

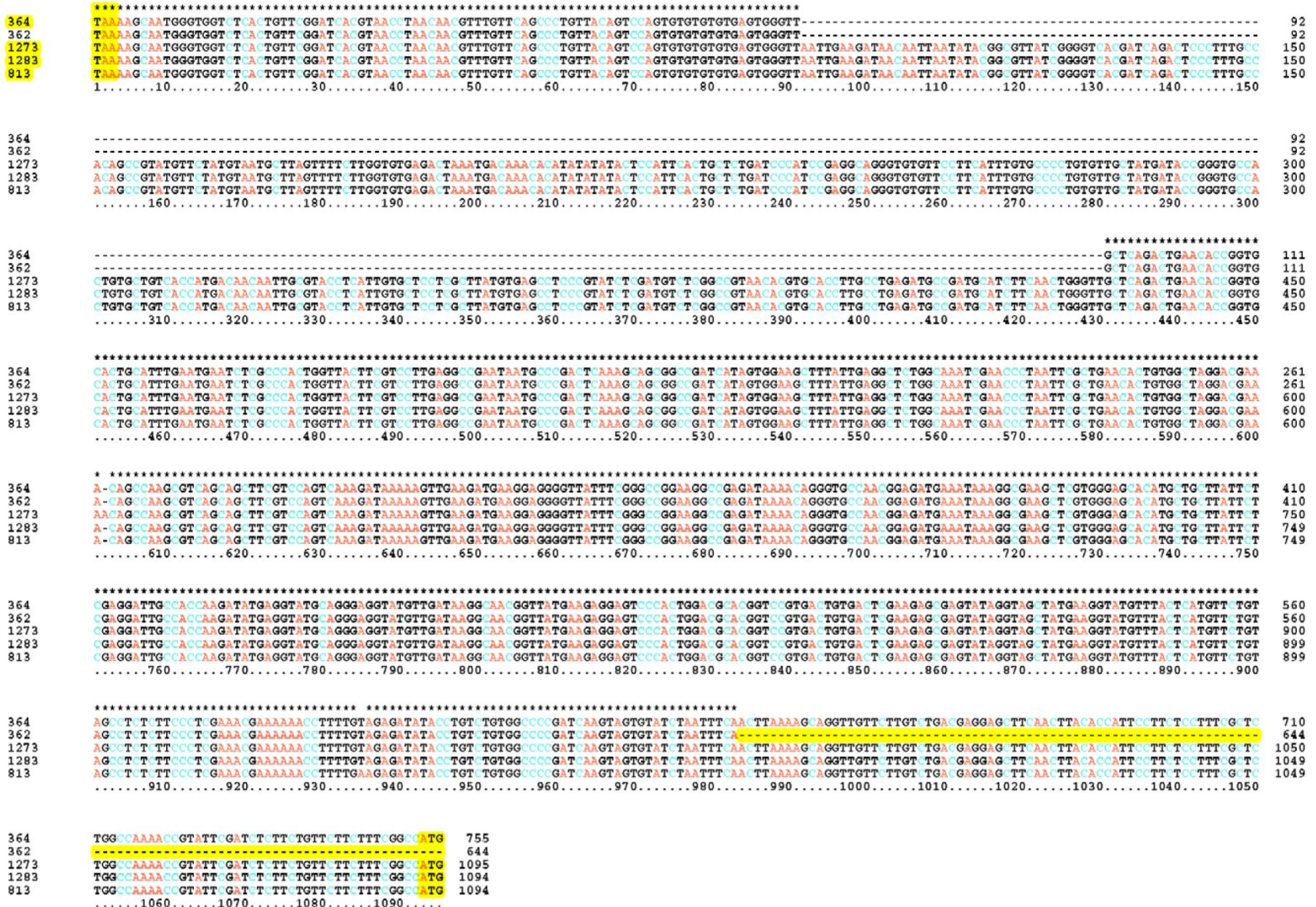


# Figure S3A, continued

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UHOR_10021-818 ----- 722
UHOR_10021-820 ----- 722
UHOR_10021-822 ----- 728
UHOR_10021-815 ----- 728
UHOR_10021-811 ----- 703
UHOR_10021-805 ----- 702
UHOR_10021-813 GCAATGGGTGGTTCACCTGTTGGGATCACGTAACTAACCAACGTTTGTTCAGCCCTGTTACAGTCCAGTGTGTGTGAGTGGGTTAATTGAAGATAA 811
UHOR_10021-1273 GCAATGGGTGGTTCACCTGTTGGGATCACGTAACTAACCAACGTTTGTTCAGCCCTGTTACAGTCCAGTGTGTGTGAGTGGGTTAATTGAAGATAA 660
UHOR_10021-1283 GCAATGGGTGGTTCACCTGTTGGGATCACGTAACTAACCAACGTTTGTTCAGCCCTGTTACAGTCCAGTGTGTGTGAGTGGGTTAATTGAAGATAA 661
UHOR_10021-362 GCAATGGGTGGTTCACCTGTTGGGATCACGTAACTAACCAACGTTTGTTCAGCCCTGTTACAGTCCAGTGTGTGTGAGTGGGTTGTCAGACTGAAA 772
UHOR_10021-364 GCAATGGGTGGTTCACCTGTTGGGATCACGTAACTAACCAACGTTTGTTCAGCCCTGTTACAGTCCAGTGTGTGTGAGTGGGTTGTCAGACTGAAA 773
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....
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# Figure S3B

