Table S1: PCR cycling conditions

	Initiation	Denaturation	Annealing	Extension	Final Extension	Hold
Tp1, Tp2	95°C, 11 min	41 cycles: 95°C, 1 min	50°C, 1 min	72°C, 1 min	72°C, 10 min	10°C
Tp3, Tp4, Tp7	95°C, 11 min	43 cycles: 95°C, 30 s	50°C, 1 min	72°C, 1.5 min	72°C, 10 min	10°C
Tp5	95°C, 11 min	40 cycles: 95°C, 30 s	50°C for 45s	72°C, 30 s	72°C, 10 min	10°C
Tp6	95°C, 11 min	42 cycles: 95°C, 30 s	55°C, 1 min	72°C, 1.5 min	72°C, 10 min	10°C
Tp8, Tp10	95°C, 11 min	40 cycles: 95°C, 30 s	55°C, 1 min	72°C, 2 min	72°C, 10 min	10°C
Tp9	95°C, 11 min	30 cycles: 95°C, 30 s	55°C, 1 min	72°C, 1.5 min	72°C, 10 min	10°C

Table S2a: Stabilate information and accession numbers

Sample ID	Stabilate Name	Tp1	Tp2[2]	Tp3	Tp4	Tp5	Tp6	Tp7	Tp8	Tp10
Buffalo-derived *T. parva*										
BD1	Mara 3[1]	*JF451995*	*JF451900*	KY556754	KY556860	KY556797	KY581701	KY556818	KY556832	KY556721
BD2	Mara 4 [1]	*JF451954*	*JF451901*	KY556755	-	KY556798	KY581702	KY556821	-	-
BD3	Mara 18[1]	*JF451996*	*JF451902*	KY556756	KY556877	KY556799	KY581703	KY556819	-	KY556722
BD4	Mara 30 [1]	*JF451955*	*JF451903*	KY556758	KY556878	KY556781	KY581704	KY556803	KY556834	KY556723
BD5	Mara 32 [1]	*JF451956*	*JF451904*	KY556761	KY556879	KY556782	KY581705	KY556817	KY556835	KY556724
BD6	Mara 42 [1]	*JF451997*	*JF451905*	KY556760	KY556882	KY556800	KY581706	KY556802	KY556838	KY556726
BD7	6998 [1,2]	*JF451957*	*JF451906*	KY556769	KY556869	KY556791	KY581716	KY556809	KY556849	KY556734
BD8	6999[2]	*JF451998*	*JF451898*	KY556771	KY556870	KY556792	KY581718	KY556811	KY556851	KY556736
BD9	7001[2]	*JF451999*	*JF451907*	KY556772	KY556872	KY556793	KY581720	KY556812	-	KY556737
BD10	7546[3]	*JF452000*	*JF451908*	KY556775	KY556875	KY556795	KY581723	KY556816	-	KY556739
BD14	7014[2]	*JF451958*	*JF451912*	KY556773	-	KY556794	KY581721	KY556813	KY556854	KY556738
BD15	7698[3]	*JF451991*	*JF451913*	KY556776	KY556876	KY556796	KY581724	KY556829	KY556856	KY556740
BD16	7344[3]	*JF452003*	*JF451899*	KY556774	KY556874	-	KY581722	KY556815	KY556853	-
BD17	Mara 41[1]	-	-	KY556759	KY556881	-	-	KY556820	KY556837	KY556725
BD18	4740[4]	KY556886	KY556753	KY556762	KY556861	-	KY581707	KY556804	KY556839	KY556727
BD19	5012[6]	KY556887	KY556744	KY556763	KY556862	KY556784	KY581708	KY556801	KY556840	KY556728
BD20	5489[4]	KY556888	KY556745	KY556764	KY556863	-	KY581709	KY556805	KY556841	KY556729
BD21	6666[2]	KY556889	KY556746	KY556765	KY556864	-	KY581711	KY556806	KY556843	KY556730
BD22	6807[2]	KY556890	-	-	KY556865	KY556785	-	KY556807	KY556844	KY556731
BD23	6818[2]	KY556891	-	KY556766	KY556866	KY556786	KY581712	KY556808	KY556845	-
BD24	6819[1]	KY556892	KY556747	KY556767	KY556867	KY556787	KY581713	KY556828	KY556846	KY556732
BD25	6998 cl. 11[3]	KY556893	KY556748	KY556770	KY556868	-	KY581717	KY556810	KY556850	KY556735
BD26	7065[2]	-	-	-	KY556873	-	KY581727	KY556814	KY556855	-
Cattle-derived *T. parva*										
CD16	Tc867 Bt106[3]	KY556896	KY556752	KY556779	KY556885	-	KY581726	-	KY556859	KY556743
CD17	Tc841 IL57[3]	KY556897	KY556751	KY556778	KY556884	-	KY581725	KY556831	KY556858	KY556742

CD28	Tc120F344[5]	KY556895	KY556750	KY556777	KY556883	-	-	KY556830	KY556857	KY556741

Italicized accession numbers indicate previously published sequences. – indicates samples were not run or no sequence data was available. [1] Conrad et al., 1987, [2] Baldwin et al. 1988, [3] Pelle et al., 2011, [4] ILRI biorepository, [5] Pelle, personal communication, [4] Grootenhuis et al., 1987, [6] unknown origin.

Table S2b: Tp9 Accession numbers

Sample ID	Stabilate name	Genomic DNA[1]	Cloned DNA[1]
Buffalo-derived *T. parva*			
BD1	Mara 3	KY563669	KY563670
BD2	Mara 4	-	KY563671
BD3	Mara 18	KY563673	KY563672
BD4	Mara 30	KY563675	KY563674
BD5	Mara 32	-	KY563676
BD6	Mara 42	KY563678	KY563677
BD7	6998	KY563682	KY563683
BD8	6999	-	KY563685
BD9	7001	-	KY563686
BD10	7546	-	KY563690
BD14	7014	-	KY563687
BD15	7698	-	KY563691
BD16	7344	KY563689	KY563688
BD18	4740	KY563679	-
BD19	5012	KY563680	-
BD25	6998 cl. 11	-	KY563684
Cattle-derived *T. parva*			
CD16	Tc 867 Bt106	-	KY563694
CD17	Tc 841 IL57	-	KY563693
CD28	Tc 120 F344	-	KY563692

Table S3a: Tp1 nucleotide variant Clustal alignment

```
TP03_0849(genomic)      TATGGCCACTTCAATTGCATTTGCCGCTGATCCTGGATTCTGTTATTTTCTATTAATACC      720
XM_757880(mRNA)         TATGGCCACTTCAATTGCATTTGCCGCTGATCCTGGATTCTGTTATTTTCTATTAATACC      720
V1(3)                   -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V2(1)                   -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V13(2)                  -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V36(1)                  -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V37(1)                  -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V38(1)                  -------------------------TCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V39(1)                  -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
V40(1)                  -------------------------GCTGATCCTGGATTCTGTTATTTTCTATTAATACC      35
                                                  **********************************

TP03_0849(genomic)      AGGCCCTGACTCGAAACCAATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      780
XM_757880(mRNA)         AGGCCCTGACTCGAAACCAATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      780
V1(3)                   AGGCCCTGACTCGAAACCAATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V2(1)                   AGGCCCTGACTCGAAACCCATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V13(2)                  AGGCCCTGACTCGAAACCTATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V36(1)                  AGGCCCTGACTCGAAACCAATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V37(1)                  AGGCCCTGACTCGAAACCAATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V38(1)                  AGGCCCTGACTCGAAACCTATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V39(1)                  AGGCCCTGACTCGAAACCAATATTCCTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
V40(1)                  AGGCCCTGACTCGAAACCTATATTCTTCAAAAACGACGGAGATAAATTTTTACGTTGCGT      95
                        ****************** ****** **********************************

TP03_0849(genomic)      AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      840
XM_757880(mRNA)         AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      840
V1(3)                   AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      155
V2(1)                   AGGGTATCCAAAGGTTAAAGAAGAAATTATAGAAATGGCTACAAAATTCAATAGACTACC      155
V13(2)                  AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      155
V36(1)                  AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      155
V37(1)                  AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      155
V38(1)                  AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGATTACC      155
V39(1)                  AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGATTACC      155
V40(1)                  AGGGTATCCAAAGGTTAAAGAAGAAATGCTAGAAATGGCTACAAAATTCAATAGACTACC      155
                        ***************************  ************************** ****

TP03_0849(genomic)      AAAGGGCGTGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC      900
XM_757880(mRNA)         AAAGGGCGTGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC      900
V1(3)                   AAAGGGCGTGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC      215
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V2(1)                 AAAGGGCGTGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
V13(2)                AAAGGGCATGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
V36(1)                AAAGGGCATGGAAATACCTTCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
V37(1)                AAAGGGCATGGAAATACCTTCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
V38(1)                AAAGGGCGTGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
V39(1)                AAAGGGCGTGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
V40(1)                AAAGGGCATGGAAATACCTGCACCTCCAGGAGTAAAACCAGAGGCTCCCACACCTACACC    215
                      ******* *********** ****************************************

TP03_0849(genomic)    AACGACAATAACTCCTTCTGTACCTCCTACTATACCAACGCCAATAACTCCTTCGGCACC    960
XM_757880(mRNA)       AACGACAATAACTCCTTCTGTACCTCCTACTATACCAACGCCAATAACTCCTTCGGCACC    960
V1(3)                 AACGACAATAACTCCTTCTGTACCTCCTACTATACCAACGCCAATAACTCCTTCGGCACC    275
V2(1)                 AACGACAATAACTCCTTCTGTACCTCCTACTATACCAACGCCAATAACTCCTTCGGCACC    275
V13(2)                AACGACAATAACTCCTTCTGTACCTCCTACTATACCAACTCCAATAACTCCTTCTGCACC    275
V36(1)                AACGACAATAACTCCCTCTGTACCTCCTACTATACCAACTCCAATAACTCCTTCGGCACC    275
V37(1)                AACGACAATAACTCCCTCTGTACCTCCTACTATACCAACTCCAATAACTCCTTCGGCACC    275
V38(1)                AACGACAATAACTCCTTCTGTACCTCCTACTATACCAACGCCAATAACTCCTTCGGCACC    275
V39(1)                AACTCCAATA------------------------------------ACTCCTTCTGCACC    239
V40(1)                AACGACAATAACTCCCTCTGTACCTCCTACTATACCAACTCCAATAACTCCTTCTGCACC    273
                      ***  *****                                    ******** ***

TP03_0849(genomic)    TCCTA------------CTACACCACCTACGGGACTAAATTTTAACTTGACAGTTCAGAA    1008
XM_757880(mRNA)       TCCTA------------CTACACCACCTACGGGACTAAATTTTAACTTGACAGTTCAGAA    1008
V1(3)                 TCCTA------------CTACACCACCTACGGGACTAAATTTTAACTTGACAGTTCAGAA    323
V2(1)                 TCCTA------------CTACACCACCTACGGGACTAAATTTTAACTTGACAGTTCAGAA    323
V13(2)                TCCTTCTGCACCTCCTACTACACCACCTAAGGGACTAAATTTTAACTTGACACTTCAGAA    335
V36(1)                TCCTACTACACCACCTACTACACCACCTACGGGACTAAATTTTAACTTGACAGTTCAGAA    335
V37(1)                TCCTACTACACCTCCTACTACACCACCTAAGGGACTAAATTTTAACTTGACAGTTCAGAA    335
V38(1)                TCCTA------------CTACACCAACTACGGGACTAAATTTTAACTTGACACGTCAGAA    323
V39(1)                TCCTACTACACCTCCTACTACACCACCTAAGGGACTAAATTTTAACTTGACAGTTCAGAA    299
V40(1)                TCCTA------------CTACACCACCTACGGGACTAAATTTTAACTTGACACTTCAGAA    323
                                       ******** *** **********************  ******

TP03_0849(genomic)    CAAATTCATGATAGGTTCGCAAGAAGTTAAGTTAAATATAACTCACGAATACGAGGGTGT    1068
XM_757880(mRNA)       CAAATTCATGATAGGTTCGCAAGAAGTTAAGTTAAATATAACTCACGAATACGAGGGTGT    1068
V1(3)                 CAAATTCATGATAGGTTCGCAAGAAGTTAAGTTAAATATAACTCACGAATACGAGGGTGT    383
V2(1)                 CAAATTCATGGTAGGTTCGCAAGAAGTTAAGTTAAATATAACTCACGAATACGATGGTGT    383
V13(2)                CAAATTCATGATAGGTTCGCAAGAAGTTAAGTTAAGTATAACTCACGAATACGATGGTGT    395
V36(1)                CAAATTCATGGTAGGTTCGCAAGAAGTTAAGTTAAGTATAACTTACGAATACGATGGTGT    395
V37(1)                CAAATTCATGGTAGGCTCGCAAGAAGTTAAGTTAAGTATAACTTACGAATACGATGGTGT    395
V38(1)                CAAATTCATGATAGGTTCGCAAGAAGTTAAGTTAAATATAACTTACGAATACGATGGTGT    383
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V39(1)                   CAAATTCATGGTAGGTTCGCAAGAAGTTAAGTTAAATATAACTCACGAATACGAGGGTGT        359
V40(1)                   CAAATTCATGATAGGTTCGCAAGAAGTTAAGTTAAGTATAACTCACGAATACGATGGTGT        383
                         ********** **** ******************* ******* ********** *****

TP03_0849(genomic)       ATACGAAGCTCATAAATATTTCATTGAAAGGGGCAGCTTTACCCCTACCTCATTCTCAAT        1128
XM_757880(mRNA)          ATACGAAGCTCATAAATATTTCATTGAAAGGGGCAGCTTTACCCCTACCTCATTCTCAAT        1128
V1(3)                    ATAC--------------------------------------------------------        387
V2(1)                    ATAC--------------------------------------------------------        387
V13(2)                   ATAC--------------------------------------------------------        399
V36(1)                   ATAC--------------------------------------------------------        399
V37(1)                   ATAC--------------------------------------------------------        399
V38(1)                   ATAC--------------------------------------------------------        387
V39(1)                   ATAC--------------------------------------------------------        363
V40(1)                   ATAC--------------------------------------------------------        387
                         ****
```

Primer regions are in bold, underlined and italicized text.

Table S3b: Tp1 protein variant Clustal alignment

```
XP_762973         FAADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGVEIP      240
V1(3)             --ADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGVEIP      58
V2(1)             --ADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEIIEMATKFNRLPKGVEIP      58
V11(2)            --ADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGMEIP      58
V13(1)            --ADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGMEIP      58
V17(1)            --ADPGFCYFLLIPGPDSKPIFLKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGVEIP      58
V35(1)            --ADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGMEIP      58
V36(1)            --ADPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGMEIP      58
V37(1)            --SDPGFCYFLLIPGPDSKPIFFKNDGDKFLRCVGYPKVKEEMLEMATKFNRLPKGVEIP      58
                    :*******************:*******************::************:***

XP_762973         APPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPT----TPPTGLNFNLTVQNKFMIGS      296
V1(3)             APPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPT----TPPTGLNFNLTVQNKFMIGS      114
V2(1)             APPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPT----TPPTGLNFNLTVQNKFMVGS      114
V11(2)            APPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPSAPPTTPPKGLNFNLTLQNKFMIGS      118
V13(1)            SPPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPTTPPTTPPTGLNFNLTVQNKFMVGS      118
V17(1)            APPGVKPEAPTPTPT------------PITPSAPPTTPPTTPPKGLNFNLTVQNKFMVGS      106
V35(1)            SPPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPTTPPTTPPKGLNFNLTVQNKFMVGS      118
V36(1)            APPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPT----TPPTGLNFNLTLQNKFMIGS      114
V37(1)            APPGVKPEAPTPTPTTITPSVPPTIPTPITPSAPPT----TPTTGLNFNLTRQNKFMIGS      114
                  :**************            ********:     * .******* *****:**

XP_762973         QEVKLNITHEYEGVYEAHKYFIERGSFTPTSFSIGDLPQTGLPVNQTVDTIVVYFHRVTM      356
V1(3)             QEVKLNITHEYEGVY---------------------------------------------      129
V2(1)             QEVKLNITHEYDGVY---------------------------------------------      129
V11(2)            QEVKLSITHEYDGVY---------------------------------------------      133
V13(1)            QEVKLSITYEYDGVY---------------------------------------------      133
V17(1)            QEVKLNITHEYEGVY---------------------------------------------      121
V35(1)            QEVKLSITYEYDGVY---------------------------------------------      133
V36(1)            QEVKLSITHEYDGVY---------------------------------------------      129
V37(1)            QEVKLNITYEYDGVY---------------------------------------------      129
                  *****.**:**:***
```

Eptiope region highlighted in grey.

