

Supplemental Table 1. Molecular inversion probes included in the DR23K panel. Vol column indicates the volume (in μL) of 10 μM probe stock pooled for phosphorylation as described in **Supplemental Methods**.

MIP	Vol	Targeted Region	Probe Sequence
PM2_S0_Sub0_mip0	4	chr14:293316-293526	AACATTTGATGGATTAAACATTGACAATTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAGAGTAATCCATAATAATTTGTATGAGA
PM2_S0_Sub0_mip1	2	chr14:293507-293714	ATGTTTAAATCATGTTCTTACTGTAATATCCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGTGCATTTTCAACTTTAAATCCAA
PM2_S0_Sub0_mip2	2	chr14:293696-293906	TTGGAGATAACCAACAACCATTTACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAGAGATAATGAAATGAATGAAATTTTAAAA
PM2_S0_Sub0_mip3	2	chr14:293861-294062	GATATTATCATTTGAACTACCTAAATAATTTGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCAGTTCCTGACACATAATTCATTT
PM2_S0_Sub0_mip4	2	chr14:294045-294227	AAGATTTATCAATAGGTTCACTAGATCCAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGATTCATCTAAATCAAGAACATATGAAA
PM2_S0_Sub0_mip5	2	chr14:294152-294357	AATAAATTTATATGGAAGAGATAAATTACCAACAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGGTCTTCATAAAATCTTTCTTCAATA
PM2_S0_Sub0_mip6	2	chr14:294316-294515	ACTTTTTAAATAAAATGTTGCAGAATTTAGATGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAAATGCTCTTTTCACCTTTTACTT
PM2_S0_Sub0_mip7	2	chr14:294434-294640	TAAAGTTATTTGCCAATATAAATCGTGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAAAGGTAGTATTACAGTTCTTAATGT
PM2_S0_Sub0_mip8	2	chr14:294632-294843	TGGAAACCAAAGGAAAAACATAATTATATAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCAACTTTTGAATTTACCTCAGAAAAAT
PM2_S0_Sub0_mip9	2	chr14:294700-294914	ATACATAATCCTGGACCAACATCTTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGGTTCATTATGGATAAAATATGTTTTCT
PM3_S0_Sub0_mip0	2	chr14:297348-297544	AACTAAAGTAAAAAGATGGAATGCTAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTGAAAGCCGTAATAAAAGTTAAA
PM3_S0_Sub0_mip1	2	chr14:297501-297680	GGTAAATCTTCTTTTAAATGTTTAAATTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCTGTGCAATATTTTGAAGTCTTAATTAT
PM3_S0_Sub0_mip10	4	chr14:298754-298965	TATATATTTGTGATGTCGTTTGATTATATTGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTGTTCTAGGTGACCCATTTAT
PM3_S0_Sub0_mip2	2	chr14:297615-297826	TTATTTAGGTAGTGAGTTTGATAATGTGGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATTATTTGTGACAGTTTTCATAGTTTTG
PM3_S0_Sub0_mip3	2	chr14:297773-297967	TTTAATTTATGCTCTTTAATTGTTTTCATAAGTCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTACAAGACTCTGATGTACATTTTATA
PM3_S0_Sub0_mip4	2	chr14:297891-298076	ACAATAAGTGGAATATTTAGTAAAGATTTAGTAACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAGATTTAGCAAATGTATTATCTTTTGGAA
PM3_S0_Sub0_mip5	2	chr14:298048-298240	TATCATCTTTTTCATATGTTTTTGATTTTGATGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGTGTTTTTAATCTACAATATATGGATCTATA
PM3_S0_Sub0_mip6	2	chr14:298153-298359	AAAGATTCTTTGATGGACCATTGAACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTCAGTACCCTATAAATTTATTGAAATGA
PM3_S0_Sub0_mip7	2	chr14:298339-298537	AATAACCTTTATTTTTGTTTTCTGTTGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAGAATGGAACCTTTGAAACACTT
PM3_S0_Sub0_mip8	2	chr14:298434-298629	TATATACTTTAGAACCTAAACAATACCTTGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATGTGGCAAGTTGATTAGATGTA
PM3_S0_Sub0_mip9	2	chr14:298589-298798	TTACCACAAGTGTTACATACAAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCTTTATAAATTTTTGGCTAAAGCAAAT
crt_S0_Sub0_mip1	4	chr7:403099-403307	ATTTTAAATATTTATGTCATATATGTGGAAGACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTCCATTTTGGATACTTACTTCCT
crt_S0_Sub0_mip10	4	chr7:404323-404479	AACAATAAATACTGCTCCGAGATAATTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATAATAAAACAAAGTTTAAGTGTTAATATATAT
crt_S0_Sub0_mip11	4	chr7:404375-404577	TTTCTTCTGTGTTTCAAAAGATAATTTCCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTATTTCCCTTGTCATGTTTGAAAA
crt_S0_Sub0_mip12	2	chr7:404588-404802	TGTTTGAAAGCATACAGGCTAAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTGGAAGGGTGATACAGGTAATAT
crt_S0_Sub0_mip13	2	chr7:404756-404915	GTATAATTTTCCCTTTTGTATTTACCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAACGCATTATAATTATTTCTGTTATTTTATT
crt_S0_Sub0_mip14	4	chr7:404809-404999	TAATATAAGACAAGAAGTGAACAATTGGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTACCTCTACGACTGTGTTTCTT
crt_S0_Sub0_mip15	2	chr7:404997-405192	ATGGGTAAAGAAGCTTATAATAAAATTTCAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAAATGGTTTCGCATGTTTATTCTT
crt_S0_Sub0_mip16	2	chr7:405158-405363	AAGACCACAATTCTGAAGAGGAAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCATAGCTGGTTATTAAATTATCACAAT
crt_S0_Sub0_mip17	2	chr7:405353-405571	ATTGTTAGTTGTATACAAGGTCCAGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTAGAAAACCTTCGCATTGTTTT

crt_S0_Sub0_mip18	2	chr7:405569-405736	ATATGTCATGGTAGAAAAATTTGTCGATAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTACGTTGTACCATCATAAACATTTAAAT
crt_S0_Sub0_mip19	2	chr7:405653-405843	CAAGATTATTAGATTTTCGTAACTTTGGTAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNCTTAGCCGTAAGAATAAAAAGATATA
crt_S0_Sub0_mip2	4	chr7:403184-403345	AATGAATGTATAATAAATAATATGACTGCGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNCCAATAGGTTGATTTATCTATTCAATTA
crt_S0_Sub0_mip20	4	chr7:405837-406030	TACAACATCACCTATAAAATTAAGAAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNCCCTACACGGTAAATTATAGAACCA
crt_S0_Sub0_mip21	4	chr7:405979-406163	ATTTTATATTTCCATCTGCTCTTTTATTCTATTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATGGCTTGTTCTGTTTATAAATATTTA
crt_S0_Sub0_mip22	2	chr7:406082-406280	TTTGTATTACTTTCTAAGATAATATTTCTACACGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTTGAATCGACGTTGGTTAATTCT
crt_S0_Sub0_mip23	4	chr7:406274-406465	AATAATGTTGAAGGTATAGAGATCTCTTTATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNAAATGAGAAATGAAGAAAATGAAGATT
crt_S0_Sub0_mip3	4	chr7:403291-403507	GAGGTTCTTGCTTGGTAAATGTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAATGACGAGCGTTATAGAGAATTA
crt_S0_Sub0_mip4	2	chr7:403492-403702	ATCTGTTAAGGTGCACAAGGGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAAGGAATAACAATAAAGAACATAATCA
crt_S0_Sub0_mip5	2	chr7:403592-403787	GATTTATAAGAGAATCTATTCCACCTACCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAGAGATTAAGGATAATATTTTATTATATTTAA
crt_S0_Sub0_mip6	2	chr7:403780-403972	TAATATATTGATTTATCTTACTTTTGAATTTCCCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGAACAGGCATCTAACATGGATATA
crt_S0_Sub0_mip7	2	chr7:403933-404082	TCTTCTGCTTTTTAATATTAAGATATAGGTAAGTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTTGTTTATATATTTATATTTCTTATGACCTT
crt_S0_Sub0_mip8	4	chr7:404081-404279	ATATTAATAGGAATACTTAATTGAAGAACAATGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTCCGAGATAATGTATAAGTGATATCTA
crt_S0_Sub0_mip9	4	chr7:404129-404324	AACAATAGCTCTTGTAAGAAATGAAATTATCTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTTAAATATTAAGATATAGGTAAGTATACTATTTAA
dhfr-ts_S0_Sub0_mip1	2	chr4:748093-748266	AGTTACAACATATGTGAATGAATCAAAATATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTTATTTATATATTTATATTTCTCCTTTTATGAT
dhfr-ts_S0_Sub0_mip10	2	chr4:749309-749518	AATGTAAAGATCTTGACCAATGGCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAATGTAAGGATATGGGAAGCTAAT
dhfr-ts_S0_Sub0_mip11	2	chr4:749460-749638	TTTTTAATTGATCCACTCCTTTATTTTCATAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTAGAATAAGAAGCAATATTTAAAGGTAC
dhfr-ts_S0_Sub0_mip12	2	chr4:749579-749756	TTGATAGTTAAAAATTCAACTTAACAGAATACCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNCCCTTGTCATATTTTATGTCAGTTTTAT
dhfr-ts_S0_Sub0_mip13	2	chr4:749711-749926	CGCAGGTTGCAAATTACAGACTTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNATTTTGTATCATTTTGTTCATATATTTTT
dhfr-ts_S0_Sub0_mip2	2	chr4:748114-748299	AAAACGTCGCAGACTTGTTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNGTTTAAATATTTACATCTCTTATATTTCAATTTT
dhfr-ts_S0_Sub0_mip3	2	chr4:748217-748428	TTTATTTCTAGACCTCTAAATGTGTAGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNATCCTATTGCTTAAAGGTTTAAATTTT
dhfr-ts_S0_Sub0_mip4	2	chr4:748374-748585	TCCGTTGTTTATCAAGAAATTTTAGAAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNGATAATGTAATGATATGCCTAATTCTA
dhfr-ts_S0_Sub0_mip5	2	chr4:748548-748746	CAAGTAAACTATTAGATCTTCAACTTTGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNCGTTTTCTTATAAATGATAAAATCCAAT
dhfr-ts_S0_Sub0_mip6	2	chr4:748719-748908	TAAAATTAATTATGAAATGATGATGATGATGAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTGAAATGAGTATCAAATTATTTCTGTTA
dhfr-ts_S0_Sub0_mip7	2	chr4:748870-749072	ATATGACATGTATCTTTGTCATCTCTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTTCCATTATCATAATATCATAAATAATATTTA
dhfr-ts_S0_Sub0_mip8	2	chr4:749038-749237	TTTGGTTTATTAGAGGAGAAACAAATGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNCTATACATCCAAATGATTTTCAAATATATAATAG
dhfr-ts_S0_Sub0_mip9	2	chr4:749183-749371	ATATTGACTTAAATCAAATTTTATAATATATCCGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNATGTCTCCATTGAAAACCATAAAT
dhps_S0_Sub0_mip0	2	chr8:548152-548314	ACCTTGTCGAAAAATATTTAGGTAAGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATAATAAATTTGCGTAAAGAAATCTAAT
dhps_S0_Sub0_mip1	4	chr8:548309-548472	CAGTTTCTAGAATCAACACAGCGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNGTGAAAAATAAAATATATAGAATCAAGAGT
dhps_S0_Sub0_mip10	2	chr8:549625-549827	AACTATAATGTTTTTAAAGAAATGTGTTGATAATGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAACCTAAACGTGCTGTTCAAA
dhps_S0_Sub0_mip11	2	chr8:549823-549996	TATCAATACTTATAATTGGTTTCGCATCACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNTTATATCATAAAGTATATCATAATTTGTTA