## UHOR\_10021 - UHOR\_10022 intergenic region



## Figure S3C

### UHOR\_10021 - *Uhavr1* locus region in virulent isolates

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                                983
Uh364brk CAAGTAGTGTATCTAATTTCA-----
Uh822    CAAGTAGTGTATCTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTTGGCGTCATTTCGTCAGAGNTTGGGGTTGAGGTGTCTTTTGTTGATGATGGTAG
Uh811    CAAGTAGTGTATCTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTTGGCGTCATTTCGTCAGAGGTTGGGGTTGAGGTGTCTTTTGTTGATGATGGTAG
Uh818    CAAGTAGTGTATCTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTTGGCGTCATTTCGTCAGAGGTTGGGGTTGAGGTGTCTTTTGTTGATGATGGTAG
Uh815    CAAGTAGTGTATCTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTTGGCGTCATTTCGTCAGAGGTTGGGGTTGAGGTGTCTTTTGTTGATGATGGTAG
Uh805    CAAGTAGTGTATCTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTTGGCGTCATTTCGTCAGAGGTTGGGGTTGAGGTGTCTTTTGTTGATGATGGTAG
Uh362    CAAGTAGTGTATCTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTTGGCGTCATTTCGTCAGAGGTTGGGGTTGAGGTGTCTTTTGTTGATGATGGTAG
Uh820    CAAGTAGTGTATGTAATTTTCAGTTGAAGTCATTTCGTCAGCGTCTNNGNGTCATTTCGTCAGAGGTTGGGGNTGAGGTGTCTTTTGTTGATGATGGTAG
*****

Uh364brk -----
Uh822    GAGAGAGAGAGAGC-----TAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
Uh811    GAGAGAGAGAGAGC-----TAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
Uh818    GAGAGAGAGAGAGC-----TAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
Uh815    GAGAGAGAGAGAGCGAGAGAGAGCTAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
Uh805    GAGAGAGAGAGAGCGAGAGAGAGCTAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
Uh362    GAGAGAGAGAGAGCGAGAGAGAGCTAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
Uh820    GAGAGAGAGAGAGCGAGAGAGAGCTAGGAGTCTATATATACAAAAGTAGAGCGGCGGACTGCCGAGCATAACAAAGCATTTCGCTTGAGTAGGTTGTGA
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Comparison of *Uhavr1* locus sequences among seven virulent isolates, focusing on the region after the 'breakpoint' where Uh362 (grey) diverges from sequences in avirulent isolate Uh364 (brk, highlighted in yellow). The 10-bp repeat unit is in red. The base position is as in panel B.