Table S4a: Tp2 nucleotide variant Clustal alignment

```
TP01_0056(genomic)      ATAAAAAGATGAAATTGGCCGCCAGATTAATTAGCCTTTACTTTATTATTTACATTTTAC      180
XM_765583(mRNA)         ATAAAAAGATGAAATTGGCCGCCAGATTAATTAGCCTTTACTTTATTATTTACATTTTAC      180
V1(2)                   -----------------------------ATTAGCCTTTACTTTATTATTTACATTTTAC      31
V44(1)                  -----------------------------ATTAGTCTTTACTTTGTTATTTTCATTCTAC      31
V45(1)                  -----------------------------ATTAGCCTTTACTTTATTATTTTCATTCTAC      31
V46(1)                  -----------------------------ATTAGCCTTTACTTTATTATTTTCATTCTAC      31
V47(1)                  -----------------------------ATTAGCCTTTACTTTATTATTTTCATTCTAC      31
V48(2)                  -----------------------------ATTAGCCTTTACTTTATTATTTTCATTCTAC      31
V49(1)                  -----------------------------ATTAGCCTTTACTTTATTATTTTCATTCTAC      31
                                                     ***** *********.******:**** ***

TP01_0056(genomic)      ATTCCCCAGTGCTGGGAGGTAATTGT---AGTCATGAAGAACTAAAAAAATTGGGAATGC      237
XM_765583(mRNA)         ATTCCCCAGTGCTGGGAGGTAATTGT---AGTCATGAAGAACTAAAAAAATTGGGAATGC      237
V1(2)                   ATTCCCCAGTGCTGGGAGGTAATTGT---AGTCATGAAGAACTAAAAAAATTGGGAATGC      88
V44(1)                  CTTCCTCAGTCTTGGGAGGTAATTGT---ACTAATGAAGAACTAAAAAAATTGGGAATGG      88
V45(1)                  CTTCCTCAGTCTTGGGAAATAATAATTGTAGTGATAGTGAGCTAGAAACTTTGGGTATGT      91
V46(1)                  CTTCCTCAGTCTTGGGAGGTAATTGT---ACTGAGGAAGAACTAAAAAAAATGGGAATGG      88
V47(1)                  CTTCCTCAGTCTTGGGAGGTAATTGT---AGTGACAATGAGCTGGATACTTTGGGTTTGT      88
V48(2)                  CTTCCTCAGTCTTGGGAGGTAATTGT---AGTGACAATGAGCTGGATACTTTGGGTTTGT      88
V49(1)                  CTTCCTCAGTCTTGGGAGGTAATTGT---AGTGATGATGAACTAAGAAAATTGGGAATGT      88
                        .**** ****  *****. **** .*   * * * .. **.**. .:*.::****::**

TP01_0056(genomic)      TAGAGGGCGATGGTTTCGACAGGGATGCATTGTTCAAATCATCACATGGTATGGGAAAGG      297
XM_765583(mRNA)         TAGAGGGCGATGGTTTCGACAGGGATGCATTGTTCAAATCATCACATGGTATGGGAAAGG      297
V1(2)                   TAGAGGGCGATGGTTTCGACAGGGATGCATTGTTCAAATCATCACATGGTATGGGAAAGG      148
V44(1)                  TAGTGGGTGAAGGTTTAGATATGGAGGCATTGTTCAAAACATCTAAGGGTATGACGAAAG      148
V45(1)                  TGGACAAACCGGATCCTGACAAGCAAAGATTGTTCTTAACATCTAAGGCTATGTCGACAG      151
V46(1)                  TAGAGGGTGAAGGTTTCGATAAGGAAAAATTGTTCAAATCATCAAAGAGTATGGGAATAG      148
V47(1)                  TGGACAAACCAGATCTTGACAAGAATAGATTGTTTTTAACATCACATGGAATGGGAAAGA      148
V48(2)                  TGGACAAACCAGATCTTGACAAGAATAGATTGTTCTTAACATCACATGGAATGGGAAAGA      148
V49(1)                  TAAAGGGCGATGGTTTCGACAGGGATGCATTGTTCAAATCATCACATGGAATGGGAAAGG      148
                        *..: ..  . *.*   ** * * * . ****** : . ****:.* . :***  .* ..

TP01_0056(genomic)      TAGGAAAAAGGTATGGTCTTAAAACTACTCCAAAAGTAGATAAAGTCTTAGCAGATCTTG      357
XM_765583(mRNA)         TAGGAAAAAGGTATGGTCTTAAAACTACTCCAAAAGTAGATAAAGTCTTAGCAGATCTTG      357
V1(2)                   TAGGAAAAAGGTATGGTCTTAAAACTACTCCAAAAGTAGATAAAGTCTTAGCAGATCTTG      208
V44(1)                  TAGGGAGAAAGTATGGTATTAGACCTGGAACTACAAAAGATAAACTTACTAAAGAACTTA      208
V45(1)                  TAGGGAAAAAATATGGTATTAGACCTGGAACAAAAACAGAAAAATTTCTAAAAGAACTTA      211
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V46(1)                  TAGGGAGAAATCATGGTCTTAAACCAAAACCAAGATTAGAGAGTGTATTTGAAGATCTTG        208
V47(1)                  TAGCTAGAAGGTTTGGTATTAGACCTGGAACAAAAACAGAAAAATTCTTAAAAGAACTTA        208
V48(2)                  TAGGTAGAAGGTTTGGTATTAGACCTGGAACAAAAACAGAAAAATTCTTAAAAGAACTTA        208
V49(1)                  TAGGTAGAATGCATGGTCTTAAAACGACTCCAAAAGTAGAGAGAGTCTTAGAAGATCTTG        208
                        ***  *.**   :**** *:*.*.* . :.*:* *  *** ..: *   :..:**:.**

TP01_0056(genomic)      AAACACTGTTTGGAAAACACGGTCTTGGTGGTATTAGTAAAGATTGTCTTAAATGTTTTG        417
XM_765583(mRNA)         AAACACTGTTTGGAAAACACGGTCTTGGTGGTATTAGTAAAGATTGTCTTAAATGTTTTG        417
V1(2)                   AAACACTGTTTGGAAAACACGGTCTTGGTGGTATTAGTAAAGATTGTCTTAAATGTTTTG        268
V44(1)                  CTAGACTTCTTGAAAAAATCGGTATTATAGGAGTTAGTGAGTCTTGTCTTAGTTGTTTTG        268
V45(1)                  CTACTCTTCTTACACAACTAGGTATTACAGGAATTAGAGAACAATGTCTTGCCTGTTTTG        271
V46(1)                  AAAAACTGTTTGGAAAACACGGTCTTGGTGGTATTAGTAAAAATTGTCTTACTTGTTTTG        268
V47(1)                  CTAAATTATTTACAGAAATTGGTATTACAGGTGTTGGTGAGAAGTGCCTCGAATGTTTAG        268
V48(2)                  CTAAATTATTTACAGAAATTGGTATTACAGGTGTTGGTGAGAAGTGCCTCGAATGTTTAG        268
V49(1)                  AAACACTGTTTGGAAAAATCGGTCTTGGTGGTATTAGTAAAGATTGTCTTAAATGTTTTG        268
                          * : *  **. * ** : ***.**. :** .* .*:... . ** **    *****:*

TP01_0056(genomic)      CACAAAGCCTAGTGTGCGTATTAATGAAATGTAGAGGAGCATGTCTCAAAGGACCATGTA        477
XM_765583(mRNA)         CACAAAGCCTAGTGTGCGTATTAATGAAATGTAGAGGAGCATGTCTCAAAGGACCATGTA        477
V1(2)                   CACAAAGCCTAGTGTGCGTATTAATGAAATGTAGAGGAGCATGTCTCAAAGGACCATGTA        328
V44(1)                  GACAAAGCATTAAGTGTGTAGCACAACATTGCAAGGGAGCGTGTCTTAGGGGACCATGTA        328
V45(1)                  CACAAAGCATATATTGCGTTGCGAATAATTGCAGGGGAGCATGTCTTAGGGGTCCATGTA        331
V46(1)                  TGCAAAGCATTATGTGTGTTATAAATAAATGTAGAGGAGCATGTCTCAAAGGCCCATGTA        328
V47(1)                  CAGCAAGCATTAAGTGTGTATCACACCATTGCAAGGGAGCGTGTCTAAAGGGACCATGTA        328
V48(2)                  CAGCAAGCATTAAGTGTGTATCACAACATTGCAAGGGAGCGTGTCTAAAGGGACCATGTA        328
V49(1)                  TGGAAAGCATTATGTGTGTTATAAAAAAATGTAGAACAGCATGTCTCAGAGGACCATGTA        328
                         . .****.*  : ** .*:  ..: .* ** *... ***.***** ...*. *******

TP01_0056(genomic)      CTGACGACTGCCAAAATTGCTTTGATAGAAACTGTAAATCTGCATTGCTGGAATGCATTG        537
XM_765583(mRNA)         CTGACGACTGCCAAAATTGCTTTGATAGAAACTGTAAATCTGCATTGCTGGAATGCATTG        537
V1(2)                   CTGACGACTGCCAAAATTGCTTTGATAGAAACTGTAAATCTGCATTGCTGGAATGCATTG        388
V44(1)                  CAGAAGACTGCCAAAAATGCATTGAAAAAAATTGTAAACAGGCATTGCTGGAATGTATTG        388
V45(1)                  CTAAAGAGTGTCAAGAATGCATTAAAAAAAATTGTAAACAGGCATTGCTGGAATGTATTG        391
V46(1)                  CCGACGGATGTCAAAAGTGTATTAATACTAATTGTAAACCGGCACTGCTGGAATGCATTG        388
V47(1)                  CAGAAGGCTGTCAAGAATGCATTAAAAGAAATTGTATGGAAGCATTGCTGCAATGCATTG        388
V48(2)                  CAGATGGCTGTCAAGAATGCATTAAAAGAAATTGTATGGAAGCATTGCTGGAATGCATTG        388
V49(1)                  CTGATGACTGCCAAAATTGCATTAAAAGAAATTGTAAGCAAGGATTGCTGGAATGCATTG        388
                        * .* *. ** ***.* ** :**.*:* :** ***.:. . * * ***** *.** ****

TP01_0056(genomic)      GGAAAACAAGTATTCCAAATCCATGTAAATGGAAAGAAGATTATCTAAAATACAAATTTC        597
XM_765583(mRNA)         GGAAAACAAGTATTCCAAATCCATGTAAATGGAAAGAAGATTATCTAAAATACAAATTTC        597
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V1(2)                   GGAAAACAAGTATTCCAAATCCATGTAAATGGAAAGAAGATTATCTAAAATACAAATTTC        448
V44(1)                  GAAAAGGTGATGTTCCGAATCCTTGCGATTGGGAGAAAGAATATCTAAGTTACAAACTTC        448
V45(1)                  GAAAAGGTGATGTTCCGAATCCTTGTCAATGGAAAGATGATTATCTAAAATTCAAACTTC        451
V46(1)                  GAGTAAATGATATTCCAAATCCATGTAAATGGAAAGAAGATTATCTAAAATACAAACTTC        448
V47(1)                  GGAAACCAAGTGTTCCAAATCCTTGTGATTGGAAAGATGATTATCTAAAATTCAAATTTC        448
V48(2)                  GGAAACCAAGTATTCCAAATCCTTGTGATTGGAAAGATGATTATCTAAAATTCAAATTTC        448
V49(1)                  GAAAAGAGGATGTTCCAAATCCTTGCGATTGGGACAAAGAATATCTAAAATACAAACTTC        448
                        *..:*   ..:.**...*****:**  *:***.* .*:** *******.:*:**** ***

TP01_0056(genomic)      CTGAAACAGATGAGGACGAATCTACGAAAAAAAGGAGAAGCCTCCGGCACTTCATAGGGAT        657
XM_765583(mRNA)         CTGAAACAGATGAGGACGAATCTACGAAAAAAAGGAGAAGCCTCCGGCACTTCATAGGGAT        657
V1(2)                   CTGAAACAGATGAGGACGAATCTACGAAAAAA----------------------------        480
V44(1)                  CTGAAACA----------------------------------------------------        456
V45(1)                  CTGAAACA----------------------------------------------------        459
V46(1)                  CTGAAACAGATGAGGAC-------------------------------------------        465
V47(1)                  CTGAAACAGGTGAGGATGAGGCTCA-----------------------------------        473
V48(2)                  CTGAAACAGATAGTGACGAATCTGAGAAAAA-----------------------------        479
V49(1)                  CTGATACAGATGGGGATGAGTCTCA-----------------------------------        473
                        **** ***
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Primer regions are in bold, underlined and italicized text.

Table S4b: Tp2 protein variant Clustal alignment

```
XP_765583        MKLAARLISLYFIIYILHSPVLGG-NCSHEELKKLGMLEGDGFDRDALFKSSHGMGKVGK 59
V1(2)            -------ISLYFIIYILHSPVLGG-NCSHEELKKLGMLEGDGFDRDALFKSSHGMGKVGK 52
V42(1)           -------ISLYFIIFILPSSVLGNNNCSDSELETLGMLDKPDPDKQRLFLTSKAMSTVGK 53
V43(1)           -------ISLYFVIFILPSSVLGG-NCTNEELKKLGMVVGEGLDMEALFKTSKGMTKVGR 52
V44(1)           -------ISLYFIIFILPSSVLGG-NCTEEELKKMGMVEGEGFDKEKLFKSSKSMGIVGR 52
V45(1)           -------ISLYFIIFILPSSVLGG-NCSDDELRKLGMLKGDGFDRDALFKSSHGMGKVGR 52
V46(1)           -------ISLYFIIFILPSSVLGG-NCSDNELDTLGLLDKPDLDKNRLFLTSHGMGKIAR 52
V47(2)           -------ISLYFIIFILPSSVLGG-NCSDNELDTLGLLDKPDLDKNRLFLTSHGMGKIGR 52
                        ***** *:** * ***  **:..** .:*::   . * : ** :*:.*  :.:
XP_765583        RYGLKTTPKVDKVLADLETLFGKHGLGGISKDCLKCFAQSLVCVLMKCRGACLKGPCTDD 119
V1(2)            RYGLKTTPKVDKVLADLETLFGKHGLGGISKDCLKCFAQSLVCVLMKCRGACLKGPCTDD 112
V42(1)           KYGIRPGTKTEKFLKELTTLLTQLGITGIREQCLACFAQSIYCVANNCRGACLRGPCTKE 113
V43(1)           KYGIRPGTTKDKLTKELTRLLEKIGIIGVSESCLSCFGQSIKCVAQHCKGACLRGPCTED 112
V44(1)           NHGLKPKPRLESVFEDLEKLFGKHGLGGISKNCLTCFVQSIMCVINKCRGACLKGPCTDG 112
V45(1)           MHGLKTTPKVERVLEDLETLFGKIGLGGISKDCLKCFVESIMCVIKKCRTACLRGPCTDD 112
V46(1)           RFGIRPGTKTEKFLKELTKLFTEIGITGVGEKCLECLAASIKCVSHHCKGACLKGPCTEG 112
V47(2)           RFGIRPGTKTEKFLKELTKLFTEIGITGVGEKCLECLAASIKCVSQHCKGACLKGPCTDG 112
                  .*::     : .  :*  *: : *: *:  .** *:  *: **  :*: *** ***:.

XP_765583        CQNCFDRNCKSALLECIGKTSIPNPCKWKEDYLKYKFPETDEDESTKKGEASGTS      174
V1(2)            CQNCFDRNCKSALLECIGKTSIPNPCKWKEDYLKYKFPETDEDESTKK-------      160
V42(1)           CQECIKKNCKQALLECIGKGDVPNPCQWKDDYLKFKLPET---------------      153
V43(1)           CQKCIEKNCKQALLECIGKGDVPNPCDWEKEYLSYKLPET---------------      152
V44(1)           CQKCINTNCKPALLECIGVNDIPNPCKWKEDYLKYKLPETDED------------      155
V45(1)           CQNCIKRNCKQGLLECIGKEDVPNPCDWDKEYLKYKLPDTDGDES----------      157
V46(1)           CQECIKRNCMEALLQCIGKPSVPNPCDWKDDYLKFKFPETGEDEA----------      157
V47(2)           CQECIKRNCMEALLECIGKPSIPNPCDWKDDYLKFKFPETDSDESEK--------      159
                 **:*:. **  .**:***  .:****.*  :**.:* * *
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Eptiope region highlighted in grey. Eptiopes in close proximity or overlapping are denoted by underlined regions or highlighted in a different shade of grey.