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dhps_S0_Sub0_mip14	4	chr8:550203-550406	AAATGAGTATACAAAAGTAACAATTCTATATATGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCCACTTTTTATTGGATATTCAAGAAAA
dhps_S0_Sub0_mip15	2	chr8:550323-550526	AAACATCCAATTGTGTGATTTGTCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGAACTCTTATTAGATCTACCTTTTTATAATA
dhps_S0_Sub0_mip16	4	chr8:550515-550726	ATTTGTTGTTCTTTTTCTATTTTACATGTCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTCTTTTCAGGTGGATTAGCAATT
dhps_S0_Sub0_mip17	4	chr8:550580-550787	GATTTTGTCTTCTAAAACGTCATGAACCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAGTCCACTTTTGATAATTTTATAAAATCA
dhps_S0_Sub0_mip2	2	chr8:548460-548609	ATATATGATGTTAATTATATAAACGAATTGATGCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCATACTTTTATATACATACCTTTATATACATACTT
dhps_S0_Sub0_mip3	2	chr8:548575-548752	TTTTATCTAATACAATGTATTCTGGAACGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTACATTCTAATAAATAATTTCTACATTTACT
dhps_S0_Sub0_mip4	2	chr8:548751-548955	AAAATGTAAAAGAGAAAGAAAAATTTGAAATCGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGAAAAAGTTGATAATAGTATTCTAAAG
dhps_S0_Sub0_mip5	2	chr8:548937-549125	AATATATTTTATAACTACCAACATACTAAGAGGATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATCTTTATCCATATTTACTTTAGACATATT
dhps_S0_Sub0_mip6	2	chr8:549105-549309	ATATTGAATTTTATCCATTCTCATGTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNACTCTCAAAATATATTCTTTGGAAGA
dhps_S0_Sub0_mip7	2	chr8:549299-549451	TTGTTTATTATTTCTTGTGGATCTCTAAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTCTTTAATATTTATATTATTGTTCTTTCATC
dhps_S0_Sub0_mip8	2	chr8:549370-549583	AGATGGAGGTATTTTTGTTGAACCTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCAACACACAGATATAGCATACTTTTAT
dhps_S0_Sub0_mip9	2	chr8:549583-549740	AAAAAGAATCATAATTAACATTTAATATTCCAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCATTCCATTCTTTTGAAATAATTGTAA
k13_S0_Sub0_mip1	3	chr13:1724818-1724999	TACACCATTTAGAAATTGCCATCTTTATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNAAAAATAAGAACATTTAAATTTCTTCATT
k13_S0_Sub0_mip10	3	chr13:1726199-1726378	ATATTGAAGAACAGAAATTACATGATGAAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATGATACTTATGAAAAGAAATTTATTGAA
k13_S0_Sub0_mip11	3	chr13:1726304-1726503	AGACACAAATGAATTTTATTCGAGAAAAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATATGAATCTCCATCAATTATGAATAC
k13_S0_Sub0_mip12	5	chr13:1726474-1726678	ACATATTATTAATGTTCTTGATAAATTACTTGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTAATCCAGAATCATCATTTATAAGATT
k13_S0_Sub0_mip13	3	chr13:1726531-1726741	TATGAATCTCCATCAATTATGAATACCAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGAATCCATTGATATGAGTGATTAGATT
k13_S0_Sub0_mip14	3	chr13:1726693-1726878	TTCTCGCTACTACTTCGCTTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTTCTATATTATCTTTAGACATATTATTAAT
k13_S0_Sub0_mip15	3	chr13:1726824-1727000	AATAGTTTCCTTTTAAATAATAGTAGTTATGGAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCATTCTTTATTATGTTTTGTTAATTAATTATA
k13_S0_Sub0_mip2	3	chr13:1724927-1725137	AAGTTCTAAATTCATGTCTATTCTTTTACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNACAATTTCCATATGCCTTATTAGAA
k13_S0_Sub0_mip3	3	chr13:1725079-1725274	TAGGGGTATTCAAAGGTGCCACCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGAATCTAATATGTTATGTTCTATTATCA
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k13_S0_Sub0_mip5	3	chr13:1725363-1725575	TGTACACATACGCCAGCATTGTTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCGGTATAATAGAAGGCCATCATA
k13_S0_Sub0_mip6	3	chr13:1725563-1725749	AAAAAGCTTATTTTGAAGTGCTGTATTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTAACCTCTTAAGAAATCCGTTAACTATA
k13_S0_Sub0_mip7	3	chr13:1725714-1725926	ACCAACATTAATATCAATCATAGTTTCAGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACCATAAAATCTGCTCTTTCAA
k13_S0_Sub0_mip8	3	chr13:1725921-1726121	ATTTTTGAAACATCTAGACATACCTTAACANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNATTGATATATCTAATGGTTATAACAAATAAAA
k13_S0_Sub0_mip9	3	chr13:1726086-1726264	ATAATTTATCTTTTTCTCGAATAAAATTCATTTGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNCGATTTCTTGTAATAATCTTAATCTTTC
mdr1_S0_Sub0_mip0	2	chr5:957787-957958	AACAAAAAGAGTACCGCTGAATTATTTAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNGTGTACATAGCTTATTTCAATTATAAGATTT
mdr1_S0_Sub0_mip1	2	chr5:957899-958080	TTTACCCATCTTTCAACACAAAATCAAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGTAATGTTCTCCTGATAATACA
mdr1_S0_Sub0_mip10	2	chr5:959125-959327	ACAAATGCATATGTTTTCCCTTCTTTANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCCATTGCTTCTAAATCTTTAAACTAT
mdr1_S0_Sub0_mip11	2	chr5:959261-959476	TCTGATGTTGTTGATGTGTCCAAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNTTGAAATGGTGGAGATCAAAAATT