Figure S3D

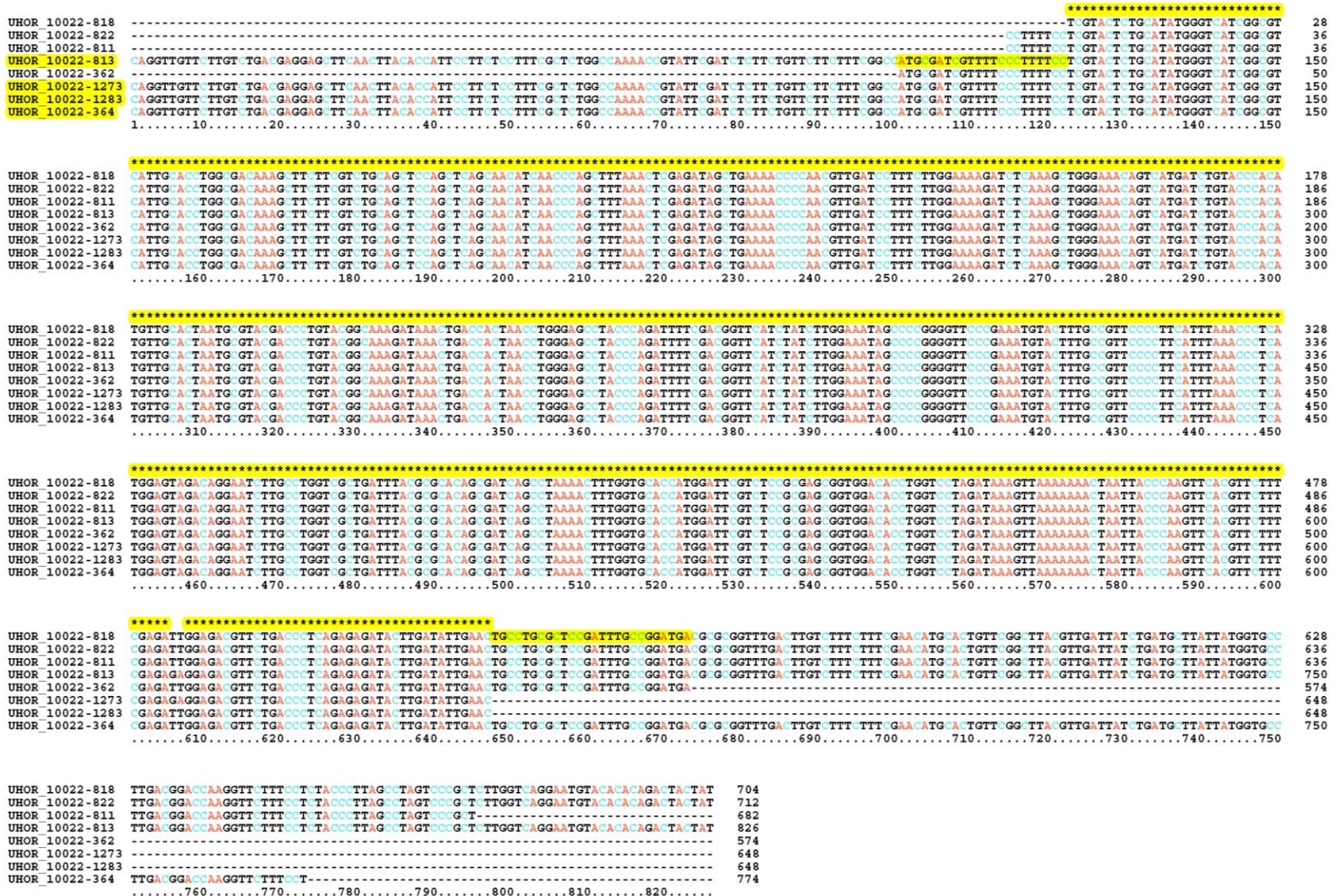


Figure S3E

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UHOR_08130-364 TGG TTGTTTACAGATGC AAAAT TTA TCACTGTGAA CAGACT TTATA TCG AGTTGTCCATGTAT TCTCCGATTGACCCCTATAG TAGGAGAAGATG TT TGACCT GAAAGTAGGATCGTCTCTCAGCATTTT TCCTTT TT 150
UHOR_08130-362 TGG TTGTTTACAGATGC AAAAT TTA TCACTGTGAA CAGACT TTATA TCG AGTTGTCCATGTAT TCTCCGATTGACCCCTATAG TAGGAGAAGATG TT TGACCT GAAAGTAGGATCGTCTCTCAGCATTTT TCCTTT TT 150
UHOR_08130-811 -----ACAGATGC AAAAT TTA TCACTGTGAA CAGACT TTATA TCG AGTTGTCCATGTAT TCTCCGATTGACCCCTATAG TAGGAGAAGATG TT TGACCT GAAAGTAGGATCGTCTCTCAGCATTTT TCCTTT TT 140
UHOR_08130-818 -----TTA TCACTGTGAA CAGACT TTATA TCG AGTTGTCCATGTAT TCTCCGATTGACCCCTATAG TAGGAGAAGATG TT TGACCT GAAAGTAGGATCGTCTCTCAGCATTTT TCCTTT TT 125
UHOR_08130-822 -----TTA TCACTGTGAA CAGACT TTATA TCG AGTTGTCCATGTAT TCTCCGATTGACCCCTATAG TAGGAGAAGATG TT TGACCT GAAAGTAGGATCGTCTCTCAGCATTTT TCCTTT TT 125
UHOR_08130-813 -----TTA TCACTGTGAA CAGACT TTATA TCG AGTTGTCCATGTAT TCTCCGATTGACCCCTATAG TAGGAGAAGATG TT TGACCT GAAAGTAGGATCGTCTCTCAGCATTTT TCCTTT TT 125
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

*****
UHOR_08130-364 CCTATAAAGTCCGAGAT GTTGAAGGTCAGGTTATACCAACCGAGGGACATCTGCGCAAGATCACAGTCCAGTGCCCTGAAACC TTCTTTGATCAG TTTTAAAGGATCAGAAC TGGATCTCGGT TTGATTTATGCCATCAC 300
UHOR_08130-362 CCTATAAAGTCCGAGAT GTTGAAGGTCAGGTTATACCAACCGAGGGACATCTGCGCAAGATCACAGTCCAGTGCCCTGAAACC TTCTTTGATCAG TTTTAAAGGATCAGAAC TGGATCTCGGT TTGATTTATGCCATCAC 300
UHOR_08130-811 CCTATAAAGTCCGAGAT GTTGAAGGTCAGGTTATACCAACCGAGGGACATCTGCGCAAGATCACAGTCCAGTGCCCTGAAACC TTCTTTGATCAG TTTTAAAGGATCAGAAC TGGATCTCGGT TTGATTTATGCCATCAC 290
UHOR_08130-818 CCTATAAAGTCCGAGAT GTTGAAGGTCAGGTTATACCAACCGAGGGACATCTGCGCAAGATCACAGTCCAGTGCCCTGAAACC TTCTTTGATCAG TTTTAAAGGATCAGAAC TGGATCTCGGT TTGATTTATGCCATCAC 275
UHOR_08130-822 CCTATAAAGTCCGAGAT GTTGAAGGTCAGGTTATACCAACCGAGGGACATCTGCGCAAGATCACAGTCCAGTGCCCTGAAACC TTCTTTGATCAG TTTTAAAGGATCAGAAC TGGATCTCGGT TTGATTTATGCCATCAC 275
UHOR_08130-813 CCTATAAAGTCCGAGAT GTTGAAGGTCAGGTTATACCAACCGAGGGACATCTGCGCAAGATCACAGTCCAGTGCCCTGAAACC TTCTTTGATCAG TTTTAAAGGATCAGAAC TGGATCTCGGT TTGATTTATGCCATCAC 275
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