Table S5a: Tp3 nucleotide variant Clustal alignment

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TP01_0868(genomic)      ATGAAATTAAATACTATCGCAATAGCCTTTTTGTATTCCTGTTTCTCACAGTTTTTAAAA        60
XM_7663892(mRNA)        ATGAAATTAAATACTATCGCAATAGCCTTTTTGTATTCCTGTTTCTCACAGTTTTTAAAA        60
V1(2)                   ------------------------------------------------------------        60
V2(1)                   ------------------------------------------------------------        0
V3(3)                   ------------------------------------------------------------        0
V4(1)                   ------------------------------------------------------------        0
V5(3)                   ------------------------------------------------------------        0
V6(3)                   ------------------------------------------------------------        0
V7(1)                   ------------------------------------------------------------        0
V8(1)                   ------------------------------------------------------------        0
V9(1)                   ------------------------------------------------------------        0
V10(5)                  ------------------------------------------------------------        0
V11(1)                  ------------------------------------------------------------        0
V12(1)                  ------------------------------------------------------------        0
V13(1)*                 ------------------------------------------------------------        0


TP01_0868(genomic)      AATGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        120
XM_7663892(mRNA)        AATGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        120
V1(2)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        120
V2(1)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTATCACCAGATGGTTCTTTTCTTCAA        58
V3(3)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTATCACCAGATGGTTCTTTTCTTCAA        58
V4(1)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTATCACCAGATGGTTCTTTTCTTCAA        58
V5(4)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTATCACCAGATGGTTCTTTTCTTCAA        58
V6(3)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTATCACCAGATGGTTCTTTTCTTCAA        58
V7(1)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
V8(1)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
V9(1)                   --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
V10(5)                  --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
V11(1)                  --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
V12(1)                  --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
V13(1)*                 --TGTGTCTGCTCTGAGGCGTAGTTCTCCAGATTTGTCACCAGATGGTTCTTTTCTTCAA        58
                          ********************************* ************************

TP01_0868(genomic)      GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA        180
XM_7663892(mRNA)        GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA        180
V1(2)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA        180
V2(1)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA        118
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V3(3)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V4(1)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTGCTAAGGTA      118
V5(4)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTGCTAAGGTA      118
V6(3)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTGCTAAGGTA      118
V7(1)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V8(1)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V9(1)                   GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V10(5)                  GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V11(1)                  GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V12(1)                  GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
V13(1)*                 GTAAAATCAGCTTCTCCTCAAGATAAACAAGATGTAATCCAAAGTTCCTCTCCTAAGGTA      118
                        *************************************************** ********

TP01_0868(genomic)      ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      240
XM_7663892(mRNA)        ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      240
V1(2)                   ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      240
V2(1)                   ACAGTGCCTGCGGTGGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V3(3)                   ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V4(1)                   ACAGTGCCTGCGGTGGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCACCAGTTCTATCA      178
V5(4)                   ACAGTGCCTGCGGTGGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCACCAGTTCTATCA      178
V6(3)                   ACAGTGCCTGCGGTGGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V7(1)                   ACAGTGCCTGCGGTGGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V8(1)                   ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTTTCA      178
V9(1)                   ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V10(5)                  ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V11(1)                  ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V12(1)                  ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
V13(1)*                 ACAGTGCCTACGGTTGACCCTGAAGGCCTCAAGAAGGCGGTTACTGCAGCAGTTCTATCA      178
                        ********* **** ********************************* ***********

TP01_0868(genomic)      AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC      300
XM_7663892(mRNA)        AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC      300
V1(2)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC      300
V2(1)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCG      238
V3(3)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCG      238
V4(1)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCCGCC      238
V5(4)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCCGCC      238
V6(3)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCCGCC      238
V7(1)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC      238
V8(1)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC      238
V9(1)                   AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTACC      238
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V10(5)                 AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC        238
V11(1)                 AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC        238
V12(1)                 AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC        238
V13(1)*                AACCAAAATCAAGCTCTACAAAACGGTGCTCTTAATCCAGCAGATTTCACTCAAGCTGCC        238
                       ******************************************************* * *

TP01_0868(genomic)     TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGTA        357
XM_7663892(mRNA)       TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGTA        357
V1(2)                  TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGTA        357
V2(1)                  GCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGC-        294
V3(3)                  GCTGTTAATTCCAT---GAGTAATGCTGTTGGTGCCATGAACAACACTGTTGGTCCAGT-        294
V4(1)                  GCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGC-        294
V5(4)                  GCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGC-        294
V6(3)                  GCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGC-        294
V7(1)                  GCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGT-        294
V8(1)                  TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGT-        294
V9(1)                  TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGTA        295
V10(5)                 TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGT-        294
V11(1)                 TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGT-        294
V12(1)                 TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGT-        294
V13(1)*                TCTGTTAATTCCAT---GAGTAATGCTGTTAGTGCCATGAACAATACTGTTGGTCCAGT-        294
                        *************   ************* ************* *************

TP01_0868(genomic)     AAAAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        417
XM_7663892(mRNA)       AAAAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        417
V1(2)                  AAAAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        417
V2(1)                  --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAACGCCTGGTGTACAG        352
V3(3)                  --AAATCCCATGACTACTGTTGGTACTATGAACTCCTTTACTGGAACGCCTGGTGTACAG        352
V4(1)                  --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAACGCCTGGTGTACAG        352
V5(4)                  --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAACGCCTGGTGTACAG        352
V6(3)                  --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAACGCCTGGTGTACAG        352
V7(1)                  --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAACGCCTGGTGTACAG        352
V8(1)                  --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        352
V9(1)                  AAAAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        355
V10(5)                 --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        352
V11(1)                 --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        352
V12(1)                 --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        352
V13(1)*                --AAATCCCATGGCTACTGTTGGTACTATGAACTCCTTTACTGGAATGCCTGGTGTACAG        352
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TP01_0868(genomic)     GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT        477
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XM_7663892(mRNA)        GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     477
V1(2)                   GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     477
V2(1)                   GATACTTTTTCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V3(3)                   GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V4(1)                   GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACTCAAGAGAACAGT     412
V5(4)                   GATACTTTTTCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V6(3)                   GATACTTTTTCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V7(1)                   GATACTTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACTCAAGAGAACAGT     412
V8(1)                   GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V9(1)                   GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     415
V10(5)                  GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACTCAAGAGAACAGT     412
V11(1)                  GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V12(1)                  GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACCCAAGAGAACAGT     412
V13(1)*                 GATAATTTTCCTCAGACACCGCCTGTTAATGTTCAAGACACCTCTACTCAAGAGAACAGT     412
                        **** **** **************************************************

TP01_0868(genomic)      CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     537
XM_7663892(mRNA)        CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     537
V1(2)                   CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     537
V2(1)                   CTTGACAACCTAAATCTCCTCTTAGATCCTTCGTTAGCAAAGATATCTCAAGCTGATAGT     472
V3(3)                   CTTGACAACCTAAATCTCCTCTTAGATCCTTCGTTACTAAAGATATCTCAAGCTGATAGT     472
V4(1)                   CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
V5(4)                   CTTGACAACCTAAATCTCCTCTTAGATCCTTCGTTACTAAAGATATCTCAAGCTGATAGT     472
V6(3)                   CTTGACAACCTAAATCTCCTCTTAGATCCTTCGTTACTAAAGATATCTCAAGCTGATAGT     472
V7(1)                   CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
V8(1)                   CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
V9(1)                   CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     475
V10(5)                  CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
V11(1)                  CTTGACAACCTAAATCTCCTCTTAGATCCTTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
V12(1)                  CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
V13(1)*                 CTTGACAACCTAAATCTCCTCTTAGATCCCTCGTTAGTAAAGATATCTCAAGCTGATAGT     472
                        ***************************** ******  **********************

TP01_0868(genomic)      CACATAAAAGAAAGCATGGTTAGTTTCATTTTTATTAATTTGTTCAGGAAAAAGCTGTAC     597
XM_7663892(mRNA)        CACATAAAAGAAAGCATG-----------------------------GAAAAAGCTGTAC     568
V1(2)                   CACATAAAAGAAAGCATGGTTAGTTTCATTTTTATTAATTTGTTCAGGAAAAAGCTGTAC     597
V2(1)                   CACATAAAAGAAAGCATGGTTAGTTTTATTTTTATTAATTTGTTCAGGAAAAAGCTGTAC     532
V3(3)                   CACATAAAAGAAAGCATGGTTAGTTTTATTTTTATTAGTTTGTTCAGGAAAAAGCTGTAC     532
V4(1)                   CACATAAAAGAAAGCATGGTTAGTTTTATTTTTACTAATTTTTTCAGGAAAAAGCTGTAC     532
V5(4)                   CACATAAAAGAAAGCATGGTTAGTTTTATTCTTATTAATTTGCTCAGGAAAAAGCTGTAC     532
V6(3)                   CACATAAAAGAAAGCATGGTTAGTTTTATTTTTATTAATTTGTTCAGGAAAAAGCTGTAC     532
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V7(1)                  CACATAAAAGAAAGCATGGTTAGTTTTATTTTTACTAATTTTTTCAGGAAAAAGCTGTAC       532
V8(1)                  CACATAAAAGAAAGCATGGTTAGTTTCATTTTTATTAATTTGTTCAGGAAAAAGCTGTAC       532
V9(1)                  CACATAAAAGAAAGCATGGTTAGTTTCATTTTTATTAATTTGTTCAGGAAAAAGCTGTAC       535
V10(5)                 CACATAAAAGAAAGCATGGTTAGTTTTATTTTTACTAATTTTTTCAGGAAAAAGCTGTAC       532
V11(1)                 CACATAAAAGAAAGCATGGTTAGTTTTATTTTTATTAGTTTGTTCAGGAAAAAGCTGTAC       532
V12(1)                 CACATAAAAGAAAGCATGGTTAGTTTTATTTTTATTAGTTTGTTCAGGAAAAAGCTGTAC       532
V13(1)*                CACATAAAAGAAAGCATGGTTAGTTTTATTTTTACTAATTTTTTCAGGAAAAAGCTGTAC       532
                       ******************                             *************

TP01_0868(genomic)     ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       657
XM_7663892(mRNA)       ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       628
V1(2)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       657
V2(1)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V3(3)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V4(1)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V5(4)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V6(3)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V7(1)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V8(1)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V9(1)                  ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       595
V10(5)                 ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V11(1)                 ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACTAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V12(1)                 ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
V13(1)*                ACAGCCTTAAAAAGGTCTTGGAGGGGCTAACCAACCTTGCGACTCTGTCTAAAAGTAGGG       592
                       ******************************* ****************************

TP01_0868(genomic)     ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       717
XM_7663892(mRNA)       ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       688
V1(2)                  ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       717
V2(1)                  ATACAGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V3(3)                  ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V4(1)                  ATACAGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V5(4)                  ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V6(3)                  ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V7(1)                  ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V8(1)                  ATACAGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V9(1)                  ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       655
V10(5)                 ATACAGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V11(1)                 ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V12(1)                 ATACAGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
V13(1)*                ATACTGAACCGTTTAATGTTCTGGGGGATGACTATACGATGCGTAACGTTTTGGACCTCA       652
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TP01_0868(genomic)      TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        777
XM_7663892(mRNA)        TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        748
V1(2)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        777
V2(1)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V3(3)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V4(1)                   TGAATAAGGAACTCAGGCAAGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V5(4)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTCGTGTTCCAATTCAACGCCT        712
V6(3)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTCGTGTTCCAATTCAACGCCT        712
V7(1)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCA--------------------------        686
V8(1)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V9(1)                   TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        715
V10(5)                  TGAATAAGGAACTCAGGCAAGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V11(1)                  TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V12(1)                  TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
V13(1)*                 TGAATAAGGAACTCAGGCAGGTTGAATCTCTTCAGAAAGTTGTGTTCCAATTCAACGCCT        712
                        ******************* **************

TP01_0868(genomic)      TTGCACTTTCCACCTTCACTAAGAGTCCAGACGATAATAAAAAATCCTAA  827
XM_7663892(mRNA)        TTGCACTTTCCACCTTCACTAAGAGTCCAGACGATAATAAAAAATCCTAA  798
V1(2)                   TTGCACTTTCC---------------------------------------  827
V2(1)                   TTGCACTTTCC---------------------------------------  723
V3(3)                   TTGCACTTTCC---------------------------------------  723
V4(1)                   TTGCACTTTCC---------------------------------------  723
V5(4)                   TTGCACTTTCC---------------------------------------  723
V6(3)                   TTGCACTTTCC---------------------------------------  723
V7(1)                   --------------------------------------------------  686
V8(1)                   TTGCACTTTCC---------------------------------------  723
V9(1)                   TTGCACTTTCC---------------------------------------  726
V10(5)                  TTGCACTTTCC---------------------------------------  723
V11(1)                  TTG-----------------------------------------------  715
V12(1)                  TTGCCCTTTCC---------------------------------------  723
V13(1)*                 TTGC----------------------------------------------  716
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Primer regions are in bold, underlined and italicized text.

* Partial sequence as defined by only having either the forward or reverse sequence of the allele available for analysis. This sequence is its own variant due to unique nucleotides.

Table S5b: Tp3 protein variant Clustal alignment

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XP_7663892(2)MKLNTIAIAFLYSCFSQFLKNVSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSPKV   60
V2(1)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSAKV   39
V3(3)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSAKV   39
V4(3)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSAKV   39
V5(1)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSPKV   39
V6(1)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSPKV   39
V7(1)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSPKV   39
V8(3)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSPKV   39
V9(9)        ---------------------VSALRRSSPDLSPDGSFLQVKSASPQDKQDVIQSSSPKV   39
                                  ************************************ **

XP_7663892(2)TVPTVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQAASV-NSMSNAVSAMNNTVGPV   119
V2(1)        TVPAVDPEGLKKAVTAPVLSNQNQALQNGALNPADFTQAAAV-NSMSNAVSAMNNTVGPA   98
V3(3)        TVPAVDPEGLKKAVTAPVLSNQNQALQNGALNPADFTQAAAV-NSMSNAVSAMNNTVGPA   98
V4(3)        TVPAVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQAAAV-NSMSNAVSAMNNTVGPA   98
V5(1)        TVPAVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQAAAV-NSMSNAVSAMNNTVGPA   98
V6(1)        TVPAVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQAAAV-NSMSNAVSAMNNTVGPV   98
V7(1)        TVPTVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQATSV-NSMSNAVSAMNNTVGPV   98
V8(3)        TVPTVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQAAAV-NSMSNAVGAMNNTVGPV   98
V9(9)        TVPTVDPEGLKKAVTAAVLSNQNQALQNGALNPADFTQAASV-NSMSNAVSAMNNTVGPV   98
             ***:************ **********************::* *******.********.

XP_7663892(2)KNPMATVGTMNSFTGMPGVQDNFPQTPPVNVQDTSTQENSLDNLNLLLDPSLVKISQADS   179
V2(1)        -NPMATVGTMNSFTGTPGVQDNFPQTPPVNVQDTSTQENSLDNLNLLLDPSLVKISQADS   157
V3(3)        -NPMATVGTMNSFTGTPGVQDTFSQTPPVNVQDTSTQENSLDNLNLLLDPSLLKISQADS   157
V4(3)        -NPMATVGTMNSFTGTPGVQDTFSQTPPVNVQDTSTQENSLDNLNLLLDPSLLKISQADS   157
V5(1)        -NPMATVGTMNSFTGTPGVQDTFSQTPPVNVQDTSTQENSLDNLNLLLDPSLAKISQADS   157
V6(1)        -NPMATVGTMNSFTGTPGVQDTFPQTPPVNVQDTSTQENSLDNLNLLLDPSLVKISQADS   157
V7(1)        KNPMATVGTMNSFTGMPGVQDNFPQTPPVNVQDTSTQENSLDNLNLLLDPSLVKISQADS   158
V8(3)        -NPMTTVGTMNSFTGTPGVQDNFPQTPPVNVQDTSTQENSLDNLNLLLDPSLLKISQADS   157
V9(9)        -NPMATVGTMNSFTGMPGVQDNFPQTPPVNVQDTSTQENSLDNLNLLLDPSLVKISQADS   157
              ***:********** ******* **************************** *******

XP_7663892(2)HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   239
V2(1)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
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V3(3)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
V4(3)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
V5(1)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
V6(1)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
V7(1)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   218
V8(3)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
V9(9)        HIKESMEKAVHSLKKVLEGLTNLATLSKSRDTEPFNVLGDDYTMRNVLDLMNKELRQVES   217
             ************************************************************

XP_7663892(2)LQKVVFQFNAFALSTFTKSPDDNKKS   265
V2(1)        LQKVVFQFNAFALS------------   231
V3(3)        LQKVVFQFNAFALS------------   231
V4(3)        LQKVVFQFNAFALS------------   231
V5(1)        LQKVVFQFNAFALS------------   231
V6(1)        L-------------------------   218
V7(1)        LQKVVFQFNAFALS------------   232
V8(3)        LQKVVFQFNAFALS------------   231
V9(9)        LQKVVFQFNAFALS------------   231
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Eptiope sequence unknown.