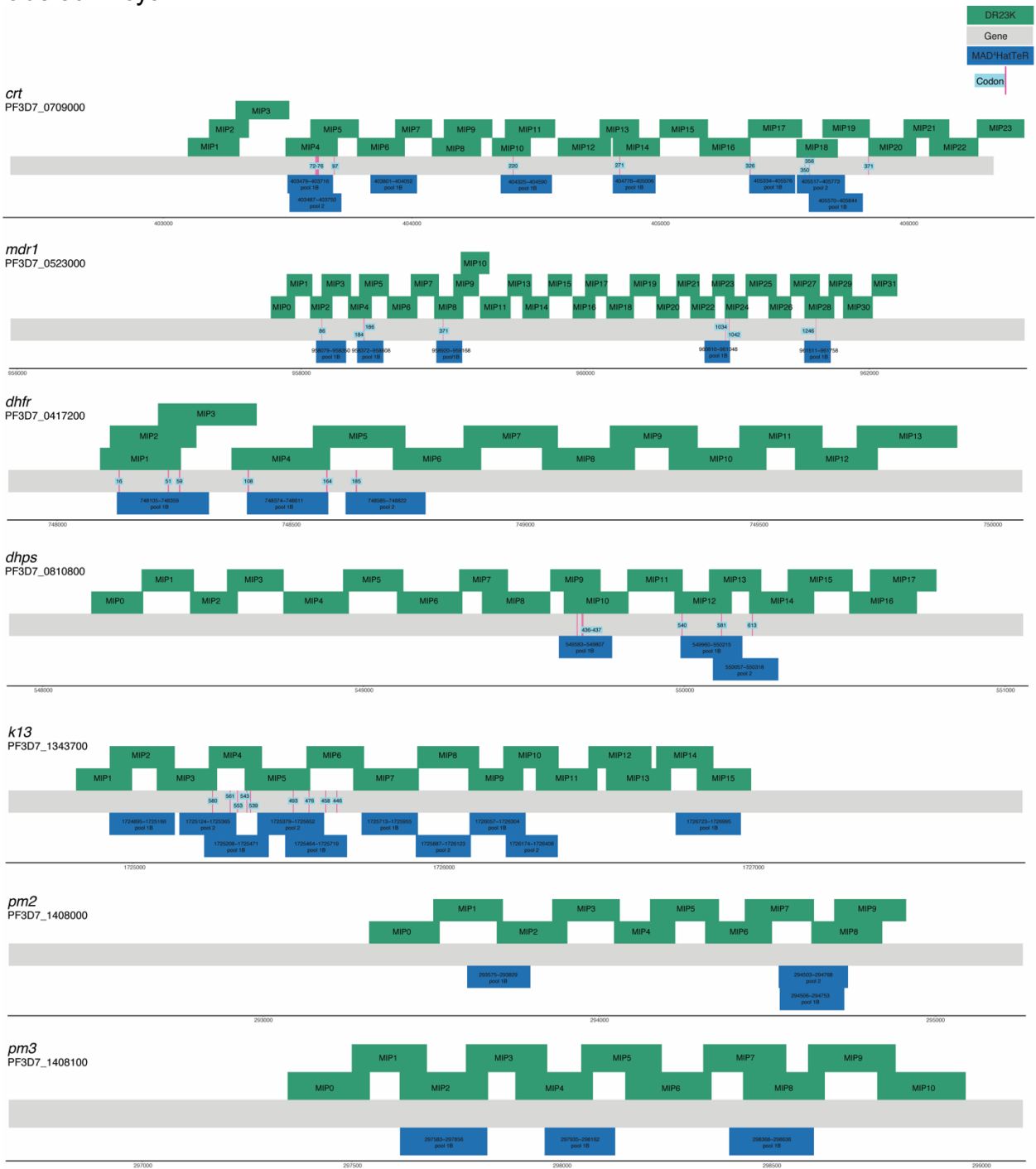
mdr1_S0_Sub0_mip13	2	chr5:959453-959625	AAATCCTAAAAATTCTAATTCTTGATGAAGCTACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGACATCAAATGAATTATTAGAAATGAAA
mdr1_S0_Sub0_mip14	2	chr5:959559-959748	CTACTAAGGTATCATATTTATCTGGTAATGATGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGCATATCTTAGTACTTAATCTATGT
mdr1_S0_Sub0_mip15	2	chr5:959738-959909	GTACACATGATAGTCTTATGAAAAATAAAATGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTTGAAAGGAAATGAAATAGAATAACT
mdr1_S0_Sub0_mip16	2	chr5:959913-960073	TACCTTGTTCAATAATATAGCTACCCCTCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTCATTTTCATGTATTGATAAACTATTTCAT
mdr1_S0_Sub0_mip17	2	chr5:960000-960158	AAGTTCCATTTTTCAAAGAATGTTTAGAAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCAAAAGATTTTCATCAAATAAATCTTCAAATA
mdr1_S0_Sub0_mip18	2	chr5:960150-960344	TTTCATTTCTGCTGTATTTTACAATTACGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNATTTGAGTTATATTCTAGATTTGCAAAAT
mdr1_S0_Sub0_mip19	2	chr5:960315-960527	ATCAAGATAAAAAATACCCAGGTGTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGGATTATATCCCGTATTTGCTTTAT
mdr1_S0_Sub0_mip2	2	chr5:958064-958221	AAATAATAATTTTCTATGTTGTGCAGGTAACATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGTAATTACATCCATACAATAACTTGAT
mdr1_S0_Sub0_mip20	2	chr5:960501-960664	TATTTTCAAATAATCTACGTTTCATAGTCTTTTCGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGCAACAATTGGACAAAAATAAAA
mdr1_S0_Sub0_mip21	2	chr5:960643-960807	TTCAGATGATGAAATGTTTAAAGATCCAAGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTTATTTTCTCTCATTTTCATAATGCTCTT
mdr1_S0_Sub0_mip22	2	chr5:960741-960916	CTCTTACAGCAAATACACGCATATTAATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGTCTTTATTTTATAATCAATAGCTTTTTTC
mdr1_S0_Sub0_mip23	2	chr5:960896-961052	GAGGTACTATATTAGTTGATGACTTTATGAAATCCNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCATACTGTTATTAATTATGGTTTAGAA
mdr1_S0_Sub0_mip24	2	chr5:960984-961147	CCCATAAAGCTGCATTACAATAATCTTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTCAAATGATAATTTTGCATTTTCTGA
mdr1_S0_Sub0_mip25	2	chr5:961131-961350	AAAAACTACAGCAATCGTTGGAGAAANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNCTGGTAGTTATGCTGGAAATTAA
mdr1_S0_Sub0_mip26	2	chr5:961292-961452	ACGGAAATTTACATCTTTAATATCAACTTTACCTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGATAATCTTGAAATTTTGTCATATCATT
mdr1_S0_Sub0_mip27	2	chr5:961444-961653	TCAAGAACCCTGTTATTTAATATGTCCANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGATTTTATGACTTGAAAAATGATCACAT
mdr1_S0_Sub0_mip28	2	chr5:961545-961755	ATCCAGATTGGTTTGAAAAATTCATTTACATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGGTAATGATTCGATAAAATCATCTATA
mdr1_S0_Sub0_mip29	2	chr5:961715-961882	ATATTATTATTAGATGAAGCAACATCATCACTTGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAAAATATCAAATTTGGAAGAGAAGAT
mdr1_S0_Sub0_mip3	4	chr5:958145-958352	CATGTTCTTTAATATTACACCAAACACAGANNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGAACTCACTTGTTCTAAATAAAAAATCTA
mdr1_S0_Sub0_mip30	2	chr5:961817-962026	ACCATATGGTCCAACATTTGTATCATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCAGGGTTATTAATACCACAATTTT
mdr1_S0_Sub0_mip31	3	chr5:962018-962199	TTTATGCATTTATATGATCCGCAAACATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNGCCACAGAATTGCATCTATAAAA
mdr1_S0_Sub0_mip4	2	chr5:958331-958498	AGGATTATTATCATGAAATTGTCCATCTTGNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNACATATGACACCACAAACATAAAATTAA
mdr1_S0_Sub0_mip5	2	chr5:958409-958619	TTGCAAGTTATTGTGGAGAAAAGACTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNAGGAATTGGTACGAAATTTATAACAATT
mdr1_S0_Sub0_mip6	2	chr5:958606-958819	ATTAAGCCTCTTCTATAATGGACATGGTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTGAGGCACCATTAATAATCATTATT
mdr1_S0_Sub0_mip7	2	chr5:958773-958971	ATTAGTTGAAAATAATGATGATGGAGAAACATTACNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTAGTTTCTTATGCATTCGGTTTTT
mdr1_S0_Sub0_mip8	2	chr5:958940-959143	TGTTGCTTCTAAAGCTTTTCATATATTCTGTTATATNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCTTCAATTAATTTTAGTAGTTGATTT
mdr1_S0_Sub0_mip9	2	chr5:959072-959253	AAAAATTGGAGTTGTTAGTCAAGATCCATTNNNNAGATCGGAAGAGCACACGTGACTCGCCAAGCTGAAGNNNNNNNNNNNTCATTATGATACTAGAAAAGATGTTGAA