*****
UHOR_08130-364 GAAATTGATCAGCAATGTCCAAGACCCACTG TGACACAGTATAT TAT GAAATGGACAAGACTTCAACCTCAAAATTGT TACCTTGGCA GGAATCCCAAGATCTGT CAGCACAT TAGCGTTAAGCGGTTTGCCCCAGATT 450
UHOR_08130-362 GAAATTGATCAGCAATGTCCAAGACCCACTG TGACACAGTATAT TAT GAAATGGACAAGACTTCAACCTCAAAATTGT TACCTTGGCA GGAATCCCAAGATCTGT CAGCACAT TAGCGTTAAGCGGTTTGCCCCAGATT 450
UHOR_08130-811 GAAATTGATCAGCAATGTCCAAGACCCACTG TGACACAGTATAT TAT GAAATGGACAAGACTTCAACCTCAAAATTGT TACCTTGGCA GGAATCCCAAGATCTGT CAGCACAT TAGCGTTAAGCGGTTTGCCCCAGATT 440
UHOR_08130-818 GAAATTGATCAGCAATGTCCAAGACCCACTG TGACACAGTATAT TAT GAAATGGACAAGACTTCAACCTCAAAATTGT TACCTTGGCA GGAATCCCAAGATCTGT CAGCACAT TAGCGTTAAGCGGTTTGCCCCAGATT 425
UHOR_08130-822 GAAATTGATCAGCAATGTCCAAGACCCACTG TGACACAGTATAT TAT GAAATGGACAAGACTTCAACCTCAAAATTGT TACCTTGGCA GGAATCCCAAGATCTGT CAGCACAT TAGCGTTAAGCGGTTTGCCCCAGATT 425
UHOR_08130-813 GAAATTGATCAGCAATGTCCAAGACCCACTG TGACACAGTATAT TAT GAAATGGACAAGACTTCAACCTCAAAATTGT TACCTTGGCA GGAATCCCAAGATCTGT CAGCACAT TAGCGTTAAGCGGTTTGCCCCAGATT 425
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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UHOR_08130-364 AGATTGG TGTGATATA TCGGAAACCGCAAGTTTACAGATGGAAAAACGAGAGGGCTGT TAGAATGAGG TTGAT GAGGAAAGGACAGAGTTTGAGGAATTAT TGG TGTGAAAGGCAAAATGACGAAAGGGATAAA 600
UHOR_08130-362 AGATTGG TGTGATATA TCGGAAACCGCAAGTTTACAGATGGAAAAACGAGAGGGCTGT TAGAATGAGG TTGAT GAGGAAAGGACAGAGTTTGAGGAATTAT TGG TGTGAAAGGCAAAATGACGAAAGGGATAAA 600
UHOR_08130-811 AGATTGG TGTGATATA TCGGAAACCGCAAGTTTACAGATGGAAAAACGAGAGGGCTGT TAGAATGAGG TTGAT GAGGAAAGGACAGAGTTTGAGGAATTAT TGG TGTGAAAGGCAAAATGACGAAAGGGATAAA 590
UHOR_08130-818 AGATTGG TGTGATATA TCGGAAACCGCAAGTTTACAGATGGAAAAACGAGAGGGCTGT TAGAATGAGG TTGAT GAGGAAAGGACAGAGTTTGAGGAATTAT TGG TGTGAAAGGCAAAATGACGAAAGGGATAAA 575
UHOR_08130-822 AGATTGG TGTGATATA TCGGAAACCGCAAGTTTACAGATGGAAAAACGAGAGGGCTGT TAGAATGAGG TTGAT GAGGAAAGGACAGAGTTTGAGGAATTAT TGG TGTGAAAGGCAAAATGACGAAAGGGATAAA 575
UHOR_08130-813 AGATTGG TGTGATATA TCGGAAACCGCAAGTTTACAGATGGAAAAACGAGAGGGCTGT TAGAATGAGG TTGAT GAGGAAAGGACAGAGTTTGAGGAATTAT TGG TGTGAAAGGCAAAATGACGAAAGGGATAAA 575
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