Table S6a: Tp4 nucleotide variant Clustal alignment

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TP03_0210       GTAGTTTTATCTAAATTGCCAATTGGTGATTTAGCAACACAATACTTTGCAGGTATTTAC 1377
XM_758135       GTAGTTTTATCTAAATTGCCAATTGGTGATTTAGCAACACAATACTTTGCAGATA----- 922
V1(2)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V2(2)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V3(4)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V4(2)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V5(2)           ------------------------------------------TACTTTGCAGGTATTTAC 18
V6(1)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V7(1)           ---------------------------------------CAATACTTTGCCGGTATTTAC 21
V8(1)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V9(2)           ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V10(1)          ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V11(1)          ---------------------------------------CAATACTTTGCAGGTATTTAC 21
V12(2)          ---------------------------------------------TTTGCAGGTATTTAC 15
V13(3)          ---------------------------------------CAATACTTTGCAGGTATTTAC 21
                                                             ***** ****

TP03_0210       GCAGCTTGTACTCCCCCACGGGAACTTAGTTATACAAATT-TATTCTAGATTACTTATAT 1436
XM_758135       ------------------------------------------------------------ 922
V1(2)           GCAGCTTGTACTCCCCCACGGGAACTTAGTTATACAAATT-TATTCTAGATTACTTATAT 80
V2(2)           GCAGCTTGTACATCCCCACGGGAACTTAGTTATACAAATT-TATTCTAGATTACTTATAT 80
V3(4)           GGAGCTTGTACATCCCCACGGGAACTTAGTTACACAAATTTAACACTAGATTAGTTATAT 81
V4(2)           GGAGCTTGTACATCCCCACGGGAACTTAGTTACACACTTTTAACACCAGATTAGTTATAT 81
V5(2)           GCAGCTTGTACTCCCCCACGGGAACTTAGTTACACAAATTTAACACTATATTAGTTATAT 78
V6(1)           GGAGCTTGTACATCCCCACGGGAACTTAGTTATACACTTTTAACACCAGATTAGTTATAT 81
V7(1)           GCAGCTTGTACTCCCCCACGGGAACTTAGTTATACACTTTTAACACCAGATTAGTTATAT 81
V8(1)           GGAGCTTGTACATCCCCACGGGAACTTAGTTACACAAATTTAACACTAGATTAGTTATAT 81
V9(2)           GGAGCTTGTACATCCCCACGGGAACTTAGTTATACACTTTTAACACCAGATTAGTTATAT 81
V10(1)          GGAGCTTGTACATCCCCACGGGAACTTAGTTATACACTTTTAACACCAGATTAGTTATAT 81
V11(1)          GCAGCTTGTACTCCCCCACGGGAACTTAGTTATATACTTTTAACACTATATTAGTTATAT 81
V12(2)          GGAGCTTGTACTCCCCCACGGGAACTTAGTTATACAAATT-TATTCTAGATTACTTATAT 74
V13(3)          GGAGCTTGTACATCCCCACGGGAACTTAGTTACACAAATTTAACACTAGATTAGTTATAT 81


TP03_0210       CCCGTACAATATTAATAATTTTCCTTAGATAAAAATGTATTTTGTGCCGGCCGGGTTGAT 1496
XM_758135       -------------------------------AAAATGTATTTTGTGCCGGCCGGGTTGAT 951
V1(2)           CCCGTACAATATTAATAATTTTCCTTAGATAAAAATGTATTTTGTGCCGGCCGGGTTGAT 140
V2(2)           CCCGTACAATATTAATAATTTTCCTTAGATAAAAATGTATTTTGTGCCGGCCGGGTTGAT 140
V3(4)           ACTATACAATATTAATAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGTCGCGTTGAT 141
V4(2)           TGCATACAATATTAACAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGTCGCGTTGAT 141
V5(2)           TGCATACAATATTAACAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGTCGTGTTGAT 138
V6(1)           ACTATACAATATTAACAATTTTTTATAGATAAGAATGTATTTTGTGCCGGTCGTGTTGAT 141
V7(1)           TGCATACAATATTAACAATTTTTTATAGATAAGAATGTATTTTGTGCCGGTCGTGTTGAT 141
V8(1)           ACTATACAATATTAATAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGCCGGGTTGAT 141
V9(2)           ACTATACAATATTAACAATTTTTTATAGATAAGAATGTATTTTGTGCCGGTCGTGTTGAT 141
V10(1)          ACTATACAATATTAACAATTTTTTATAGATAAGAATGTATTTTGTGCCGGTCGTGTTGAT 141
V11(1)          TGCATACAATATTAACAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGTCGCGTTGAT 141
V12(2)          GCCATACAATATTAATAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGTCGTGTTGAT 134
V13(3)          ACTATACAATATTAATAATTTTCCTTAGATAAGAATGTATTTTGTGCCGGCCGGGTTGAT 141
                                               * ***************** ** ******

TP03_0210       GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 1556
XM_758135       GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 1011
V1(2)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 200
V2(2)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 200
V3(4)           GAAAATGATCTTGTAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 201
V4(2)           GAAAATGATCTTATAAGAACGAGTAAAGCCACTGGTGCTTCTATTCAAACCACTCTCAAC 201
V5(2)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCCATTCAAACCACTCTCAAT 198
V6(1)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCCATTCAAACCACTCTCAAT 201
V7(1)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 201
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V8(1)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 201
V9(2)           GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCCATTCAAACCACTCTCAAT 201
V10(1)          GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCCATTCAAACCACTCTCAAT 201
V11(1)          GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCYATTCAAACCACTCTCAAT 201
V12(2)          GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACTCTCAAT 194
V13(3)          GAAAATGATCTTATAAGAACGAGTAAAGCTACTGGTGCTTCTATTCAAACCACCCTCAAT 201
                ************ **************** *********** *********** *****

TP03_0210       AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGTCAATTCCTGCTACAATCTA 1616
XM_758135       AACCTTTCAGTTGACGT------------------------------------------- 1028
V1(2)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGTCAATTCCTGCTACAATCTA 260
V2(2)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATCTA 260
V3(4)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGTCAATTCCTGCTACAATCTA 261
V4(2)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCGTGCAGGCAATTCCTGCTACAATCTA 261
V5(2)           AATCTTTCAGTTGACGTCTTAGGTACTGCGTTTCTTGCAGGCAATTCCTGCTACAATCTA 258
V6(1)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATCTA 261
V7(1)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATCTA 261
V8(1)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGTCAATTCCTGCTACAATCTA 261
V9(2)           AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATCTA 261
V10(1)          AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATCTA 261
V11(1)          AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATATA 261
V12(2)          AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCTTGCAGGCAATTCCTGCTACAATCTA 254
V13(3)          AACCTTTCAGTTGACGTCTTAGGTACTGCGTTGCGTGCAGGCAATTCCTGCTACAATCTA 261
                ** **************

TP03_0210       CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 1675
XM_758135       ------------------------------------------------------------ 1028
V1(2)           CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 319
V2(2)           CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTACTTATCCCATCCTGGA-TTCTA 319
V3(4)           CTCAGTTTACTAGTTATTCATCACCTACTTTGCACTTATTTATCCCATCCTGGA-TTCTA 320
V4(2)           CTCAGTTTACTAGTTATTCATCACCTACTTTGCACTTATTTATCCCATCCTGGGTTTGTA 321
V5(2)           CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 317
V6(1)           CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 320
V7(1)           CTCAGTTTACTAGTTATTTATACCCTACTTTGCAGTTATTTATCCCATCCTGGA-TTCTA 320
V8(1)           CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 320
V9(2)           CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 320
V10(1)          CTCAGCCTACTAGTTATTTATACTTTAGTGTTCACTTATTTATCCCATCCTGGA-TTCTA 320
V11(1)          CTCAGTTTAATAGTTATTTATCACCTACTKTGCAGTTATTTATCCCATCCTGGA-TTCTA 320
V12(2)          CTCAGTTTAATAGTTATTTATCACCTACTGTGCACTTATTTATCCCATCCTGGGTTTGTA 314
V13(3)          CTCAGTTTAATAGTTATTTATCACCTACTGTGCACTTATTTATCCCATCCTGGA-TTCTA 320


TP03_0210       TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACTTTTTAAATATAAT 1735
XM_758135       ------------------------------------------------------------ 1028
V1(2)           TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACTTTTTAAATATAAT 379
V2(2)           TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACTTTTTAAATATAAT 379
V3(4)           TTCATCATTTACACCAGATTTACATGCTTTATTTATTGTATTCCACTTTTTAAATATAAT 380
V4(2)           TTCATCATTTACACTAGATTTACATGCTACTTATGAGTTATTCCACTTTTTAAATATAAT 381
V5(2)           TTCATCATTTAAACTAGATTTACATGGTTTCTTTATTGTATTCCACTTT-TAAATACAAT 376
V6(1)           TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACCTTTTAAATATAAT 380
V7(1)           TTCATCATTTACACCAGATTTACATTCTTTATTTATTGTATTTCACCTTTTAAATATAAT 380
V8(1)           TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACTTTTTAAATATAAT 380
V9(2)           TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACTTTTTAAATATAAT 380
V10(1)          TTCATCATTTACACTAGATTTACATGTTTTATTTATTGTATTCCACCTTTTAAATATAAT 380
V11(1)          TTCATCATTTACACTAGATTTACATGGTTTCTTTGTTGTATTTCACCTTTTAAATATAAT 380
V12(2)          TTCATCATTTAAACTAGATTTACATTCTTTATTTATTGTATTCCACTTTTTAAATATAAT 374
V13(3)          TTCATCATTTACACCAGATTTACATGGTTTCTTTATTGTATTCCACTTTTTAAATATAAT 380


TP03_0210       TTTATAATGGTTTATTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 1795
XM_758135       -------------CTTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 1075
V1(2)           TTTATAATGGTTTATTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 439
V2(2)           TTTATAATGGTTTATTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 439
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V3(4)          TTTATAATGGTTTATTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 440
V4(2)          TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAGGTCCAAATTGGCTCTGAAC 441
V5(2)          TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAGGTCCAAATTGGCTCTGAAC 436
V6(1)          TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 440
V7(1)          TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAAGTCCAAATTGGGTCTGAAC 440
V8(1)          TTTATAATGGTTTATTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 440
V9(2)          TTTATAATGGTTTATTAGGAACTTGTGGTGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 440
V10(1)         TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAAGTGCAAATTGGGTCTGAAC 440
V11(1)         TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAAGTCCAAATTGGMTCTGAAC 440
V12(2)         TTTATAATGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAGGTCCAAATTGGGTCTGAAC 434
V13(3)         TTTATACTGGTTTATTAGGAACTTGTGGAGTGTTTGAGGAGGTCCAAATTGGCTCTGAAC 440
                             ************** *********** ** ******** *******

TP03_0210      GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 1855
XM_758135      GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 1135
V1(2)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 499
V2(2)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 499
V3(4)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
V4(2)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 501
V5(2)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 496
V6(1)          GTTACAATATGTTCACAGATTGCAAGAGTTCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
V7(1)          GTTACAATTTGTTCACCGATTGCAAGAGTGCAAAAACCTGTACAATTGTGCTGAGAGGTG 500
V8(1)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
V9(2)          GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
V10(1)         GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
V11(1)         GTTACAATATGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
V12(2)         GTTACAATTTGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 494
V13(3)         GTTACAATTTGTTCACAGATTGCAAGAGTGCAAAAACCTGTACAATTGTGTTGAGAGGTG 500
               ******** ******* ************ ******************** *********

TP03_0210      GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 1915
XM_758135      GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 1195
V1(2)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 559
V2(2)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 559
V3(4)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 560
V4(2)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 561
V5(2)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCAATTATGATTGTCA 556
V6(1)          GGGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCAATTATGATTGTCA 560
V7(1)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCAATTATGATTGTCA 560
V8(1)          GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 560
V9(2)          GGGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 560
V10(1)         GGGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCAATTATGATTGTCA 560
V11(1)         GGGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 560
V12(2)         GGGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCAATTATGATTGTCA 554
V13(3)         GAGGTCAGCAGTTCATTGATGAATCTGAACGTTCACTCCATGACGCGATTATGATTGTCA 560
               * ******************************************** *************

TP03_0210      GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGTGCCATTGAGATGTTGCTCT 1975
XM_758135      GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGTGCCATTGAGATGTTGCTCT 1255
V1(2)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGTGCCATTGAGATGTTGCTCT 619
V2(2)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGCGCTATTGAGATGTTGCTCT 619
V3(4)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGCGCCGGCGCCATTGAAATGTTACTCT 620
V4(2)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGTGCCATTGAGATGTTACTCT 621
V5(2)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGCGCCATTGAGATGTTGCTCT 616
V6(1)          GAAGAGCAACTAAGTGTAATACTATTCTTCCCGGCGCCGGCGCCATTGAGATGTTACTCT 620
V7(1)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGCGCCATTGAGATGTTACTCT 620
V8(1)          GAAGAGCAACTAAGTGTAATACTATTCTTCCCGGCGCCGGCGCCATTGAGATGTTGCTCT 620
V9(2)          GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGCGCCATTGAGATGTTGCTCT 620
V10(1)         GAAGAGCAACTAAGTGTAATACTATTCTTCCCGGCGCCGGCGCCATTGAGATGTTACTCT 620
V11(1)         GAAGAGCAACTAAATGTAATACTATCCTTCCCGGMGCCGGCGCCATTGAGATGTTACTCT 620
V12(2)         GAAGAGCAACTAAATGTAATACTATCCTTCCCGGAGCTGGTGCCATTGAGATGTTGCTCT 614
V13(3)         GAAGAGCAACTAAATGTAATACTATTCTTCCCGGCGCCGGCGCCATTGAGATGTTGCTCT 620
               ************* *********** ******** ** ** ** ***** ***** ****
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```
TP03_0210      CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCTGTCAACCATG 2035
XM_758135      CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCTGTCAACCATG 1315
V1(2)          CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCTGTCAACCATG 679
V2(2)          CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 679
V3(4)          CAACTTATCTCCTACACTACTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V4(2)          CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 681
V5(2)          CAACTTATCTCCTCCACTATTCTCTCAACACTATCAATCCCACAGACTCAGTTAACCATG 676
V6(1)          CAACTTATCTCCTACACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V7(1)          CAACTTATCTCCTACACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V8(1)          CAACTTATCTCCTACACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V9(2)          CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V10(1)         CAACTTATCTCCTACACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V11(1)         CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
V12(2)         CAACTTATCTCCTACACTACTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 674
V13(3)         CAACTTATCTCCTCCACTATTCTCTCAACACTATTAATCCCACAGACTCAGTTAACCATG 680
               ************* ***** ************** ************** ** *******

TP03_0210      TTAACTGCGTTAACTCCGTAAATCATGTTAATGGAGTTACTGGGGTGAATAAGAGTCTGG 2095
XM_758135      TTAACTGCGTTAACTCCGTAAATCATGTTAATGGAGTTACTGGGGTGAATAAGAGTCTGG 1375
V1(2)          TTAACTGCGTTAA----------------------------------------------- 692
V2(2)          TTAACTGCGTTAA----------------------------------------------- 692
V3(4)          TTAACTGCGTTAA----------------------------------------------- 693
V4(2)          TTAACTGCGTTAA----------------------------------------------- 694
V5(2)          TTAACTGCGTTAA----------------------------------------------- 689
V6(1)          TTAACTGCGTTAA----------------------------------------------- 693
V7(1)          TTAACTGCGTTAA----------------------------------------------- 693
V8(1)          TTAACTGCCTTAA----------------------------------------------- 693
V9(2)          TTAACTTCGTTAA----------------------------------------------- 693
V10(1)         TTAACTGCGTTAA----------------------------------------------- 693
V11(1)         TTAACTGCGTTAA----------------------------------------------- 693
V12(2)         TTAACTGCGTTAA----------------------------------------------- 687
V13(3)         TTAACTGCGTTAA----------------------------------------------- 693
               ****** * ****
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Primer regions are in bold, underlined and italicized text.

Table S6b: Tp4 protein variant Clustal alignment

```
XP_763228      ATQYFADKNVFCAGRVDENDLIRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 360
V1(10)         --QYFADKNVFCAGRVDENDLIRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 58
V2(1)          --QYFADKNVFCAGRVDENDLIRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 58
V3(6)          --QYFADKNVFCAGRVDENDLIRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 58
V4(4)          --QYFADKNVFCAGRVDENDLVRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 58
V5(2)          --QYFADKNVFCAGRVDENDLIRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 58
V6(1)          --QYFADKNVFCAGRVDENDLIRTSKATGASIQTTLNNLSVDVLGTCGVFEEVQIGSERY 58
                 ******************* **************************************

XP_763228      NMFTDCKSAKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 420
V1(10)         NMFTDCKSAKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 118
V2(1)          NMFTDCKSSKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 118
V3(6)          NLFTDCKSAKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 118
V4(4)          NMFTDCKSAKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 118
V5(2)          NMFTDCKSAKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 118
V6(1)          NMFTDCKSAKTCTIVLRGGGQQFIDESERSLHDAIMIVRRATKCNTILPGAGAIEMLLST 118
               * ****** ***************************************************

XP_763228      YLLHYSLNTINPTDSVNHVNCVNSVNHVNGVTGVNKSLVGKRHIIMNGFAKALECIPRNL 480
V1(10)         YLLHYSLNTINPTDSVNHVNCV-------------------------------------- 140
V2(1)          YLLHYSLNTINPTDSVNHVNCV-------------------------------------- 140
V3(6)          YLLHYSLNTINPTDSVNHVNCV-------------------------------------- 140
V4(4)          YLLHYSLNTINPTDSVNHVNCV-------------------------------------- 140
V5(2)          YLLHYSLNTINPTDSVNHVNFV-------------------------------------- 140
V6(1)          YLLHYSLNTINPTDSVNHVNCL-------------------------------------- 140
               ********************
```

Eptiope region highlighted in grey.