Supplemental Table 2. Number of genotype calls discordant between MAD⁴HatTeR and DR23K by SNP.

SNP	Number of discordant / Number of comparisons (%)	Prevalence of mutant allele (mixed or mutant) by MAD ⁴ HatTeR	Prevalence of mutant allele (mixed or mutant) by DR23K
CRT C72S	0 / 56 (0%)	0 / 65 (0%)	0 / 56 (0%)
CRT M74I / N75E / K76T	1 / 56 (2%)	1 / 65 (2%)	0 / 56 (0%)
MDR1 N86Y/F	0 / 54 (0%)	0 / 64 (0%)	0 / 55 (0%)
MDR1 Y184F	13 / 59 (22%)	51 / 65 (79%)	41/59 (70%)
MDR1 S1034C	0 / 63 (0%)	0 / 65 (0%)	0 / 63 (0%)
MDR1 N1042D	0 / 63 (0%)	0 / 65 (0%)	0 / 63 (0%)
MDR1 D1246Y	2 / 61 (3%)	2 / 65 (3%)	2 / 61 (3%)
DHFR A16V	0 / 57 (0%)	0 / 65 (0%)	0 / 57 (0%)
DHFR N51I	2 / 64 (3%)	64 / 65 (99%)	63 / 64 (98%)
DHFR C59R	8 / 64 (13%)	64 / 65 (99%)	61 / 64 (95%)
DHFR S108N	13 / 66 (20%)	67 / 67 (100%)	66 / 66 (100%)
DHFR I164L	23 / 66 (35%)	31 / 67 (46%)	8 / 66 (12%)
DHPS I431V	0 / 59 (0%)	0 / 65 (0%)	0 / 59 (0%)
DHPS S436A	1 / 58 (2%)	1 / 65 (2%)	0 / 58 (0%)
DHPS S436F	0 / 58 (0%)	0 / 65 (0%)	0 / 58 (0%)
DHPS A437G	19 / 58 (33%)	63 / 65 (97%)	54 / 58 (93%)
DHPS K540E	10 / 61 (16%)	66 / 66 (100%)	58 / 61 (95%)
DHPS A581G	2 / 64 (3%)	4 / 66 (6%)	2 / 64 (3%)
DHPS A613S/T	0 / 63 (0%)	0 / 65 (0%)	0 / 63 (0%)
K13 P441A	0 / 50 (0%)	1 / 65 (2%)	1 / 50 (2%)
K13 C469Y	9 / 57 (16%)	26 / 66 (40%)	20 / 57 (35%)
K13 M476I	0 / 62 (0%)	0 / 66 (0%)	0 / 62 (0%)
K13 Y493H	0 / 56 (0%)	0 / 66 (0%)	0 / 56 (0%)
K13 R539T	0 / 61 (0%)	0 / 65 (0%)	0 / 61 (0%)

K13 I543R	0 / 61 (0%)	0 / 65 (0%)	0 / 61 (0%)
K13 R561H	0 / 58 (0%)	0 / 66 (0%)	0 / 58 (0%)
K13 A578S	2 / 59 (3%)	4 / 66 (6%)	3 / 59 (5%)
K13 C580Y	0 / 63 (0%)	0 / 66 (0%)	0 / 63 (0%)
K13 A675V	8 / 64 (13%)	18 / 65 (28%)	15 / 64 (23%)

Supplemental Figure 1. Genomic regions of drug resistance genes targeted by DR23K and MAD⁴HatTeR. The genomic region is indicated in gray, regions targeted by DR23K in green, and regions targeted by MAD⁴HatTeR in blue. Known SNPs of interest are labeled in cyan.