*****
UHOR_08130-364 ATGGGAAGCCGTACAGACATT GATCAG TGC AAGG GAT TCGAGTTTGGGTGTAATTGAAAGGGCTTTG ATATAT ACCCGTGAAGGAAAGTGAG GGGT CAGTG CATTGCAACCCGGG TGGGGTCTTACTTCACAGTTGATAGTAA 750
UHOR_08130-362 ATGGGAAGCCGTACAGACATT GATCAG TGC AAGG GAT TCGAGTTTGGGTGTAATTGAAAGGGCTTTG ATATAT ACCCGTGAAGGAAAGTGAG GGGT CAGTG CATTGCAACCCGGG TGGGGTCTTACTTCACAGTTGATAGTAA 750
UHOR_08130-811 ATGGGAAGCCGTACAGACATT GATCAG TGC AAGG GAT TCGAGTTTGGGTGTAATTGAAAGGGCTTTG ATATAT ACCCGTGAAGGAAAGTGAG GGGT CAGTG CATTGCAACCCGGG TGGGGTCTTACTTCACAGTTGATAGTAA 740
UHOR_08130-818 ATGGGAAGCCGTACAGACATT GATCAG TGC AAGG GAT TCGAGTTTGGGTGTAATTGAAAGGGCTTTG ATATAT ACCCGTGAAGGAAAGTGAG GGGT CAGTG CATTGCAACCCGGG TGGGGTCTTACTTCACAGTTGATAGTAA 694
UHOR_08130-822 ATGGGAAGCCGTACAGACATT GATCAG TGC AAGG GAT TCGAGTTTGGGTGTAATTGAAAGGGCTTTG ATATAT ACCCGTGAAGGAAAGTGAG GGGT CAGTG CATTGCAACCCGGG TGGGGTCTTACTTCACAGTTGATAGTAA 725
UHOR_08130-813 ATGGGAAGCCGTACAGACATT GATCAG TGC AAGG GAT TCGAGTTTGGGTGTAATTGAAAGGGCTTTG ATATAT ACCCGTGAAGGAAAGTGAG GGGT CAGTG A .....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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UHOR_08130-364 TGG TCTGATGAAAAGCAATCAATTACAACATTATG TTGACCTTTA 797
UHOR_08130-362 TGG TCTGATGAAAAGCAATCAATTACAACATTATG TTGACCTTTT 797
UHOR_08130-811 TG----- 743
UHOR_08130-818 ----- 694
UHOR_08130-822 T----- 727
UHOR_08130-813 ----- 686
.....760.....770.....780.....790.....

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Figure S3F

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UHOR_08132-811 -----GTTTGCATTGCCAGTAGAAACTCCTTGGACGTTTATGTCGGAAGGGCAACCCGGTGGAAATCGGTATGATGTAATAAACTCGTGTGTAGGTTTACCCGAGG TGGATTGCTTGTGGGTCACTCTCGA 145
UHOR_08132-818 AGAGGGTTTGCATTGCCAGTAGAAACTCCTTGGACGTTTATGTCGGAAGGGCAACCCGGTGGAAATCGGTATGATGTAATAAACTCGTGTGTAGGTTTACCCGAGG TGGATTGCTTGTGGGTCACTCTCGA 150
UHOR_08132-364 -----CCCGGTGGAAATCGGTATGATGTAATAAACTCGTGTGTAGGTTTACCCGAGG TGGATTGCTTGTGGGTCACTCTCGA 91
UHOR_08132-822 -GAGGGTTTGCATTGCCAGTAGAAACTCCTTGGACGTTTATGTCGGAAGGGCAACCCGGTGGAAATCGGTATGATGTAATAAACTCGTGTGTAGGTTTACCCGAGG TGGATTGCTTGTGGGTCACTCTCGA 149
UHOR_08132-362 -----CCCGGTGGAAATCGGTATGATGTAATAAACTCGTGTGTAGGTTTACCCGAGG TGGATTGCTTGTGGGTCACTCTCGA 91
UHOR_08132-813 --AGGGTTTGCATTGCCAGTAGAAACTCCTTGGACGTTTATGTCGGAAGGGCAACCCGGTGGAAATCGGTATGATGTAATAAACTCGTGTGTAGGTTTACCCGAGG TGGATTGCTTGTGGGTCACTCTCGA 148
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

*****
UHOR_08132-811 TCAATGCCATGGCCACAACTACTTTACGGCGTGTGACCTTAACCTCTTATTTTGTCTGTTTTGCAGTACTGGGAGTGTGCCAATGATCCGTGGGATCCAGAGAGT TTTTGTGATCATGACCCC 295
UHOR_08132-818 TCAATGCCATGGCCACAACTACTTTACGGCGTGTGACCTTAACCTCTTATTTTGTCTGTTTTGCAGTACTGGGAGTGTGCCAATGATCCGTGGGATCCAGAGAGT TTTTGTGATCATGACCCC 300
UHOR_08132-364 TCAATGCCATGGCCACAACTACTTTACGGCGTGTGACCTTAACCTCTTATTTTGTCTGTTTTGCAGTACTGGGAGTGTGCCAATGATCCGTGGGATCCAGAGAGT TTTTGTGATCATGACCCC 241
UHOR_08132-822 TCAATGCCATGGCCACAACTACTTTACGGCGTGTGACCTTAACCTCTTATTTTGTCTGTTTTGCAGTACTGGGAGTGTGCCAATGATCCGTGGGATCCAGAGAGT TTTTGTGATCATGACCCC 299
UHOR_08132-362 TCAATGCCATGGCCACAACTACTTTACGGCGTGTGACCTTAACCTCTTATTTTGTCTGTTTTGCAGTACTGGGAGTGTGCCAATGATCCGTGGGATCCAGAGAGT TTTTGTGATCATGACCCC 241
UHOR_08132-813 TCAATGCCATGGCCACAACTACTTTACGGCGTGTGACCTTAACCTCTTATTTTGTCTGTTTTGCAGTACTGGGAGTGTGCCAATGATCCGTGGGATCCAGAGAGT TTTTGTGATCATGACCCC 298
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