Table S7a: Tp5 nucleotide variant Clustal alignment

```
TP02_0767(genomic)      TAGAGGAAAGATGAGGAAGCGAGTTTGGGTAAATGCCGGCGATATTATTTTGGTATCGCT        539
XM_765334(mRNA)         TAGAGGAAAGATGAGGAAGCGAGTTTGGGTAAATGCCGGCGATATTATTTTGGTATCGCT        301
V1(10)                  ------------------------------------------------------------        0
V2(1)*                  ------------------------------------------------------------        0
V3(2)                   -----------------------------TAAATGCCGGCGATATTATTTTGGTATCGCT        31
V4(1)                   -----------------------------TAAATGCCGGCGATATTATTTTGGTATCGCT        31
V5(1)*                  -----------------------------TAAATGCCGGCGATATTATTTTGGTATCGCT        31
V6(1)*                  ------------------------------------------------------------        0


TP02_0767(genomic)      TAGAGATTTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACTGCTGAGGAGGCTCG        599
XM_765334(mRNA)         TAGAGATTTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACTGCTGAGGAGGCTCG        361
V1(10)                  -------TTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACTGCTGAGGAGGCTCG        53
V2(1)*                  -------TTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACTGCTGAGGAGGCTCG        53
V3(2)                   TAGAGATTTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACTGCTGAGGAGGCTCG        91
V4(1)                   TAGAGATTTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACCGCTGAGGAGGCGCG        91
V5(1)*                  -------TTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACCGCTGAGGAGGCGCG        53
V6(1)*                  -------TTCCAGGACAGCAAGGCTGACGTGATCGCAAAGTACACTGCTGAGGAGGCTCG        53
                               ************************************** *********** **

TP02_0767(genomic)      TACTCTGAAGGCTTACGGCGAGTTGCCTGAAGCGACCAAAATCAACGAAACTGACGTGTA        659
XM_765334(mRNA)         TACTCTGAAGGCTTACGGCGAGTTGCCTGAAGCGACCAAAATCAACGAAACTGACGTGTA        421
V1(10)                  TACTCTGAAGGCTTACGGCGAGTTGCCTGAAGCGACCAAAATCAACGAAACTGACGTGTA        113
V2(1)*                  TACTCTGAAGGCTTACGGGGAGTTGCCTGAAGCGACCAAAATCAACGAAACTGACGTGTA        113
V3(2)                   TACTCTGAAGGCTTACGGGGAGTTGCCTGAAGCGACCAAAATCAACGAAACTGACGTGTA        151
V4(1)                   TACTCTCAAGGCTTACGGAGAATTACCTGAAGCAACTAAAATCAACGAAACAGATGTGTA        151
V5(1)*                  TACTCTCAAGGCTTACGGAGAATTACCTGAAGCAACTAAAATCAACGAAACAGATGTGTA        113
V6(1)*                  TACTCTGAAGGCTTACGGTGAGTTGCCTGAAGCGACCAAAATCAACGAAACTGACGTGTA        113
                        ****** *********** ** ** ******** ** ************** ** *****

TP02_0767(genomic)      CGACGACGAGGCCGACAACTGCATTGACTTCCAGGACGTATCGTCTGAATCAGAACCTGA        719
XM_765334(mRNA)         CGACGACGAGGCCGACAACTGCATTGACTTCCAGGACGTATCGTCTGAATCAGAACCTGA        481
V1(10)                  CGACGACGAGGCCGACAACTGCATTGACTTCCAGGACGTATCGTCTGAATCAGAACCTGA        173
V2(1)*                  CGACGACGAGGCCGACAACTGCATTGACTTCCAGGACGTATCCTCTGAATCAGAACCTGA        173
V3(2)                   CGACGACGAGGCCGACAACTGCATTGACTTCCAGGACGTATCGTCTGAATCAGAACCTGA        211
V4(1)                   CGACGACCAGGCTGACAACTGCATTGACTTCCCGGACGTTTCCTCCGAGTCCGAACCCGA        211
V5(1)*                  CGACGACGAGGCTGACAACTGCATTGACTTCCAGGACGTTTCATCCGAGTCAGAACCCGA        173
V6(1)*                  CGACGACGAGGCCGACAATTGCATTGACTTCCAGGACGTATCCTCTGAATCAGAACCTGA        173
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                        ******* **** ***** ************* ****** ** ** ** ** ***** **

TP02_0767(genomic)      GGATGAGTCACAAGAGGAGTCGGATTT-------------------      746
XM_765334(mRNA)         GGATGAGTCACAAGAGGAGTCGGATTTCGATATCGATGATTTATAA      527
V1(10)                  GGATGAGTCACAAGAGGAGTCGGATTT-------------------      200
V2(1)*                  GGATGAGTCACAAGAGGAGTCGGATTT-------------------      200
V3(2)                   GGATGAGTCACAAGAGGAGTCGGATTT-------------------      238
V4(1)                   AGATGAATCTCAAGAGGAGTCGGATTT-------------------      238
V5(1)*                  AGATGAATCTCAAGAGGAATCAGAGTT-------------------      200
V6(1)*                  GGATGAGTCACAAGAGGAGTCGGATTT-------------------      200
                         ***** ** ******** ** ** **
```

Primer regions are in bold, underlined and italicized text.

* Partial sequence as defined by only having either the forward or reverse sequence of the allele available for analysis. This sequence is its own variant due to unique nucleotides.

Table S7b: Tp5 protein variant Clustal alignment

```
XP_765334        IRGKMRKRVWVNAGDIILVSLRDFQDSKADVIAKYTAEEARTLKAYGELPEATKINETDV 120
V1(14)           -----------NAGDIILVSLRDFQDSKADVIAKYTAEEARTLKAYGELPEATKINETDV 49
V2(1)            -----------NAGDIILVSLRDFQDSKADVIAKYTAEEARTLKAYGELPEATKINETDV 49
V3(1*           -----------------------FQDSKADVIAKYTAEEARTLKAYGELPEATKINETDV  37
                                        *************************************

XP_765334        YDDEADNCIDFQDVSSESEPEDESQEESDFDIDDL  155
V1(14)           YDDEADNCIDFQDVSSESEPEDESQEESD------  78
V2(1)            YDDQADNCIDFPDVSSESEPEDESQEESD------  78
V3(1)*           YDDEADNCIDFQDVSSESEPEDESQEESE------  66
                 *** ******* ****************
```

* Partial sequence as defined by only having either the forward or reverse sequence of the allele available for analysis. This sequence is its own variant due to unique nucleotides.

Eptiope region highlighted in grey.

Table S8a: Tp6 nucleotide variant Clustal alignment

```
TP01_0188(genomic)      ATTATTTGTAATGGCTCAGATTCCTGTTGATAAATTCGCTAAATTAGTTACTGGAGCCGG     60
XM_765715(mRNA)         ATTATTTGTAATGGCTCAGATTCCTGTTGATAAATTCGCTAAATTAGTTACTGGAGCCGG     0
V1(4)                   ------------------------------------------------------------     0
V2(1)                   ------------------------------------------------------------     0
V3(1)                   ------------------------------------------------------------     0
V4(1)                   ------------------------------------------------------------     0
V5(1)                   ------------------------------------------------------------     0
V6(1)                   ------------------------------------------------------------     0
V7(1)                   ------------------------------------------------------------     0
V8(1)                   ------------------------------------------------------------     0
V9(2)                   ------------------------------------------------------------     0
V10(1)                  ------------------------------------------------------------     0
V11(1)                  ------------------------------------------------------------     0
V12(2)                  ------------------------------------------------------------     0
V13(6)                  ------------------------------------------------------------     0


TP01_0188(genomic)      CTCTGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     120
XM_765715(mRNA)         CTCTGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATG-     120
V1(4)                   -TCTGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     59
V2(1)                   -TCCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTTAATTCCAGTTTATACGATGG     59
V3(1)                   -TCCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTTAATTCCAGTTTATACGATGG     59
V4(1)                   -TCCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTTAATTCCAGTTTATACGACGG     59
V5(1)                   ------------------------------------------------------------     0
V6(1)                   --CCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     58
V7(1)                   ----GCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     56
V8(1)                   -TCCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     59
V9(2)                   ----GCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTTAATTCCAGTTTATACGATGG     56
V10(1)                  -TCCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTTAATTCCAGTTTATACGATGG     59
V11(1)                  -TCTGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     59
V12(2)                  -TCCGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTTAATTCCAGTTTATACGATGG     59
V13(6)                  -TCTGCTCTCTTATTATTCGGTTCAGGTGCCTGGCTTGTCAATTCCAGTTTATACGATGG     59


TP01_0188(genomic)      TAAGATTCTACTCTACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAGA     180
XM_765715(mRNA)         ------------------------------------------------------------     120
V1(4)                   TAAGATTCTACTCTACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAGA     119
V2(1)                   TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAAA     119
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V3(1)                  TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATTTTATATATATAAA    119
V4(1)                  TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATATA    119
V5(1)                  -----------------------------------TATTTTATTATATAATATATATAAA    25
V6(1)                  TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAAA    118
V7(1)                  TAAGATTCTATTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAAA    116
V8(1)                  TAAGATTCTATTCGACTTCCACTTTATATTAGCTTTATTTTATTATTTTATATATATAAA    119
V9(2)                  TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATTTTATATATATAAA    116
V10(1)                 TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATTTTATATATATAAA    119
V11(1)                 TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAAA    119
V12(2)                 TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAAA    119
V13(6)                 TAAGATTCTACTCGACTTCCACTTTATATTAGCTTTATTTTATTATATAATATATATAAA    119


TP01_0188(genomic)     ATTGTAAAAACAATCTTTAAAAACCTTTATCATTAATTTTTATTGATTTTTTTATTGT      238
XM_765715(mRNA)        ----------------------------------------------------------      120
V1(4)                  ATTGTAAAAACAATCTTTAAAAACCTTTATCATTAATTTTTATTGATTTTTTTATTGT      177
V2(1)                  ATTGTAAAAATACCCTTTTAAATCCTTTATCATTGATTTTTATTGATTTTTTTATTGT      177
V3(1)                  ATTGTAAAAATAATCTTTAAAAACCTTTATCATTAATTTTTATTGATTTTTTTATTGT      177
V4(1)                  ATTGTAAAAATACCCTTTTAAATCCTTTATCATTAATTTTTATTGATTTTTTTATTGT      177
V5(1)                  ATTGTAAAAATACCCTTTTAAATCCTTTATCATTGATTTTTATTGATTTTTTTATTGT      83
V6(1)                  ATTGTAAAAATACCCTTTTAAATCCTTTATCATTGATTTTTATTGATTTTTTTATTGT      176
V7(1)                  ATTGTAAAAATACCCTTTTAAATCCTTTATCATTAATTTTTATTGATTTTTTTATTGT      174
V8(1)                  ATTGTAAAAATAATCTTTAAAAACCTTTATCATTAATTTTTATTGATTTTTTTATTGT      177
V9(2)                  ATTGTAAAAATAATCTTTAAAAACCTTTATCATTAATTTTTATTGATTTTTTTATTGT      174
V10(1)                 ATTGTAAAAATAATCTTTAAAAACCTTTATCATTAATTTTTATTGATTTTTTTATTGT      177
V11(1)                 ATTGTAAAAATACCCTTTTAAATCCTTTATCATTGATTTTTATTGATTTTTTTATTGT      177
V12(2)                 ATTGTAAAAATACCCTTTTAAATCCTTTATCATTGATTTTTATTGATTTTTTTATTGT      177
V13(6)                 ATTGTAAAAATACCCTTTTAAATCCTTTATCATTGATTTTTATTGATTTTTTTATTGT      177


TP01_0188(genomic)     AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    298
XM_765715(mRNA)        ------------------------------------------------------------    120
V1(4)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    237
V2(1)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    237
V3(1)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    237
V4(1)                  AAATATATTGAACAGTAATGATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    237
V5(1)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    143
V6(1)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    236
V7(1)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    234
V8(1)                  AGTTATATTGAACAGTAATCATTTTTAGAATGACTTTTAATTTGTTAAATATTTTATAAA    237
V9(2)                  AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA    234
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V10(1)               AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA     237
V11(1)               AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA     237
V12(2)               AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA     237
V13(6)               AGTTATATTGAACAGTAATCATTTTTAGAATGATTTTTAATTTGTTAAATATTTTATAAA     237


TP01_0188(genomic)   TTTTACTATTTAATGTCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTTGT     358
XM_765715(mRNA)      -----------------------------------TTGGAGCTGGGCATAGAGCTGTTGT     144
V1(4)                TTTTACTATTTAATGTCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTTGT     297
V2(1)                TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTTGT     297
V3(1)                TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     297
V4(1)                TTTTACTATTTAATGTCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     297
V5(1)                TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTTGT     203
V6(1)                TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     296
V7(1)                TTTTACTATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTTGT     294
V8(1)                TTTTACTATTTAATGTCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     297
V9(2)                TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     294
V10(1)               TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     297
V11(1)               TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     297
V12(2)               TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTTGT     297
V13(6)               TTTTACGATTTAATATCTCTTTAATGTTGAATTAGTTGGAGCTGGGCATAGAGCTGTCGT     297
                                                        *************************

TP01_0188(genomic)   ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     418
XM_765715(mRNA)      ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     204
V1(4)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     357
V2(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     357
V3(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     357
V4(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     357
V5(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     263
V6(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     356
V7(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     354
V8(1)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     357
V9(2)                ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     354
V10(1)               ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACGCACTTCATAAT     357
V11(1)               ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     357
V12(2)               ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     357
V13(6)               ATATAACCGTATCACTGGAATAAGTGAGACTACACATGGAGAAGGAACCCACTTCATAAT     357
                     ************************************************ ***********

TP01_0188(genomic)   TCCCTGGCTAGAACGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     478
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XM_765715(mRNA)          TCCCTGGCTAGAACGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     264
V1(4)                    TCCCTGGCTAGAACGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V2(1)                    TCCCTGGCTAGAACGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V3(1)                    TCCCTGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V4(1)                    TCCCTGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V5(1)                    TCCCTGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     323
V6(1)                    TCCATGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     416
V7(1)                    TCCATGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     414
V8(1)                    TCCCTGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V9(2)                    TCCCTGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     414
V10(1)                   TCCCTGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V11(1)                   TCCATGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V12(2)                   TCCCTGGCTAGAACGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
V13(6)                   TCCATGGTTAGAGCGTCCAATAATTTACGATGTGAGGACTCGTCCTAGGACTCTGATGTC     417
                         *** *** **** ***********************************************

TP01_0188(genomic)       TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     538
XM_765715(mRNA)          TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     324
V1(4)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V2(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V3(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V4(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V5(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     383
V6(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     476
V7(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     474
V8(1)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACGTGCCGTGTGTTGTCTCGTCC     477
V9(2)                    TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     474
V10(1)                   TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V11(1)                   TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V12(2)                   TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
V13(6)                   TCTCACCGGAAGCCGTGACTTGCAGATGGTTAACATCACCTGCCGTGTGTTGTCTCGTCC     477
                         *************************************** ********************

TP01_0188(genomic)       CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGCAAAGATTACGACGAGCGAGT     598
XM_765715(mRNA)          CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGCAAAGATTACGACGAGCGAGT     384
V1(4)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGCAAAGATTACGACGAGCGAGT     537
V2(1)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT     537
V3(1)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT     537
V4(1)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT     537
V5(1)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGATTATGACGAGCGAGT     443
V6(1)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT     536
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V7(1)                    TGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        534
V8(1)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        537
V9(2)                    CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        534
V10(1)                   CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        537
V11(1)                   CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        537
V12(2)                   CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        537
V13(6)                   CGATGAGCGCAGACTCAGGGATATTTACAGGCACTTGGGGAAAGACTATGACGAGCGAGT        537
                          ************************************** ***** ** ***********

TP01_0188(genomic)       CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        658
XM_765715(mRNA)          CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        444
V1(4)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        597
V2(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        597
V3(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATAGTTGCCCAGTACAACGCCTCTCA        597
V4(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        597
V5(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        503
V6(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        596
V7(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        594
V8(1)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATAGTTGCCCAGTACAACGCCTCTCA        597
V9(2)                    CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATAGTTGCCCAGTACAACGCCTCTCA        594
V10(1)                   CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATAGTTGCCCAGTACAACGCCTCTCA        597
V11(1)                   CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        597
V12(2)                   CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        597
V13(6)                   CCTGCCTTCAATAATAAACGAGGTTCTGAAGAGTATTGTGGCCCAGTACAACGCCTCTCA        597
                         ************************************ ** ********************

TP01_0188(genomic)       GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        718
XM_765715(mRNA)          GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        504
V1(4)                    GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V2(1)                    GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V3(1)                    GCTCATTACTCAGAGAGAAAGGGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V4(1)                    GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V5(1)                    GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        563
V6(1)                    GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        656
V7(1)                    GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        654
V8(1)                    GCTCATTACTCAGAGAGAAAGGGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V9(2)                    GCTCATTACTCAGAGAGAAAGGGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        654
V10(1)                   GCTCATTACTCAGAGAGAAAGGGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V11(1)                   GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V12(2)                   GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
V13(6)                   GCTCATTACTCAGAGAGAAAGAGTTAGCAAAGCAGTCAGGGACCAGCTGGTGAACAGGGC        657
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TP01_0188(genomic)        CAGGGACTTTAATATTCTTCTCGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        778
XM_765715(mRNA)           CAGGGACTTTAATATTCTTCTCGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        564
V1(4)                     CAGGGACTTTAATATTCTTCTCGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V2(1)                     CAGGGACTTCAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V3(1)                     CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V4(1)                     CAGGGACTTTAATATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V5(1)                     CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        623
V6(1)                     CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        716
V7(1)                     CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        714
V8(1)                     CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V9(2)                     CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        714
V10(1)                    CAGGGACTTTAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V11(1)                    CAGGGACTTTAATATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V12(2)                    CAGGGACTTCAACATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
V13(6)                    CAGGGACTTTAATATTCTTCTTGATGATGTCTCCTTAACCCACTTAAGCTTCAGTCCTGA        717
                          ********* ** ******** **************************************

TP01_0188(genomic)        ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        838
XM_765715(mRNA)           ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        624
V1(4)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        777
V2(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        777
V3(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        777
V4(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAGTA        777
V5(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGTAGTAAATA        683
V6(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGTAGTAAATA        776
V7(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        774
V8(1)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        777
V9(2)                     ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        774
V10(1)                    ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        777
V11(1)                    ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAGCAGCAAGCTGAACGCAGTAAATA        777
V12(2)                    ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAACAGCAAGCTGAACGCAGTAAATA        777
V13(6)                    ATATGAAAAGGCTGTAGAGGCTAAACAAGTAGCTCAGCAGCAAGCTGAACGCAGTAAATA        777
                          ************************************ ************** ***** **

TP01_0188(genomic)        TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC        898
XM_765715(mRNA)           TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC        684
V1(4)                     TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC        837
V2(1)                     TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATC---------------------------        810
V3(1)                     TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGATTC        837
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V4(1)                  TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     837
V5(1)                  TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     743
V6(1)                  TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     836
V7(1)                  TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     834
V8(1)                  TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     837
V9(2)                  TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     834
V10(1)                 TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGATTC     837
V11(1)                 TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     837
V12(2)                 TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATC---------------------------     810
V13(6)                 TATAGTGTTGAAGGCTCAGGAGGAGAAGAAATCGACGATAATTAAGGCTCAGGGAGAGTC     837
                       *********************************

TP01_0188(genomic)     TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     958
XM_765715(mRNA)        TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     744
V1(4)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897
V2(1)                  ------------------------------------------------------------     810
V3(1)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897
V4(1)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897
V5(1)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCC------------------     785
V6(1)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     896
V7(1)                  TGAGGCTGCAAGG-----------------------------------------------     847
V8(1)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897
V9(2)                  TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     894
V10(1)                 TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897
V11(1)                 TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897
V12(2)                 ------------------------------------------------------------     810
V13(6)                 TGAGGCTGCAAGGCTTATTGGAAGTGCAATTAAGGATAACCCTGCCTTTATTACGCTTCG     897


TP01_0188(genomic)     GAGAATTGAAACCGCTAAGGAAGTGGCTAACATTCTCTCCAAATCGCAGAATAAAATCAT     1018
XM_765715(mRNA)        GAGAATTGAAACCGCTAAGGAAGTGGCTAACATTCTCTCCAAATCGCAGAATAAAATCAT     804
V1(4)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     931
V2(1)                  ------------------------------------------------------------     810
V3(1)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     931
V4(1)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     931
V5(1)                  ------------------------------------------------------------     785
V6(1)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     930
V7(1)                  ------------------------------------------------------------     847
V8(1)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     931
V9(2)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     928
V10(1)                 GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------     931
```

```
V11(1)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------        931
V12(2)                  ------------------------------------------------------------        810
V13(6)                  GAGAATTGAAACCGCTAAGGAAGTGGCTAACATT--------------------------        931


TP01_0188(genomic)      GCTCAATAGTAATACTCTCTTACTCTCAACTGATAAATAATATTATCAATCCTCCAATAT        1078
XM_765715(mRNA)         GCTCAATAGTAATACTCTCTTACTCTCAACTGATAAATAATATTATCAATCCTCCAATAT        864
V1(4)                   ------------------------------------------------------------        931
V2(1)                   ------------------------------------------------------------        810
V3(1)                   ------------------------------------------------------------        931
V4(1)                   ------------------------------------------------------------        931
V5(1)                   ------------------------------------------------------------        785
V6(1)                   ------------------------------------------------------------        930
V7(1)                   ------------------------------------------------------------        847
V8(1)                   ------------------------------------------------------------        931
V9(2)                   ------------------------------------------------------------        928
V10(1)                  ------------------------------------------------------------        931
V11(1)                  ------------------------------------------------------------        931
V12(2)                  ------------------------------------------------------------        810
V13(6)                  ------------------------------------------------------------        931


TP01_0188(genomic)      GCTATTATAT    1088
XM_765715(mRNA)         GCTATTATAT    874
V1(4)                   ----------    931
V2(1)                   ----------    810
V3(1)                   ----------    931
V4(1)                   ----------    931
V5(1)                   ----------    785
V6(1)                   ----------    930
V7(1)                   ----------    847
V8(1)                   ----------    931
V9(2)                   ----------    928
V10(1)                  ----------    931
V11(1)                  ----------    931
V12(2)                  ----------    810
V13(6)                  ----------    931
```