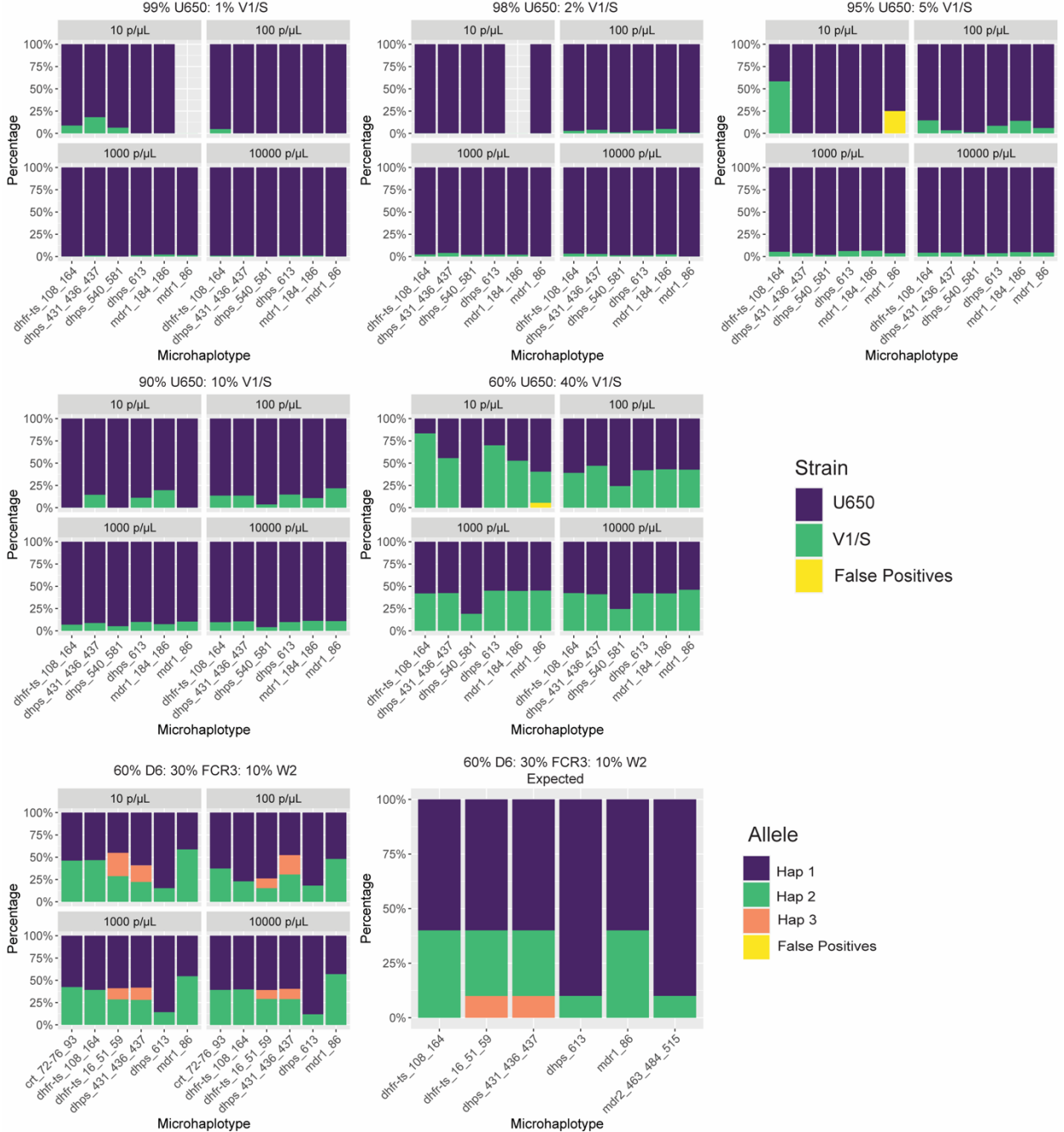
Supplemental Figure 2. Percentage of reads detecting variable drug resistance markers in DBS composed of mixed laboratory strains at varying proportions and parasite densities using MAD⁴HatTeR. Absent bars indicate missing data (e.g. no genotypes were called). For the triple strain control, the expected percentages of the reference and alternative alleles are shown in the right panel for ease of comparison to the data on the left.

