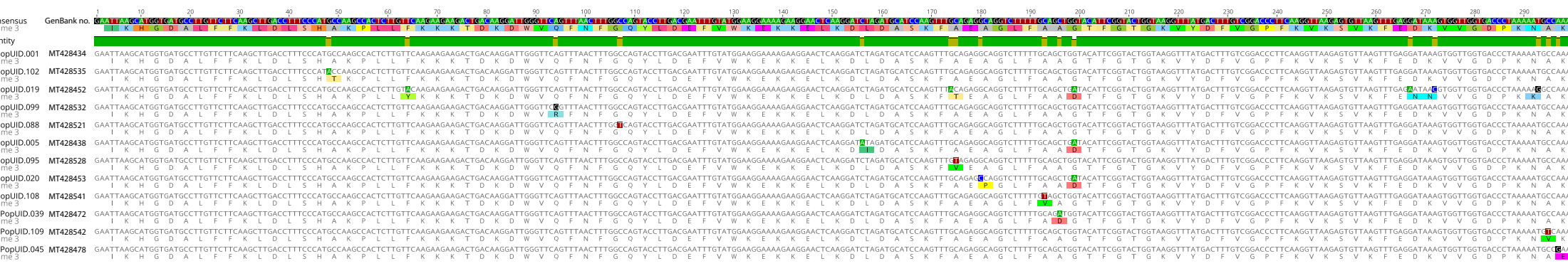


Figure S1. Nucleotide alignments of the sequence variants for the *Theileria orientalis* complex (including genotypes: *buffeli*, *chitose* (A & B) and *ikedai*), produced by targeted NGS using a region of the major piroplasm surface protein gene (*MPSP*). Alignments are compared to the most frequent sequence variant for each genotype. Synonymous nucleotide changes are in bold, and nonsynonymous amino acid changes are highlighted in colour. Genotypes *type 4* and *type 5* were omitted here, as only three sequences were recorded.

buffeli



***chitose* A**

Consensus
Frame 3

GenBank no.

1102030405060708090100110120130140150160170180190200210220230240250260270280290301

Identity

1. PopUID.003
Frame 3

MT428436

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

2. PopUID.070
Frame 3

MT428503

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

3. PopUID.079
Frame 3

MT428512

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

4. PopUID.063
Frame 3

MT428496

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

5. PopUID.083
Frame 3

MT428516

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

6. PopUID.072
Frame 3

MT428505

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

7. PopUID.084
Frame 3

MT428517

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

8. PopUID.092
Frame 3

MT428525

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

9. PopUID.075
Frame 3

MT428508

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

10. PopUID.076
Frame 3

MT428509

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

11. PopUID.080
Frame 3

MT428513

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

12. PopUID.089
Frame 3

MT428522

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

13. PopUID.057
Frame 3

MT428490

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

14. PopUID.064
Frame 3

MT428497

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

15. PopUID.042
Frame 3

MT428475

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

16. PopUID.066
Frame 3

MT428499

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

17. PopUID.053
Frame 3

MT428486

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LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

18. PopUID.027
Frame 3

MT428460

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LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

19. PopUID.029
Frame 3

MT428462

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LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

20. PopUID.074
Frame 3

MT428507

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

21. PopUID.082
Frame 3

MT428515

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

22. PopUID.069
Frame 3

MT428502

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

23. PopUID.017
Frame 3

MT428511

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

24. PopUID.055
Frame 3

MT428488

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

25. PopUID.086
Frame 3

MT428519

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

26. PopUID.047
Frame 3

MT428480

GACTGAAGCATCTGAAGACCTGTTCTTAAAGTCGACCTTCCCATCAAAACCACTTTTGTTCAGAAAGAAAGGAGCAAGGAATGGTACAGTTCAAGTTCGCTCCGCAAGTCTCGATGAAGTCTCTCTGGAAGAAAGAAAGGAATCAAGACCTGATGCTCAAGTTCTGCAAGAGCTGGCTCTTTTGCCCTGATGACTCGTACCGGAAAGTTTACAGCTTCGTGCGAAATCTCAAGTCAACAAGTCAAGTTTCGAGGATAAGGAAGTCGGAAATCAAGAAGGCCCAATA

LKHAEDLFLFKL DLSHAKPLLFKKKSDKEWVQFSFAQYLD EVLWKKEKKESESKDLDASKF AEAGLFAPDAFGTGK VYDFVGNFKVTKVKVKEFDEK EVDGSKKAK

chitose B

Consensus Frame 3	GenBank no.	<div><div><div>110120130140150160170180190200210220230240250260270280290301</div><div>CAATCAAGCATCTGATGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA</div><div>LKKHAEEDLFFFKLNNLSHAKPPLLFFKKKKSDDKEWVQFSFAQYLLDEVLLWKEKKKESKDLLDASKFAEAGLFPDAFPGTGKVVYDFVGNFKVTKVKKFEDKKEVGDSSKKAK</div></div></div>
Identity Frame 3	MT428473	GACTGAAGCATCTGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
1. PopUID.040 Frame 3	MT428471	GACTGAAGCATCTGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
2. PopUID.038 Frame 3	MT428440	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
3. PopUID.007 Frame 3	MT428485	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
4. PopUID.052 Frame 3	MT428510	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
5. PopUID.077 Frame 3	MT428534	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
6. PopUID.101 Frame 3	MT428540	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
7. PopUID.107 Frame 3	MT428437	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
8. PopUID.004 Frame 3	MT428527	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
9. PopUID.094 Frame 3	MT428523	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
10. PopUID.090 Frame 3	MT428435	GACTGAAGCATGCTGAAGACCTGTTCTTCAAGCTCAACCTTTCCCATGCAAAACCACTTTTGTTCAGAAAGAAGAGCGACAAGGAATGGGTACAGTTCAGCTTCGCCCAGTACCTTCGACGAAGTTCCTCTGGAAAGAAAAGAAGGAATCCAAGACCTCGATGCCTCCAAGTTTGCAGAACTGGTCTTTTGGCCCTGATGCTTCGGTACCGAAAAGTTTACGACTTCGTCGGAACTTCAAGGTCACCAAGGTCAAGTTCGAGGATAAGGAAATCGGAGATTCAAAGAAGGCCAAATA
11. PopUID.002 Frame 3		LKKHAEEDLFFFKLNNLSHAKPPLLFFKKKKSDDKEWVQFSFAQYLLDEVLLWKEKKKESKDLLDASKFAEAGLFPDAFPGTGKVVYDFVGNFKVTKVKKFEDKKEVGDSSKKAK

[illegible]