Primer regions are in bold, underlined and italicized text.

[1] Include X.1 variants.

Table S8b: Tp6 protein variant Clustal alignment

```
XP_765715      MAQIPVDKFAKLVTGAGSALLLFGSGAWLVNSSLYDVGAGHRAVVYNRITGISETTHGEG 60
V1(22)[1]      ------------------------------------VGAGHRAVVYNRITGISETTHGEG 24
V2(1)          ------------------------------------VGAGHRAVVYNRITGISETTHGEG 24
                                                   ************************

XP_765715      THFIIPWLERPIIYDVRTRPRTLMSLTGSRDLQMVNITCRVLSRPDERRLRDIYRHLGKD 120
V1(22)         THFIIPWLERPIIYDVRTRPRTLMSLTGSRDLQMVNITCRVLSRPDERRLRDIYRHLGKD 84
V2(1)          THFIIPWLERPIIYDVRTRPRTLMSLTGSRDLQMVNITCRVLSRPDERRLRDIYRHLGKD 84
               ************************************************************

XP_765715      YDERVLPSIINEVLKSIVAQYNASQLITQRERVSKAVRDQLVNRARDFNILLDDVSLTHL 180
V1(22)         YDERVLPSIINEVLKSIVAQYNASQLITQRERVSKAVRDQLVNRARDFNILLDDVSLTHL 144
V2(1)          YDERVLPSIINEVLKSIVAQYNASQLITQRERVSKAVRDQLVNRARDFNILLDDVSLTHL 144
               ************************************************************

XP_765715      SFSPEYEKAVEAKQVAQQQAERSKYIVLKAQEEKKSTIIKAQGESEAARLIGSAIKDNPA 240
V1(22)         SFSPEYEKAVEAKQVAQQQAERSKYIVLKAQEEKKSTIIKAQGESEAARLIGSAIKDNPA 204
V2(1)          SFSPEYEKAVEAKQVAQQQAERSKYIVLKAQEEKKSTIIKAQGDSEAARLIGSAIKDNPA 204
               ******************************************* ****************

XP_765715      FITLRRIETAKEVANILSKSQNKIMLNSNTLLLSTDK    277
V1(22)         FITLRRIETAKEVANI---------------------    220
V2(1)          FITLRRIETAKEVANI---------------------    220
               ****************
```

[1] Include X.1 variants.

Eptiope sequence unknown.

Table S9a: Tp7 nucleotide variant Clustal alignment

```
TP02_0244(genomic)      CATTCATGGAGGCACTGCAAGCAGGCTCGGACATGTCAATGATCGGACAGTTTGGTGTCG          720
XM_759717(mRNA)         CATTCATGGAGGCACTGCAAGCAGGCTCGGACATGTCAATGATCGGACAGTTTGGTGTCG          490
V1(2)                   ------------------------------------------------------------          0
V2(4)[1]                 ------------------------------------------------------------         0
V3(1)                   ------------------------------------------------------------          0
V4(1)                   ------------------------------------------------------------          0
V5(2)                   ------------------------------------------------------------          0
V6(1)                   ------------------------------------------------------------          0
V7(7)                   ------------------------------------------------------------          0
V8(7)[1]                 ------------------------------------------------------------         0
V9(1)                   ------------------------------------------------------------          0


TP02_0244(genomic)      GTTTCTACTCAGCATACCTGGTCGCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          780
XM_759717(mRNA)         GTTTCTACTCAGCATACCTGGTCGCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          550
V1(2)                   ---------------ACCTGGTCGCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          45
V2(4)                   -----------------------GCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          37
V3(1)                   -----------------------GCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          37
V4(1)                   --------------------------------------------------------GCAG          4
V5(2)                   -----------------------GCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          37
V6(1)                   -----------------------GCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          37
V7(7)                   -----------------------GCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          37
V8(7)                   -----------------------GCAGATAAGGTGACAGTAGTGTCCAAGAACAACGCAG          37
V9(1)                   -----------------------GCAGATAAGGTGACAGTAGTTTCCAAGAACAATGCAG          37
                                                                                ****

TP02_0244(genomic)      ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          840
XM_759717(mRNA)         ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          610
V1(2)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          105
V2(4)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          97
V3(1)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          97
V4(1)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          64
V5(2)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          97
V6(1)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          97
V7(7)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          97
V8(7)                   ACGACCAGTACGTCTGGGAGTCAACAGCCTCAGGCCACTTTACAGTGAAGAAGGACGACT          97
V9(1)                   ATGACCAGTACGTCTGGGAGTCAACAGCCTCAGGTCACTTTACAGTGAAGAAGGACGACT          97
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TP02_0244(genomic)        CGCACGAGCCGCTCAAAAGAGGAACTAGACTAATACTGCACTTGAAGGAGGACCAAACTG      900
XM_759717(mRNA)           CGCACGAGCCGCTCAAAAGAGGAACTAGACTAATACTGCACTTGAAGGAGGACCAAACTG      670
V1(2)                     CGCACGAGCCGCTCAAAAGAGGAACTAGACTAATACTGCACTTGAAGGAGGACCAAACTG      165
V2(4)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      157
V3(1)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      157
V4(1)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      124
V5(2)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      157
V6(1)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      157
V7(7)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      157
V8(7)                     CGCACGAGCCGCTCAAAAGAGGAACGAGACTAATACTGCACTTGAAGGAGGACCAAACTG      157
V9(1)                     CACACGAACCCCTCAAAAGAGGAACGAGACTAATAYTGCACTTGAAGGAGGAYCAGTCTG      157
                          * ***** ** ************** ********* **************** **  ***

TP02_0244(genomic)        AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      960
XM_759717(mRNA)           AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      730
V1(2)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      225
V2(4)                     AGTACCTTGAGGAGAGAAGACTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      217
V3(1)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      217
V4(1)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      184
V5(2)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      217
V6(1)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      217
V7(7)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      217
V8(7)                     AGTACCTTGAGGAGAGAAGGCTGAAAGAGCTTGTTAAGAAGCACAGCGAGTTCATTTCAT      217
V9(1)                     AGTACCTTGAGGAGAGAAGGTTGAAGGAACTTGTYAAGAAACACAGCGAGTTCATTTCRT      217
                          *******************  **** ** ***** ***** ***************** *

TP02_0244(genomic)        TCCCAATCTCGCTCTCAGTAGAGAAGACCCAGGAGACCGAGGTCACTGACGACGAGGCAG      1020
XM_759717(mRNA)           TCCCAATCTCGCTCTCAGTAGAGAAGACCCAGGAGACCGAGGTCACTGACGACGAGGCAG      790
V1(2)                     TCCCAATCTCGCTCTCAGTAGAGAAGACCCAGGAGACCGAGGTCACTGACGACGAGGCAG      285
V2(4)                     TCCCAATCTCGCTCTCGGTAGAGAAGACTCAGGAGACCGAGGTCACTGACGACGAGGCAG      277
V3(1)                     TCCCAATCTCGCTCTCGGTAGAGAAGACCCAGGAGACCGAGGTTACTGACGACGAGGCAG      277
V4(1)                     TCCCAATCTCGCTCTCAGTAGAGAAGACCCAGGAGACCGAGGTCACTGACGACGAGGCAG      244
V5(2)                     TCCCAATCTCACTCTCGGTAGAGAAGACTCAGGAGACCGAGGTCACTGACGACGAGGCAG      277
V6(1)                     TCCCAATCTCGCTCTCAGTAGAGAAGACTCAGGAGACCGAGGTCACTGACGACGAGGCAG      277
V7(7)                     TCCCAATCTCGCTCTCAGTAGAGAAGACCCAGGAGACCGAGGTCACTGACGACGAGGCAG      277
V8(7)                     TCCCAATCTCGCTCTCGGTAGAGAAGACTCAGGAGACCGAGGTCACTGACGACGAGGCAG      277
V9(1)                     TCCCAATCTCACTCTCAGTAGAGAAGACTCAAGAGACCGAAGTTACTGACGATGAGGCCG      277
                          ********** ***** *********** ** ******** ** ******** ***** *
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TP02_0244(genomic)      AGCTAGACGAGGACAAGAAGCCCGAGGAGGAGAAGCCCAAGGACGATAAGGTGGAGGACG        1080
XM_759717(mRNA)         AGCTAGACGAGGACAAGAAGCCCGAGGAGGAGAAGCCCAAGGACGATAAGGTGGAGGACG        850
V1(2)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAGAAGCCCAAGGACGATAAGGTGGAGGACG        345
V2(4)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGGCCAAGGACGATAAGGTGGA-----        332
V3(1)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGGCCAAGGACGATAAGGTGGA-----        332
V4(1)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGCCCAAGGACGATAAGGTGGA-----        299
V5(2)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGGCCAAGGACGATAAGGTGGA-----        332
V6(1)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGGCCAAGGACGATAAGGTGGA-----        332
V7(7)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGGCCAAGGACGATAAGGTGGA-----        332
V8(7)                   AGCTAGACGAGGACAAGAAGCCCGAGGAGGAAAAGGCCAAGGACGATAAGGTGGA-----        332
V9(1)                   ACCTAGATGAGGATAAGAAACCTGAGGAAGAAAAGGACAAGGACCATAAGGTGGA-----        332
                        * ***** ***** ***** ** ***** ** ***  ******* * ********

TP02_0244(genomic)      TTACTGACGAGAAAGTGACCGACGTCACTGACGAGGAGGAGAAAAAGGAGGAAAAGAAAA        1140
XM_759717(mRNA)         TTACTGACGAGAAAGTGACCGACGTCACTGACGAGGAGGAGAAAAAGGAGGAAAAGAAAA        910
V1(2)                   TTACTGACGAGA------------------------------------------------        357
V2(4)                   ------------------------------------------------------------        332
V3(1)                   ------------------------------------------------------------        332
V4(1)                   ------------------------------------------------------------        299
V5(2)                   ------------------------------------------------------------        332
V6(1)                   ------------------------------------------------------------        332
V7(7)                   ------------------------------------------------------------        332
V8(7)                   ------------------------------------------------------------        332
V9(1)                   ------------------------------------------------------------        332
```

Primer regions are in bold, underlined and italicized text.

[1] Include X.1 variants.