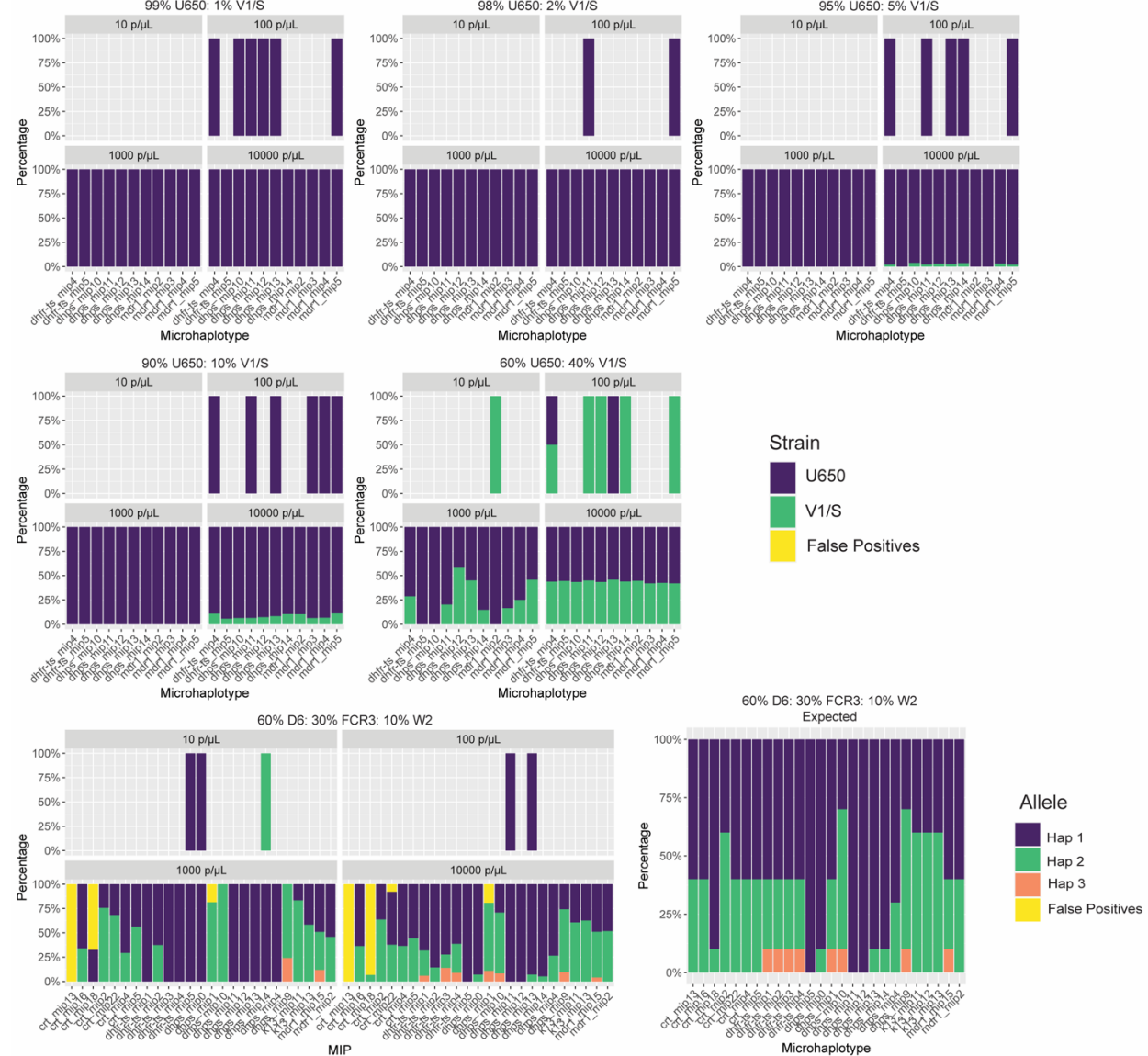


Supplemental Figure 3. Percentage of UMIs detecting variable drug resistance markers in DBS composed of mixed laboratory strains at varying proportions and parasite densities using DR23K. Absent bars indicate missing data (e.g. no genotypes were called). For the triple strain control, the expected percentages of the reference and alternative alleles are shown in the right panel for ease of comparison to the data on the left.

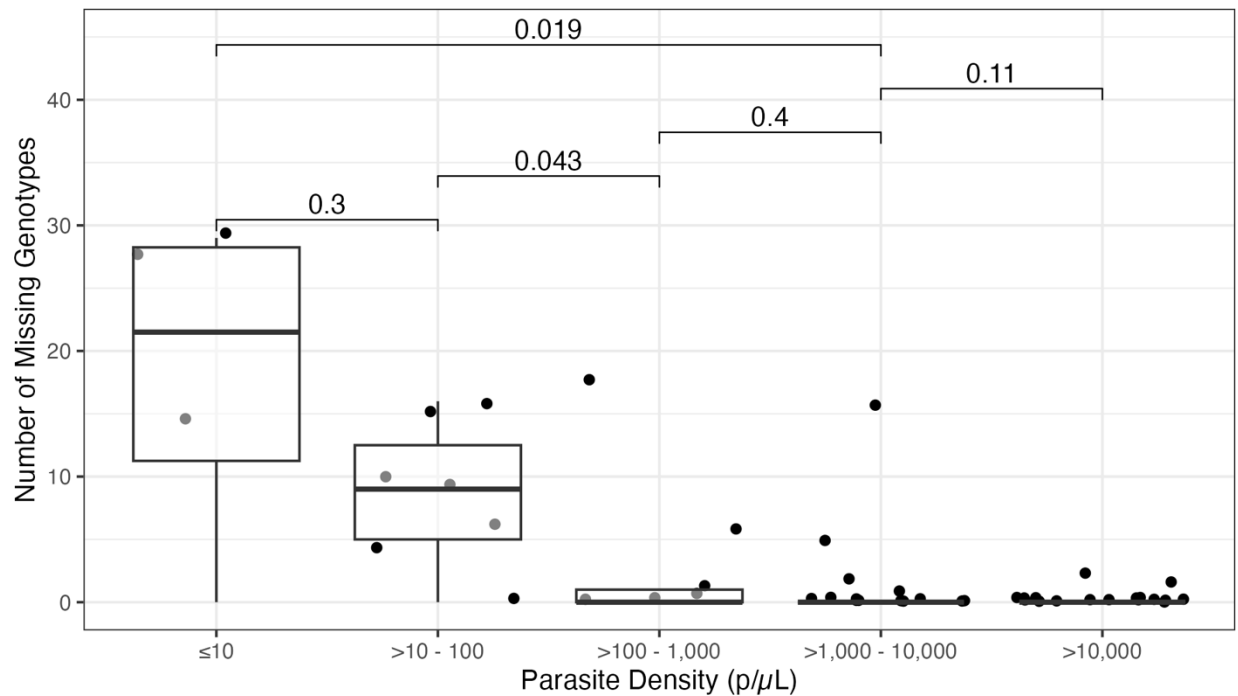


Supplemental Figure 4. Percentage of reads detecting variable microhaplotypes in DBS composed of mixed laboratory strains at varying proportions and parasite densities using MAD⁴HatTeR. Absent bars indicate missing data (e.g. no genotypes were called). For the triple strain control, the expected percentages of the reference and alternative alleles are shown in the right panel for ease of comparison to the data on the left.