*****
UHOR_08132-811 TTTGTCAA GAAC TAAG TGTGTGG TTCTTACACTTAGAATGAGTTGGATTGACCTTA GAACATGCAATTCCGAAGTCACCAAGT TTTACCGATCATTTTTTCAAGAACGGTCAAGATTGGAAATCCAGAGTCTTAC 445
UHOR_08132-818 TTTGTCAA GAAC TAAG TGTGTGG TTCTTACACTTAGAATGAGTTGGATTGACCTTA GAACATGCAATTCCGAAGTCACCAAGT TTTACCGATCATTTTTTCAAGAACGGTCAAGATTGGAAATCCAGAGTCTTAC 450
UHOR_08132-364 TTTGTCAA GAAC TAAG TGTGTGG TTCTTACACTTAGAATGAGTTGGATTGACCTTA GAACATGCAATTCCGAAGTCACCAAGT TTTACCGATCATTTTTTCAAGAACGGTCAAGATTGGAAATCCAGAGTCTTAC 391
UHOR_08132-822 TTTGTCAA GAAC TAAG TGTGTGG TTCTTACACTTAGAATGAGTTGGATTGACCTTA GAACATGCAATTCCGAAGTCACCAAGT TTTACCGATCATTTTTTCAAGAACGGTCAAGATTGGAAATCCAGAGTCTTAC 449
UHOR_08132-362 TTTGTCAA GAAC TAAG TGTGTGG TTCTTACACTTAGAATGAGTTGGATTGACCTTA GAACATGCAATTCCGAAGTCACCAAGT TTTACCGATCATTTTTTCAAGAACGGTCAAGATTGGAAATCCAGAGTCTTAC 391
UHOR_08132-813 TTTGTCAA GAAC TAAG TGTGTGG TTCTTACACTTAGAATGAGTTGGATTGACCTTA GAACATGCAATTCCGAAGTCACCAAGT TTTACCGATCATTTTTTCAAGAACGGTCAAGATTGGAAATCCAGAGTCTTAC 448
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

*****
UHOR_08132-811 CTGGGAAACACCCCGTTTCCAGACTCATATGGTGTATCGGTGTTCCACCCAAAATACAGGTGAGAAATCATTTGTGCCAAAAGTGGTTGATGAAACATGAAAGGGAAAGAACGGAGTGTGTTATAACTTGAGAGGA 595
UHOR_08132-818 CTGGGAAACACCCCGTTTCCAGACTCATATGGTGTATCGGTGTTCCACCCAAAATACAGGTGAGAAATCATTTGTGCCAAAAGTGGTTGATGAAACATGAAAGGGAAAGAACGGAGTGTGTTATAACTTGAGAGGA 600
UHOR_08132-364 CTGGGAAACACCCCGTTTCCAGACTCATATGGTGTATCGGTGTTCCACCCAAAATACAGGTGAGAAATCATTTGTGCCAAAAGTGGTTGATGAAACATGAAAGGGAAAGAACGGAGTGTGTTATAACTTGAGAGGA 541
UHOR_08132-822 CTGGGAAACACCCCGTTTCCAGACTCATATGGTGTATCGGTGTTCCACCCAAAATACAGGTGAGAAATCATTTGTGCCAAAAGTGGTTGATGAAACATGAAAGGGAAAGAACGGAGTGTGTTATAACTTGAGAGGA 599
UHOR_08132-362 CTGGGAAACACCCCGTTTCCAGACTCATATGGTGTATCGGTGTTCCACCCAAAATACAGGTGAGAAATCATTTGTGCCAAAAGTGGTTGATGAAACATGAAAGGGAAAGAACGGAGTGTGTTATAACTTGAGAGGA 541
UHOR_08132-813 CTGGGAAACACCCCGTTTCCAGACTCATATGGTGTATCGGTGTTCCACCCAAAATACAGGTGAGAAATCATTTGTGCCAAAAGTGGTTGATGAAACATGAAAGGGAAAGAACGGAGTGTGTTATAACTTGAGAGGA 598
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