Table S9b: Tp7 protein variant Clustal alignment

```
XP_764810      MSMIGQFGVGFYSAYLVADKVTVVSKNNADDQYVWESTASGHFTVKKDDSHEPLKRGTRL 180
V1(3)          -----------------ADKVTVVSKNNADDQYVWESTASGHFTVKKDDSHEPLKRGTRL 43
V2(21)         -----------------ADKVTVVSKNNADDQYVWESTASGHFTVKKDDSHEPLKRGTRL 43
V3(1)          -----------------ADKVTVVSKNNADDQYVWESTASGHFTVKKDDSHEPLKRGTRL 43
                                *******************************************

XP_764810      ILHLKEDQTEYLEERRLKELVKKHSEFISFPISLSVEKTQETEVTDDEAELDEDKKPEEE 240
V1(3)          ILHLKEDQTEYLEERRLKELVKKHSEFISFPISLSVEKTQETEVTDDEAELDEDKKPEEE 103
V2(21)         ILHLKEDQTEYLEERRLKELVKKHSEFISFPISLSVEKTQETEVTDDEAELDEDKKPEEE 103
V3(1)          ILHLKEDQSEYLEERRLKELVKKHSEFISFPISLSVEKTQETEVTDDEADLDEDKKPEEE 103
               ********:****************************************:**********

XP_764810      KPKDDKVEDVTDEKVTDVTDEEEKKEEKKKKKRKVTNVTREWEMLNKQKPIWMRLPSEVT 300
V1(3)          KPKDDKV----------------------------------------------------- 110
V2(21)         KAKDDKV----------------------------------------------------- 110
V3(1)          KDKDHKV----------------------------------------------------- 110
               * **.**
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Eptiope region highlighted in grey.

Table S10a: Tp8 nucleotide variant Clustal alignment

```
TP02_0140(genomic)      ATGCTTGGAAATCATGTCATGGGATCTAATTCCCCCCACATTAAAATTTTATCATCTGTT        60
XM_759616(mRNA)         ATGCTTGGAAATCATGTCATGGGATCTAATTCCCCCCACATTAAAATTTTATCATCTGTT        60
V1(3)                   ------------------------------------------------------------        0
V2(2)                   ------------------------------------------------------------        0
V3(1)                   ------------------------------------------------------------        0
V4(1)                   ------------------------------------------------------------        0
V5(1)                   ------------------------------------------------------------        0
V6(3)                   ------------------------------------------------------------        0
V7(1)                   ------------------------------------------------------------        0
V8(1)                   ------------------------------------------------------------        0
V9(1)                   ------------------------------------------------------------        0
V10(2)[1]                ------------------------------------------------------------       0
V11(5)[1]                ------------------------------------------------------------       0
V12(2)                  ------------------------------------------------------------        0


TP02_0140(genomic)      ACATTCTTACATATTGCTAAAATGGAAGAAGTAGAAAACGTAAAAGTCGACGCCTTGGAG        120
XM_759616(mRNA)         ACATTCTTACATATTGCTAAAATGGAAGAAGTAGAAAACGTAAAAGTCGACGCCTTGGAG        120
V1(3)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V2(2)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V3(1)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V4(1)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V5(1)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V6(3)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V7(1)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V8(1)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V9(1)                   ---------------------------------------------GTCGACGCCTTGGAG        15
V10(2)                  ---------------------------------------------GTCGACGCCTTGGAG        15
V11(5)                  ---------------------------------------------GTCGACGCCTTGGAG        15
V12(2)                  ---------------------------------------------GTCGACGCCTTGGAG        15
                                                                     ***************

TP02_0140(genomic)      CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC        180
XM_759616(mRNA)         CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC        180
V1(3)                   CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC        75
V2(2)                   CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC        75
V3(1)                   CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC        75
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V4(1)                 CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V5(1)                 CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V6(3)                 CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V7(1)                 CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V8(1)                 CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V9(1)                 CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V10(2)                CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V11(5)                CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
V12(2)                CGTGTTGACACTGAGTCTGTCCTTAATTATGACACTGTGTTAGAAAAGAAACCATTGCGC      75
                      ************************************************************

TP02_0140(genomic)    AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      240
XM_759616(mRNA)       AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      240
V1(3)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V2(2)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V3(1)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V4(1)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V5(1)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V6(3)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V7(1)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V8(1)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V9(1)                 AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V10(2)                AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V11(5)                AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
V12(2)                AGCAGTGTTGCCTCTTTCTTCAAAAGATACAGTGCTGTTCTCGTAATATTAACTGCCGTG      135
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TP02_0140(genomic)    CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      300
XM_759616(mRNA)       CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      300
V1(3)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V2(2)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V3(1)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V4(1)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V5(1)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V6(3)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V7(1)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V8(1)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V9(1)                 CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V10(2)                CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V11(5)                CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
V12(2)                CTATTATTCACATTCACTTTTGCAGCAATAGCATTGTCATCAGGCAGAAGCGCAATCAGA      195
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TP02_0140(genomic)      AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        360
XM_759616(mRNA)         AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        360
V1(3)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V2(2)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTACGTGACA        255
V3(1)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V4(1)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V5(1)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V6(3)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V7(1)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V8(1)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V9(1)                   AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V10(2)                  AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V11(5)                  AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
V12(2)                  AAGAACAGAGAACTCCTGTCAGTCGAATTTGAAAAGCTTCAGTTCGATAATTTCGTGACA        255
                        **************************************************** *******

TP02_0140(genomic)      ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAGGTT        420
XM_759616(mRNA)         ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAGGTT        420
V1(3)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAGGTT        315
V2(2)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V3(1)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V4(1)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V5(1)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V6(3)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V7(1)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V8(1)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V9(1)                   ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V10(2)                  ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V11(5)                  ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAAGTT        315
V12(2)                  ATTAAGGGAGAAAGGGAAGAGGACTTCCCCAAGATGGTAGCTGAAGTTCTTTACAAGGTT        315
                        ******************************************************** ***

TP02_0140(genomic)      GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC        480
XM_759616(mRNA)         GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC        480
V1(3)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC        375
V2(2)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCTTTGATCTACGTCCAGTTCAATGACTTTAAC        375
V3(1)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCTTTGATCTACGTCCAGTTCAATGACTTTAAC        375
V4(1)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC        375
V5(1)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC        375
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V6(3)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
V7(1)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
V8(1)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
V9(1)                   GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
V10(2)                  GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
V11(5)                  GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
V12(2)                  GCAGTCGAGTTTGACCCAAAAGAAGAGGCCTTGATCTACGTCCAGTTCAATGACTTCAAC     375
                        ***************************** ************************** ***

TP02_0140(genomic)      AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     540
XM_759616(mRNA)         AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     540
V1(3)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V2(2)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V3(1)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V4(1)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V5(1)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V6(3)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V7(1)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V8(1)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V9(1)                   AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V10(2)                  AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V11(5)                  AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
V12(2)                  AAGCAACACGACAAGAAGCACAACAATTACAGGCACAAGAAGACCTCGTACACCAACTTC     435
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TP02_0140(genomic)      AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     600
XM_759616(mRNA)         AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     600
V1(3)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V2(2)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V3(1)                   AGAGACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCCTACACCAAG     495
V4(1)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V5(1)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V6(3)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V7(1)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V8(1)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V9(1)                   AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V10(2)                  AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V11(5)                  AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
V12(2)                  AGAAACAACCTTAATGATATAAACGAGCACAACGCAAAACCAAACCTGTCGTACACCAAG     495
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TP02_0140(genomic)      AACATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       660
XM_759616(mRNA)         AACATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       660
V1(3)                   AACATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V2(2)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V3(1)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V4(1)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V5(1)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V6(3)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V7(1)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V8(1)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V9(1)                   AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V10(2)                  AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V11(5)                  AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
V12(2)                  AGCATGAACCACTTCGGTGACATATCATCCAAGGATTTCATGAAGAGATACACCAAGAAA       555
                        * **********************************************************

TP02_0140(genomic)      GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       720
XM_759616(mRNA)         GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       720
V1(3)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V2(2)                   GTACTCTTGAACTTGCCAAAAGACCACGCGTCCACCTATAACAACAACAGACCAATGTCA       615
V3(1)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V4(1)                   GTACTCTTGAACTTGCCAAAAGACCACGCGTCCACCTATAACAACAACAGACCAATGTCA       615
V5(1)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAATAACAACAGACCAATGTCA       615
V6(3)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAATAACAACAGACCAATGTCA       615
V7(1)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V8(1)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V9(1)                   GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V10(2)                  GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V11(5)                  GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
V12(2)                  GTACTCTTGAACTTGCCAAAAGACCACGTGTCCACCTATAACAACAACAGACCAATGTCA       615
                        **************************** ************ ******************

TP02_0140(genomic)      GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       780
XM_759616(mRNA)         GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       780
V1(3)                   GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
V2(2)                   GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
V3(1)                   GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
V4(1)                   GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
V5(1)                   GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
V6(3)                   GTTGATCTCAGAAGCCATGGTGTATTAACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
V7(1)                   GTTGATCTCAGAAGCCATGGTGTATTAACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC       675
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V8(1)                     GTTGATCTCAGAAGCCATGGTGTATTAACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC        675
V9(1)                     GTTGATCTCAGAAGCCATGGTGTATTAACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC        675
V10(2)                    GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC        675
V11(5)                    GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC        675
V12(2)                    GTTGATCTCAGAAGCCATGGTGTATTGACTCCAGTCAAGTGCCAAGAAGAAAATGAACTC        675
                          ************************** *********************************

TP02_0140(genomic)        TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        840
XM_759616(mRNA)           TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        840
V1(3)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V2(2)                     TCATGGCCGTACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V3(1)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAATCATTCGTTAAGAAGACATCACAAAAG        735
V4(1)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V5(1)                     TCATGGCCGTACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V6(3)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V7(1)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V8(1)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V9(1)                     TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V10(2)                    TCATGGCCATACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V11(5)                    TCATGGCCGTACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
V12(2)                    TCATGGCCGTACTCCGTAGTAGCAGTCGCCGAGTCATTCGTTAAGAAGACATCACAAAAG        735
                          ******** *********************** ***************************

TP02_0140(genomic)        ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        900
XM_759616(mRNA)           ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        900
V1(3)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V2(2)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V3(1)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCAGCAAAC        795
V4(1)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTCACAGATAAGAAATCTGCAAAC        795
V5(1)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V6(3)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V7(1)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGTAAAC        795
V8(1)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V9(1)                     ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V10(2)                    ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V11(5)                    ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
V12(2)                    ACCGTATCCCTCAGCGAAAAACAATTAGTAGATTGCGTTACAGATAAGAAATCTGCAAAC        795
                          ************************************** ************** * ****

TP02_0140(genomic)        AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA        960
XM_759616(mRNA)           AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA        960
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V1(3)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V2(2)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V3(1)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V4(1)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V5(1)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V6(3)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V7(1)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V8(1)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V9(1)                   AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V10(2)                  AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V11(5)                  AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
V12(2)                  AACCCATTCTTGGGTTACAAATACCTTAAGGACTTGGGTCTGTTCGAATCAGAACTCGTA       855
                        ************************************************************

TP02_0140(genomic)      GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       1020
XM_759616(mRNA)         GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       1020
V1(3)                   GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V2(2)                   GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V3(1)                   GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V4(1)                   GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V5(1)                   GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V6(3)                   GACAAATCCACAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V7(1)                   GACAAATCCGCAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCGTCATAC       915
V8(1)                   GACAAATCCGCAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCGTCATAC       915
V9(1)                   GACAAATCCGCAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V10(2)                  GACAAATCCGCAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V11(5)                  GACAAATCCGCAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
V12(2)                  GACAAATCCGCAACCAAGTGCCCAGCATTGGAAGGTGAAAGATTCAAAGTCCCATCATAC       915
                        ********* ******************************************** *****

TP02_0140(genomic)      TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       1080
XM_759616(mRNA)         TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       1080
V1(3)                   TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V2(2)                   TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V3(1)                   TCATACTCATATGAGCCCGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V4(1)                   TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V5(1)                   TCATACTCATATGAGCCCGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V6(3)                   TCATACTCATATGAGCCCGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V7(1)                   TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V8(1)                   TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
V9(1)                   TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA       975
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V10(2)                    TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA        975
V11(5)                    TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA        975
V12(2)                    TCATACTCATATGAGCCAGATTTGGTGGCACTCTTGTTGAATGCAGGACCACTCACTGTA        975
                          ***************** ******************************************

TP02_0140(genomic)        CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTATGCGGT        1140
XM_759616(mRNA)           CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTATGCGGT        1140
V1(3)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTATGCGGT        1035
V2(2)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V3(1)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V4(1)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V5(1)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V6(3)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V7(1)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V8(1)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V9(1)                     CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V10(2)                    CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V11(5)                    CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
V12(2)                    CCAGTTGCAGTGAGCGAGGATTGGCAATTCTACGCTGATGGAACCTTGGATGTGTGCGGT        1035
                          ***************************************************** ******

TP02_0140(genomic)        GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1200
XM_759616(mRNA)           GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1200
V1(3)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V2(2)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V3(1)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V4(1)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V5(1)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V6(3)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V7(1)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V8(1)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V9(1)                     GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V10(2)                    GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V11(5)                    GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
V12(2)                    GCTGAATTGAACCACTTCTTGACCCTAGTAGGTGTCAGCTTTGACGAAAAAGGCAATCAC        1095
                          ************************************************************

TP02_0140(genomic)        TGGATACTCAAAAACTCATTCGGTGAAGGCTGGGGAAACAAGGGATACCTACTGTTGACT        1260
XM_759616(mRNA)           TGGATACTCAAAAACTCATTCGGTGAAGGCTGGGGAAACAAGGGATACCTACTGTTGACT        1260
V1(3)                     TGGATACTCAAAAA----------------------------------------------        1109
V2(2)                     TGGATACTCAAAAA----------------------------------------------        1109
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V3(1)                   TGGATACTCAAAAA----------------------------------------------   1109
V4(1)                   TGGATACTCAAAAA----------------------------------------------   1109
V5(1)                   TGGATACTCAAAAA----------------------------------------------   1109
V6(3)                   TGGATACTCAAAAA----------------------------------------------   1109
V7(1)                   TGGATACTCAAAAA----------------------------------------------   1109
V8(1)                   TGGATACTCAAAAA----------------------------------------------   1109
V9(1)                   TGGATACTCAAAAA----------------------------------------------   1109
V10(2)                  TGGATACTCAAAAA----------------------------------------------   1109
V11(5)                  TGGATACTCAAAAA----------------------------------------------   1109
V12(2)                  TGGATACTCAAAAA----------------------------------------------   1109
                        **************
TP02_0140(genomic)      CGCAATAGCAAGGAATACAAAGATGATTGTGGATTGACCTCCTTCGCAGTGTACGCAGTT   1320
XM_759616(mRNA)         CGCAATAGCAAGGAATACAAAGATGATTGTGGATTGACCTCCTTCGCAGTGTACGCAGTT   1320
V1(3)                   ------------------------------------------------------------   1109
V2(2)                   ------------------------------------------------------------   1018
V3(1)                   ------------------------------------------------------------   1109
V4(1)                   ------------------------------------------------------------   1107
V5(1)                   ------------------------------------------------------------   1107
V6(3)                   ------------------------------------------------------------   1109
V7(1)                   ------------------------------------------------------------   1109
V8(1)                   ------------------------------------------------------------   1109
V9(2)                   ------------------------------------------------------------   1109
V10(2)                  ------------------------------------------------------------   1109
V11(5)                  ------------------------------------------------------------   1109
V12(2)                  ------------------------------------------------------------   1109


TP02_0140(genomic)      TAAAGATCAAAAATTGATATTTAATTATAATTGTACCACAAATTCTGTCCAAAGCTTTAG   1380
XM_759616(mRNA)         TAAAGATCAAAAATTGATATTTAATTATAATTGTACCACAAATTCTGTCCAAAGCTTTAG   1380
V1(3)                   ------------------------------------------------------------   1109
V2(2)                   ------------------------------------------------------------   1018
V3(1)                   ------------------------------------------------------------   1109
V4(1)                   ------------------------------------------------------------   1107
V5(1)                   ------------------------------------------------------------   1107
V6(3)                   ------------------------------------------------------------   1109
V7(1)                   ------------------------------------------------------------   1109
V8(1)                   ------------------------------------------------------------   1109
V9(1)                   ------------------------------------------------------------   1109
V10(2)                  ------------------------------------------------------------   1109
V11(5)                  ------------------------------------------------------------   1109
V12(2)                  ------------------------------------------------------------   1109
```

Primer regions are in bold, underlined and italicized text.

[1] Include X.1 variants.

Table S10b: Tp8 protein variant Clustal alignment

```
XP_764709          MLGNHVMGSNSPHIKILSSVTFLHIAKMEEVENVKVDALERVDTESVLNYDTVLEKKPLR      60
V1(3)              -----------------------------------VDALERVDTESVLNYDTVLEKKPLR      25
V2(1)              -----------------------------------VDALERVDTESVLNYDTVLEKKPLR      25
V3(1)              -----------------------------------VDALERVDTESVLNYDTVLEKKPLR      25
V4(2)              -----------------------------------VDALERVDTESVLNYDTVLEKKPLR      25
V5(1)              -----------------------------------VDALERVDTESVLNYDTVLEKKPLR      25
V6(5)[1]            -----------------------------------VDALERVDTESVLNYDTVLEKKPLR     25
V7(10)[1]           -----------------------------------VDALERVDTESVLNYDTVLEKKPLR     25
                                                      *************************

XP_764709          SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      120
V1(3)              SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      85
V2(1)              SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      85
V3(1)              SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      85
V4(2)              SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNYVT      85
V5(1)              SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      85
V6(5)              SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      85
V7(10)             SSVASFFKRYSAVLVILTAVLLFTFTFAAIALSSGRSAIRKNRELLSVEFEKLQFDNFVT      85
                   ************************************************************

XP_764709          IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      180
V1(3)              IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
V2(1)              IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
V3(1)              IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
V4(2)              IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
V5(1)              IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
V6(5)              IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
V7(10)             IKGEREEDFPKMVAEVLYKVAVEFDPKEEALIYVQFNDFNKQHDKKHNNYRHKKTSYTNF      145
                   ************************************************************

XP_764709          RNNLNDINEHNAKPNLSYTKNMNHFGDISSKDFMKRYTKKVLLNLPKDHVSTYNNNRPMS      240
V1(3)              RNNLNDINEHNAKPNLSYTKNMNHFGDISSKDFMKRYTKKVLLNLPKDHVSTYNNNRPMS      205
V2(1)              RNNLNDINEHNAKPNLSYTKSMNHFGDISSKDFMKRYTKKVLLNLPKDHVSTYNNNRPMS      205
V3(1)              RDNLNDINEHNAKPNLSYTKSMNHFGDISSKDFMKRYTKKVLLNLPKDHVSTYNNNRPMS      205
V4(2)              RNNLNDINEHNAKPNLSYTKSMNHFGDISSKDFMKRYTKKVLLNLPKDHASTYNNNRPMS      205
V5(1)              RNNLNDINEHNAKPNLSYTKSMNHFGDISSKDFMKRYTKKVLLNLPKDHASTYNNNRPMS      205
V6(5)              RNNLNDINEHNAKPNLSYTKSMNHFGDISSKDFMKRYTKKVLLNLPKDHVSTYNNNRPMS      205
V7(10)             RNNLNDINEHNAKPNLSYTKSMNHFGDISSKDFMKRYTKKVLLNLPKDHVSTYNNNRPMS      205
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XP_764709           VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      300
V1(3)               VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      265
V2(1)               VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSVN      265
V3(1)               VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      265
V4(2)               VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      265
V5(1)               VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      265
V6(5)               VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      265
V7(10)              VDLRSHGVLTPVKCQEENELSWPYSVVAVAESFVKKTSQKTVSLSEKQLVDCVTDKKSAN      265
                    **********************************************************.*

XP_764709           NPFLGYKYLKDLGLFESELVDKSTTKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      360
V1(3)               NPFLGYKYLKDLGLFESELVDKSTTKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
V2(1)               NPFLGYKYLKDLGLFESELVDKSATKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
V3(1)               NPFLGYKYLKDLGLFESELVDKSTTKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
V4(2)               NPFLGYKYLKDLGLFESELVDKSTTKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
V5(1)               NPFLGYKYLKDLGLFESELVDKSTTKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
V6(5)               NPFLGYKYLKDLGLFESELVDKSTTKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
V7(10)              NPFLGYKYLKDLGLFESELVDKSATKCPALEGERFKVPSYSYSYEPDLVALLLNAGPLTV      325
                    ***********************:************************************

XP_764709           PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILKNSFGEGWGNKGYLLLT      420
V1(3)               PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
V2(1)               PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
V3(1)               PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
V4(2)               PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
V5(1)               PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
V6(5)               PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
V7(10)              PVAVSEDWQFYADGTLDVCGAELNHFLTLVGVSFDEKGNHWILK----------------      369
                    ********************
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Eptiope region highlighted in grey.