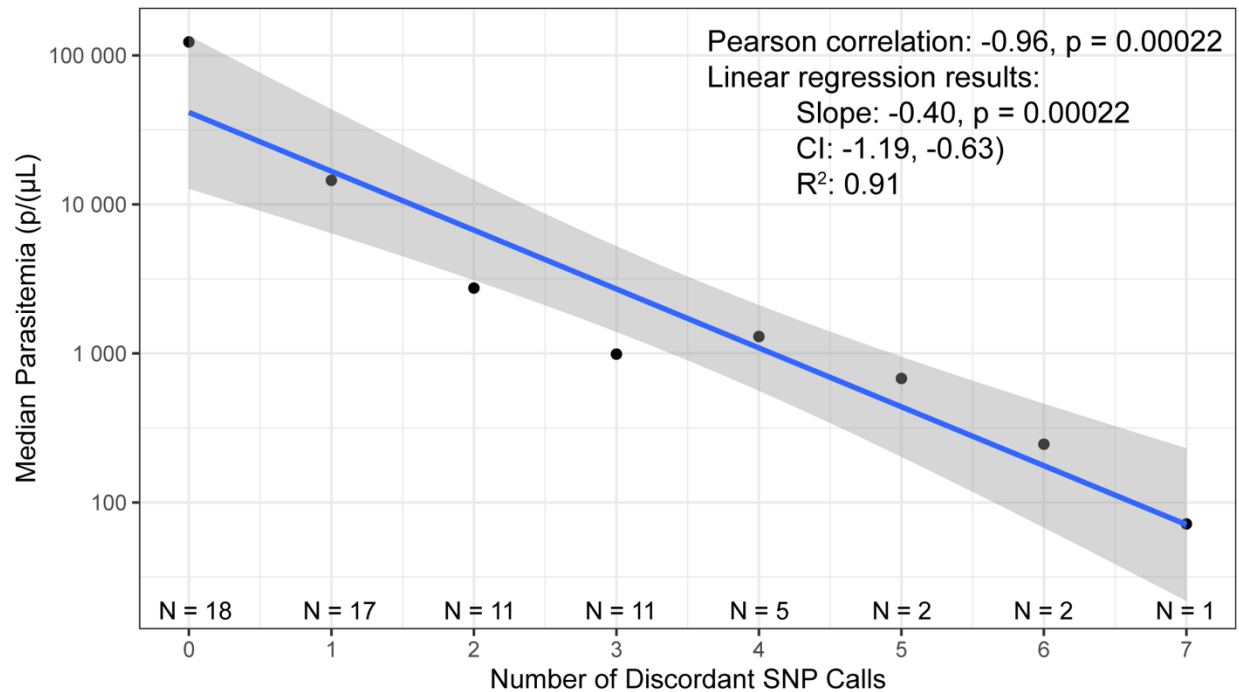




Supplemental Figure 6. Relationship between varATS qPCR-determined parasite densities and number of SNPs without successful genotype calls by DR23K. Each dot represents a field sample. Boxes show the first to third quartiles, and whiskers extend to the largest values no more than 1.5X the interquartile ranges. Statistical differences evaluated using pairwise Wilcoxon tests implemented in ggpubr:stat_compare_means function.



Supplemental Figure 7. The relationship between the number of genotype calls discordant between MAD⁴HatTeR and DR23K and varATS qPCR-determined parasite densities in field samples. A linear model of the log median parasite density as a function of the number of discordant SNP calls for a sample was fit to the data. A summary of the Pearson correlation and linear regression results are provided. The number of field samples contributing to the mean parasitemia for each category is indicated above the x-axis.



Supplemental methods

MAD⁴HatTeR sample pooling

The purpose is to combine samples to be run in Illumina sequencer as a pool.

A sample sheet was made and doublechecked to make sure that the sample names and indexes were not duplicated. The plates were briefly spun down and placed on the magnetic stand to separate beads. The samples were mixed into a single 1.5 mL microcentrifuge tube depending on the parasite concentrations as below.

- 30 µL for <10 parasites/µL
- 20 µL for 10 to <100 parasites/µL
- 15 µL for 100 to <1000 parasites/µL
- 10 µL for 1000 to <10000 parasites/µL
- 6 µL for 10000 to <100000 parasites/µL
- 3 µL for 100000 parasites/µL and above

After pooling, 1X volume of beads were added to the pool, vortexed and briefly spun down to collect liquids. The mixture was incubated for 5 minutes at room temperature, placed on a microcentrifuge tube magnetic stand, and incubated for 3 minutes or until the solution was clear. The supernatant was removed, the tube briefly spun down, placed back on the magnetic stand to remove the rest of the supernatant. 1.5 mL of 70% ethanol was added to the beads, and the tube rotated until the beads migrated to the opposite wall. After moving to the opposite wall, the ethanol supernatant was removed, the tube briefly spun down, placed back in the magnetic stand and the rest of the supernatant removed. The beads were left to dry at room temperature, until they looked matte and not shiny, but avoided cracking. The beads were resuspended with 43 µL TE buffer, incubated for 2 minutes and then put back on the magnetic stand for 3 minutes or until the liquid was clear. The TE was transferred to a clean, labeled tube ready for assessing the library purity with capillary electrophoresis.

MIP capture, amplification, and sequencing

Oligonucleotides were synthesized as 200 nmole µL trimers (Integrated DNA Technologies) with equimolar hand-mix option for random bases. The oligonucleotides were pooled as indicated in Supplemental Table 1 to create the DR23K panel. Pools were 5' phosphorylated using 1 µl (10 units) T4 polynucleotide 7 kinase (NEB) for every

nmole of probe, in 1X T4 DNA ligase buffer (NEB). Phosphorylation reactions were split into 50 µl aliquots, incubated in a thermocycler at 37°C for 45 min, followed by heat inactivation at 65°C for 20 min. Split reactions were pooled together for homogeneity, re-aliquoted, and kept at -20°C. Probes were diluted 1:8 in TE buffer (10 mM Tris, 1 mM EDTA, pH 8) to bring them to 1 µM working solution. Capture reactions were carried out as follows. 10 µl capture reactions for each sample containing Ampligase buffer (1X), Phusion DNA polymerase (0.0008 units/µl), Ampligase (0.04 units/µl), pooled MIPs (40 nM), dNTP (4 µM), and template DNA (5µl) were incubated in a preheated thermocycler at 95°C for 10 min, 60°C for 1h, and then 4°C. Next, 2 µl of exonuclease mix containing 1X Ampligase buffer, 10 units exonuclease I, and 50 units exonuclease III were added to reactions with incubations at 37°C for 1 h, 95°C for 2 min, and then 4°C. The entire capture reaction (12 µl) was amplified in a 25 µl PCR reaction containing: 1X Phusion polymerase buffer, 1X Macromolecular Crowding (MMC) solution, 200 nM each dNTP, 0.02 units/µl Phusion DNA polymerase, and 500 nM each forward and reverse primer. PCR was performed using a preheated thermocycler at 98°C for 30 s, 22 cycles (98°C 10 s, 63°C 30 s, 68°C 30 s), 68°C for 2 min, and then 4°C. 50 ml 5X MMC was prepared by mixing the following components in water and filter sterilizing using a 0.2 µ nylon syringe filter: 3.75 g Ficoll 70 (GE Healthcare), 1.25 g Ficoll 400 (Sigma), and 0.125 g polyvinylpyrrolidone (Sigma). 5 µl of each capture was run on an agarose gel to assess reaction performance and inform sample pooling. Specifically, 5 µl of captures with a clear band on the gel and 10 µl of captures without a band were combined in a single tube, vortexed briefly, and centrifuged for 10 minutes. 90% of the supernatant was then transferred to a new tube, and cleaned using Ampure XP beads (Beckman Coulter) at 1.2x bead:DNA ratios using the manufacturer's protocol. Beads were eluted in 43 µl of TE buffer. 40 µl of the eluted sample was then run on a 1.5% agarose gel, and the band observed at ~500 bp was excised and underwent gel extraction using the Monarch DNA extraction kit (NEB). Libraries were then sequenced on an Illumina MiSeq instrument using 150 bp paired-end sequencing with dual indexing using Mid-output Kit v2.