGAGAGCGA
AMPL4339706	pvmrp2_22	Pool=2	TATGTGATTCATACCCTCTTCCTCA	GAGATCACCACGATGTGCAGGTGGA
AMPL4340054	pvmrp2_23	Pool=1	ATAGAGGAAGATGCCGCGATAGAGT	GAATTGGCATTCGGCTTCATCCTAG
AMPL4339868	pvmrp2_24	Pool=2	GCGTTACAGCGCTTCATCGCTACAG	CACAGAATAACCCAAGTGAACGACC
AMPL4591745	PvP01_14_v1_2841138	Pool=2	CACCGCTAATCGCTTCCCGCTAATC	AACCTGTCTGATACTCTCATTATGC

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Nationalestraat 155 | 2000 Antwerpen | Belgium | Tel: +32 (0)3 247 66 66 | Fax: +32 (0)3 216 14 31 | E-mail: info@itg.be | Website: www.itg.be

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Nationalestraat 155 | 2000 Antwerpen | Belgium | Tel: +32 (0)3 247 66 66 | Fax: +32 (0)3 216 14 31 | E-mail: info@itg.be | Website: www.itg.be