*****
UHOR_08132-811 AATGAGAGCTGAGTTTGTGGGGGTGTGGTGAAGAGCCATGAGCAGTGAATGTGTGGAGCGAGTGGAAATGTGATTGAAACGAGGTGAGGAGAGGTACCCGATTGATAGATTTACAGGAGTCATACATCTGCAACCCGTT 745
UHOR_08132-818 AATGAGAGCTGAGTTTGTGGGGGTGTGGTGAAGAGCCATGAGCAGTGAATGTGTGGAGCGAGTGGAAATGTGATTGAAACGAGGTGAGGAGAGGTACCCGATTGATAGATTTACAGGAGTCATACATCTGCAACCCGTT 750
UHOR_08132-364 AATGAGAGCTGAGTTTGTGGGGGTGTGGTGAAGAGCCATGAGCAGTGAATGTGTGGAGCGAGTGGAAATGTGATTGAAACGAGGTGAGGAGAGGTACCCGATTGATAGATTTACAGGAGTCATACATCTGCAACCCGTT 691
UHOR_08132-822 AATGAGAGCTGAGTTTGTGGGGGTGTGGTGAAGAGCCATGAGCAGTGAATGTGTGGAGCGAGTGGAAATGTGATTGAAACGAGGTGAGGAGAGGTACCCGATTGATAGATTTACAGGAGTCATACATCTGCAACCCGTT 749
UHOR_08132-362 AATGAGAGCTGAGTTTGTGGGGGTGTGGTGAAGAGCCATGAGCAGTGAATGTGTGGAGCGAGTGGAAATGTGATTGAAACGAGGTGAGGAGAGGTACCCGATTGATAGATTTACAGGAGTCATACATCTGCAACCCGTT 691
UHOR_08132-813 AATGAGAGCTGAGTTTGTGGGGGTGTGGTGAAGAGCCATGAGCAGTGAATGTGTGGAGCGAGTGGAAATGTGATTGAAACGAGGTGAGGAGAGGTACCCGATTGATAGATTTACAGGAGTCATACATCTGCAACCCGTT 748
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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UHOR_08132-811 CCAGGCCCGTACAGGACCGTGGGACTGTTGGATGAGTGACAGACTTGTATGATGAGAGCGGTTTATTATGTGGAGGGCTATGCTGTACCGACTTGTATCA----- 851
UHOR_08132-818 CCAGGCCCGTACAGGACCGTGGGACTGTTGGATGAGTGACAGACTTGTATGATGAGAGCGGTTTATTATGTGGAGGGCTATGCTGTACCGACTTGTATCA----- 856
UHOR_08132-364 CCAGGCCCGTACAGGACCGTGGGACTGTTGGATGAGTGACAGACTTGTATGATGAGAGCGGTTTATTATGTGGAGGGCTATGCTGTACCGACTTGTATCA----- 723
UHOR_08132-822 CCAGGCCCGTACAGGACCGTGGGACTGTTGGATGAGTGACAGACTTGTATGATGAGAGCGGTTTATTATGTGGAGGGCTATGCTGTACCGACTTGTATCAGAAATGGTGTGAGTTGTCCGA 877
UHOR_08132-362 CCAGGCCCGTACAGGACCGTGGGACTGTTGGATGAGTGACAGACTTGTATGATGAGAGCGGTTTATTATGTGGAGGGCTATGCTGTACCGACTTGTATCAGAAATGGTGTGAGTTGTCCGA 746
UHOR_08132-813 CCAGGCCCGTACAGGACCGTGGGACTGTTGGATGAGTGACAGACTTGTATGATGAGAGCGGTTTATTATGTGGAGGGCTATGCTGTACCGACTTGTATCAGAAATGGTGTGAGTTGTCCGA 817
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....
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# Figure S3H

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UHOR_10033-813 --AAGTGGAGGTATGGTACGATGGGTTTACCGTGGTTAAAAGANGGAAAGTGAAGGAAAGGACCCGTGATAGCAGACCCATCCGTGATGAGGCCCTTGAGTTGATTGAAATGATGGGAGAGAGGCTCCGTGTCAATGTGTTG 148
UHOR_10033-822 CAAAGTGGAGGTATGGTACGATGGGTTTACCGTGGTTAAAAGATGGAAGTGAAGGAAAGGACCCGTGATAGCAGACCCATCCGTGATGAGGCCCTTGAGTTGATTGAAATGATGGGAGAGAGGCTCCGTGTCAATGTGTTG 150
UHOR_10033-818 CAAAGTGGAGGTATGGTACGATGGGTTTACCGTGGTTAAAAGATGGAAGTGAAGGAAAGGACCCGTGATAGCAGACCCATCCGTGATGAGGCCCTTGAGTTGATTGAAATGATGGGAGAGAGGCTCCGTGTCAATGTGTTG 150
UHOR_10033-811 ----- 1
UHOR_10033-364 ----- CTTGAGTTGATTGAAATGATGGGAGAGAGGCTCCGTGTCAATGTGTTG 54
UHOR_10033-362 ----- CTTGAGTTGATTGAAATGATGGGAGAGAGGCTCCGTGTCAATGTGTTG 53
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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UHOR_10033-813 TTAACCTTATCTCAAACTCAAGTCAACAACTGACACAACCAATCAAGATGAGGTTGCATCCCTCGTCATCCCTCCTTAATCTCTCTCCACTGCGCTTCGATCCATGGAGTGGAAAGAACAGAAATCAGAACCCACACCCCGACATCCT 298
UHOR_10033-822 TTAACCTTATCTCAAACTCAAGTCAACAACTGACACAACCAATCAAGATGAGGTTGCATCCCTCGTCATCCCTCCTTAATCTCTCTCCACTGCGCTTCGATCCATGGAGTGGAAAGAACAGAAATCAGAACCCACACCCCGACATCCT 300
UHOR_10033-818 TTAACCTTATCTCAAACTCAAGTCAACAACTGACACAACCAATCAAGATGAGGTTGCATCCCTCGTCATCCCTCCTTAATCTCTCTCCACTGCGCTTCGATCCATGGAGTGGAAAGAACAGAAATCAGAACCCACACCCCGACATCCT 300
UHOR_10033-811 -----ATGAGGTTGCATCCCTCGTCATCCCTCCTTAATCTCTCTCCACTGCGCTTCGATCCATGGAGTGGAAAGAACAGAAATCAGAACCCACACCCCGACATCCT 104
UHOR_10033-364 TTAACCTTATCTCAAACTCAAGTCAACAACTGACACAACCAATCAAGATGAGGTTGCATCCCTCGTCATCCCTCCTTAATCTCTCTCCACTGCGCTTCGATCCATGGAGTGGAAAGAACAGAAATCAGAACCCACACCCCGACATCCT 204
UHOR_10033-362 TTAACCTTATCTCAAACTCAAGTCAACAACTGACACAACCAATCAAGATGAGGTTGCATCCCTCGTCATCCCTCCTTAATCTCTCTCCACTGCGCTTCGATCCATGGAGTGGAAAGAACAGAAATCAGAACCCACACCCCGACATCCT 203
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

*****
UHOR_10033-813 TCAATCCATTTTCAAATCCCTTGTCACACCAAGTGAATCCGTATCTTAACCTTTCAATCCCTTTCCACCATTACCCCGTGTAGACCCACCCGATTACAGACCCGACCTTGTTCCCTTGTCCATGACAACACCGACAGTCC 448
UHOR_10033-822 TCAATCCATTTTCAAATCCCTTGTCACACCAAGTGAATCCGTATCTTAACCTTTCAATCCCTTTCCACCATTACCCCGTGTAGACCCACCCGATTACAGACCCGACCTTGTTCCCTTGTCCATGACAACACCGACAGTCC 450
UHOR_10033-818 TCAATCCATTTTCAAATCCCTTGTCACACCAAGTGAATCCGTATCTTAACCTTTCAATCCCTTTCCACCATTACCCCGTGTAGACCCACCCGATTACAGACCCGACCTTGTTCCCTTGTCCATGACAACACCGACAGTCC 450
UHOR_10033-811 TCAATCCATTTTCAAATCCCTTGTCACACCAAGTGAATCCGTATCTTAACCTTTCAATCCCTTTCCACCATTACCCCGTGTAGACCCACCCGATTACAGACCCGACCTTGTTCCCTTGTCCATGACAACACCGACAGTCC 254
UHOR_10033-364 TCAATCCATTTTCAAATCCCTTGTCACACCAAGTGAATCCGTATCTTAACCTTTCAATCCCTTTCCACCATTACCCCGTGTAGACCCACCCGATTACAGACCCGACCTTGTTCCCTTGTCCATGACAACACCGACAGTCC 354
UHOR_10033-362 TCAATCCATTTTCAAATCCCTTGTCACACCAAGTGAATCCGTATCTTAACCTTTCAATCCCTTTCCACCATTACCCCGTGTAGACCCACCCGATTACAGACCCGACCTTGTTCCCTTGTCCATGACAACACCGACAGTCC 353
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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UHOR_10033-813 TGAAGAGTCCCTTTGTGATGTGACGAAACCTGTGATGGTCTTGTGAAGAACTTGACAGTATAATAGAAGAGGTGAGATGGAAAAGAGGGAAGAGTGTGTGATGACCGAGG----- 567
UHOR_10033-822 TGAAGAGTCCCTTTGTGATGTGACGAAACCTGTGATGGTCTTGTGAAGAACTTGACAGTATAATAGAAGAGGTGAGATGGAAAAGAGGGAAGAGTGTGTGATGACCGAGGTT----- 571
UHOR_10033-818 TGAAGAGTCCCTTTGTGATGTGACGAAACCTGTGATGGTCTTGTGAAGAACTTGACAGTATAATAGAAGAGGTGAGATGGAAAAGAGGGAAGAGTGTGTGATGACCGAGGTT----- 571
UHOR_10033-811 TGAAGAGTCCCTTTGTGATGTGACGAAACCTGTGATGGTCTTGTGAAGAACTTGACAGTATAATAGAAGAGGTGAGATGGAAAAGAGGGAAGAGTGTGTGATGACCGAGGTT----- 319
UHOR_10033-364 TGAAGAGTCCCTTTGTGATGTGACGAAACCTGTGATGGTCTTGTGAAGAACTTGACAGTATAATAGAAGAGGTGAGATGGAAAAGAGGGAAGAGTGTGTGATGACCGAGGTTGACCGAGGAGGAGGAGGTTGGAGCCAGC 504
UHOR_10033-362 TGAAGAGTCCCTTTGTGATGTGACGAAACCTGTGATGGTCTTGTGAAGAACTTGACAGTATAATAGAAGAGGTGAGATGGAAAAGAGGGAAGAGTGTGTGATGACCGAGGTTGACCGAGGAGGAGGTTGGAGCCAGC 503
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

UHOR_10033-813 ----- 567
UHOR_10033-822 ----- 571
UHOR_10033-818 ----- 571
UHOR_10033-811 ----- 319
UHOR_10033-364 AGGGAATTTGCATT 518
UHOR_10033-362 AGGGAATTTGCATT 517
.....610.....

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