Table S11a: Tp9 nucleotide variant Clustal alignment

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TP02_0140       ATGAATGTTCTAACTACTGGAATAATTTTATACTCATTCTATCTTTCCATTTGTA-TGGA
XM_760370       ATGAATGTTCTAACTACTGGAATAATTTTATACTCATTCTATCTTTCCATTTGTA-TGGA
V1(3)           ---------------------ATAATTTTATACTCATTCTATCTTTCCATTTGTA-TGGA
V2(3)           ------------------------------------------------ATTTGTA-TGGA
V3(2)           ------------------------------------------------ACTTCTA-AGGA
V4(3)           ------------------------------------------------------------
V5(1)           ---------------------ATAATTTTATACTCATTTTACACATGCCTTTGTA-TGGA
V6(2)           ------------------------------------------------GTTTGTA-AGGA
V7(1)           -------------------------------------------------CTTGCAGTGGA
V8(1)           ----------------------------AATAATTTTATACTCATTCTATCTTTC-ATTG
V9(1)           ------------------------------------------------CTTGCAG-TGGA
V10(1)          ------------------------------------------------GCTGCTG-AGGA
V11(1)          ------------------------------------------------------------
V12(1)          ------------------------------------------------ATTTGTA-TGGA
V13(1)          ------------------------------------------------GCTGCTG-AGGA
V14(1)          ------------------------------------------------TTTAGTG-TGGA
V15(1)          ------------------------------------------------------------
V16(1)          ---------------------------GTCAGACTGGTCGTACGATGCATTTGTC-TGGA
V17(1)          ---------------------------------------------------GTTA-CAGT
V18(2)          ---ATGAATGTTCTAACTACTGGTATAATTTTATACTCATTCTACATGTCCATTT-GTAT
V19(1)          --------------------AATAATTTTATTCTCATTTTACACATGCCTTTGTA-TGGA
V20(1)          ---ATGAATGTTCTAACTACTGGAATAATTTTATACTCATTCTATCTTTCCATTT-GTAT
V21(1)          --------------------AATAATTTTATACTCATTCTATCTTTCCATTTGTA-TGGA
V22(1)          ATGAATGTTCTAACTACTGGAATAATTTTATACTCATTCTATCAATGTATTTGTA-TGGA
V23(1)          --------------------AATAATTTTATACTCATTCTACCAATGCATTTGTA-TGGA
V24(1)          --------------------AATAATTTTGTACTCATTCTACACATGCCTTTGTA-TGAA
V25(1)          --------------------AATAATTTTGTACTCATTCTACACATGCCTTTGTA-TGAA
V26(1)          --------------------AATAATTTTATACTCATTCTACATGTCCATTTGTA-TGGA
V27(1)          --------------------AATAATTTTATACTCATTCTATCTTTCCATTTGTA-TGGA
V28(1)          ATGAATGTTCTAACTACTGGAATAATTTTATACTCATTCTATCTTTCCATTTGTA-TGGA


TP02_0140       TCCTGATGATGATGTATTTGGATTCGATCCTGATGACGATGGAGACGGAAGCATGCTCCC
XM_760370       TCCTGATGATGATGTATTTGGATTCGATCCTGATGACGATGGAGACGGAAGCATGCTCCC
V1(3)           TCCTGATGATGATGTATTTGGATTCGATCCTGATGACGATGGAGACGGAAGCATGCTCCC
V2(3)           TTCTGGTG--AAGAA----GAAGATGATGTTTTCGGTGCTGAAGGAGGTAGCATGCTACC
V3(2)           TTCTGGTG--ATGAT----GATGATGATGTTTTCGGTGCTGCGGGAGGTAGCATGCAACC
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V4(3)             -TCTGGTG--ATGAT----GATGATGATGTTTTCGGTGCTGCGGGAGGTAGCATGCTACC
V5(1)             TCCTGATG--AT----------GATGATGCTTTCGGTGATGACGGAGGTAGCATGCTACC
V6(2)             TACTGGTG--ATG-------ATGATGATGTTTTCGGTGATGACGGAGGTAGCATGCTAAC
V7(1)             TTCTGATG--ATGAT----GATGATGATGTTTTCGGTGCTGCGGGAGGTAGCATGCTACC
V8(1)             TATGGATACTGTGAT----GATGATGATGTTTTCGGTGATGACGCGGATAGCATGCTCCC
V9(1)             TTCTGATG--ATGAT----GATGATGATGTTTTCGGTGCTGCGGGAGGTAGCATGCTACC
V10(1)            TCCTGGTG--AAGAA----GAAGATGATGTTTTCGGTGCTGAAGGAGGTAGCATGCAACC
V11(1)            -------------------------GATGTTTTCGGTGCTGAAGGAGGTAGCATGCTACC
V12(1)            TTCTGGTG--AAGAA----GAAGATGATGTTTTCGGTGCTGAAGGAGGTAGCATGCTACC
V13(1)            TCCTGGTG--AAGAA----GAAGATGATGTTTTCGGTGCTGAAGGAGGTAGCATGCAACC
V14(1)            TCCTGGTG--AAGAA----GAAGATGATGTTTTCGGTGCTGAAGGAGGTAGCATGCTACC
V15(1)            -----------------------------------------------------------C
V16(1)            TTCTGGTG--AAGAA----GAAGATGATGTTTTCGGTGCTGAAGGAGGTAGCATGCTCCC
V17(1)            GGATCCTG--ATGAT----AATGATGATGTTTTCGGTGATGACGAAGGTAGCATGCTCCC
V18(2)            GGATCCTG--ATGAT----AATGATGATGTTTTCGGTGATGACGAAGGTAGCATGCTCCC
V19(1)            TTCTGATG---------------ATGATGTTTTCGGTGCTGACGACGGTAGCATGCTACC
V20(1)            GGATACTG--GTGAT----GATGATGATGTTTTCGGTGCTCCGGGAGGTAGCATGCTACC
V21(1)            TCCTGATGATGATGTATTTGGATTCGATCCTGATGACGATGGAGACGGAAGCATGCTCCC
V22(1)            TTCTGGTG--ATGAT----GATGATGATGTTTTCGGTGCTGCGGGAGGTAGCATGCTACC
V23(1)            TTCTGGTG--ATGAT----GATGATGATGTTTTCGGTGCTGCGGGAGGTAGCATGCTACC
V24(1)            TTCTGACG--ATGAC----GATGATGATGCTTTCGGTGCTGAAGGAGGTAGCATGCTCCC
V25(1)            TTCTGACG--ATGAC----GATGATGATGCTTTCGGTGCTGAAGGAGGTAGCATGCTCCC
V26(1)            TACTGATG--AAGAA----GATGATGATGTTTTCGGAGATCCAGGAGGTAGCATGCTACC
V27(1)            TACTGGTG--ATG-------ATGATGATGTTTTCGGTGCTGACGGAGGTAGCATGCTCCC
V28(1)            TACTGGTG--ATG-------ATGATGATGTTTTCGGTGCTGACGGAGGTAGCATGCTCCC


TP02_0140         TCCGCACCAAAGAAGCTCTATGTTTCGTGATGATCTCGGATCATCATTTACCTCAGGTTA
XM_760370         TCCGCACCAAAGAAGCTCTATGTTTCGTGATGATCTCGGATCATCATTTACCTCAGGTTA
V1(3)             TCCGCACCAAAGAAGCTCTATGTTTCGTGATGATCTCGGATCATCATTTACCTCAGGTTA
V2(3)             TCCACGCCAAAGAAGCTCTATGTTTGGTGAGCCTCTCGGATCATTACATACAGGAGGTTA
V3(2)             TCCACGCCAAAGAAGCCCTATGTTTAGTGGTGGTCTCGGATCATCATTCACCTCAGGTTA
V4(3)             TCCACGCCAAAGAAGCCCTATGTTTAGTGGTGGTCTCGGATCATCATTCACCTCAGGTTA
V5(1)             TGAGCACAAACCATTCTCTATGATTAGCGGTGGTCTAGGATCATCACATACCGGAGGTTA
V6(2)             TCCACACCAAAGAAGCTCTATGTTTCGTGATGATCTCGGATCATCATTTACCTCAGGTTA
V7(1)             TCCACGCCAAAGAAGCCCTATGTTTAGTGGTGGTCTCGGATCATCATTCACCTCAGGTTA
V8(1)             TAAACACCAAAGAAGCTCCGTGTTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V9(1)             TCCACGCCAAAGAAGCTCTATGTTTAGTGAGCCTCTTGGATCAACATTTACCTCAGGTTA
V10(1)            TCCACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACAATTACCTCAGGTTA
V11(1)            TCCACGCCAAAGAAGCTCTATGTTTGGTGAGCCTCTCGGATCATTACATACAGGAGGTTA
V12(1)            TCCACGCCAAAGAAGCTCTATGTTTGGTGAGCCTCTCGGATCATTACTTACCGGAGGTTA
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V13(1)          TCCACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V14(1)          TCCACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V15(1)          TTCACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V16(1)          TAAACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V17(1)          TAAACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V180(2)         TAAACACCAAAGAAGCTCTATGCTTGGTAGTGGTCTCGGATCAACATTTACCTCAGGTTA
V19(1)          TCCACACCAAAGAAGCTCTATGTTTAGTGAGCCTCTCGGATCATTACATACCGGAGGTTA
V20(1)          TCCACGCCAAAGAAGCTCTGTGTTTAGTGGTGGTATAGGATCAACATTTACCTCAGGTTA
V21(1)          TCCGCACCAAAGAAGCTCCATCTTTAGTAGTGATCTAGGATCAACATTTACCACAGGTTA
V22(1)          TCCACGCCAAAGAAGCCCTATGTTTAGTGGTGGTCTCGGATCATCATTCACCTCAGGTTA
V23(1)          TCCACGCCAAAGAAGCCCTATGTTTAGTGGTGGTCTCGGATCATCATTCACCTCAGGTTA
V24(1)          TAGGCACAAAAGAAGCTCTATGTTTAGTGAGCCTCTTGGATCAACATTTACCTCAGGTTA
V25(1)          TAGGCACAAAAGAAGCTCTATGTTTAGTGAGCCTCTTGGATCAACATTTACCTCAGGTTA
V26(1)          TCCACGCCAAAGAAGCTCCGTGTTTAGTGGTGGTCTCGGATCAACATTTACCTCAGGTTA
V27(1)          TAGGCACCAAAGAAGCTCCGTGTTTAGTGGTGGTCTAGGAGAAACATTTACCTCAGGTTA
V28(1)          TAGGCACCAAAGAAGCTCCGTGTTTAGTGGTGGTCTAGGAGAAACATTTACCTCAGGTTA
                                                                 *    ** ***

TP02_0140       TACTAAACAAGATTTGGATGCCAAATTTCCAGGTATGAAAAAGAGTAAGGGGCCCAAAGA
XM_760370       TACTAAACAAGATTTGGATGCCAAATTTCCAGGTATGAAAAAGAGTAAGGGGCCCAAAGA
V1(3)           TACTAAACAAGATTTGGATGCCAAATTTCCAGGTATGAAAAAGAGTAAGGGGCCCAAAGA
V2(3)           TGGTGATGAAGAATTTGAAAATAAATTTAAAAGTATGGGAATTGGTAAGAAACCCAAAGA
V3(2)           TACTAGACAAGAGTTGGATGCAAAATTTCCAGGTATGAAAAAGGGTAAGGGATCCAAAGA
V4(3)           TACTAGACAAGAGTTGGATGCAAAATTTCCAGGTATGAAAAAGGGTAAGGGATCCAAAGA
V5(1)           TGATGATGATGAATTTCAACGAAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V6(2)           TACTAGACAAGAGTTGGATGCAAAATTTCCAAATTTGAAAGCTCGTAGAGGGCCTATAGG
V7(1)           TACTAGACAAGAGTTGGATGCAAAATTTCCAGGTATGAAAAAGGGTAAGGGATCCAAAGA
V8(1)           CAGTGATCAAGAATTGGAGGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V9(1)           CAGTGATGATGAATTTGAAGAGAAATTTAAGCGTATGGGAATGAAGAAGAAACCCAAAGA
V10(1)          CAGTGATCAAGAATTTGACGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V11(1)          TGGTGATGAAGAATTTGAAAATAAATTTAAAAGTATGGGAATTGGTAAGAAACCCAAAGA
V12(1)          TGGTGATGAAGAATTTGAAAATAAATTTAAAAGTATGGGAATTGGTAAGAAACCCAAAGA
V13(1)          CAGTGATCAAGAATTTGACGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V14(1)          CAGTGATCAAGAATTTGACGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V15(1)          CAGTGATCAAGAATTTGACGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V16(1)          CAGTGATCAAGAATTTGACGAGAAATTTAAACATATGGGAATTGGTAAGAAACCCAAAGA
V17(1)          CAGTGATCAAGAATTTGACGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V18(2)          CAGTGATCAAGAATTTGACGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V191(1)         TGGTGATGAAGAATTTGAAAATAAATTTAAACATATGAGAATTGGTAAGAAACCCAAAGA
V20(1)          CAGTGATAAAGAATTTGAGGAGAAATTTCAACGTATGGGAATTGGTAAGAAACCCAAAGA
V21(1)          TACTTGCTGGGATTTGGAAAATAAATTTCCGGGTATGAAAAAGGGTAAGGGGCATAAAGA
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V22(1)          TACTAGACAAGAGTTGGATGCAAAATTTCCAGGTATGAAAAAGGGTAAGGGATCCAAAGA
V23(1)          TACTAGACAAGAGTTGGATGCAAAATTTCCAGGTATGAAAAAGGGTAAGGGATCCAAAGA
V24(1)          CAGTGATGATGAATTTGAAGAGAAATTTAAGCGTATGGGAATGAAGAAGAAACCCAAAGA
V25(1)          CAGTGATGATGAATTTGAAGAGAAATTTAAGCGTATGGGAATGAAGAAGAAACCCAAAGA
V26(1)          CAGTGATCAAGAATTTGACGAGAAATTTAAACATATGAGAATTGGTAAGAAACCCAAAGA
V27(1)          CAGTGATCAAGAATTTGACGAGAAATTTAAACATATGGGAATTGGTAAGAAACCCAAAGA
V28(1)          CAGTGATCAAGAATTTGACGAGAAATTTAAACATATGGGAATTGGTAAGAAACCCAAAGA
                           *  *  *     *   *       **  *                 *

TP02_0140       CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
XM_760370       CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
V1(3)           CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
V2(3)           CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
V3(2)           CAAAG-------GGCAACCTAA------GCTTCCAAAGCCCGTCAAAAGTACCTTAATGC
V4(3)           CAAAG-------GGCAACCTAA------GCTTCCAAAGCCCGTCAAAAGTACCTTAATGC
V5(1)           CAAATTA-----GGAAGGACAA---------ACCAACCTCAACCGGGAGCTGCA------
V6(2)           CAAACCC-----AGAGGCCAAC---------CTCAAACTCATCAAGCAGCTGGC------
V7(1)           CAAAGCCCCGTGGAACAACCCA-CCTCAACCTCCAAAGCCTGTTAAAAGTACCTTAATTC
V8(1)           CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
V9(1)           CAAACTC-----GGAAGGACAA---------ACCAACCTCAACCAGGAACAGTA------
V10(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V11(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
V12(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCTGTCAAGAGTACCTTAATGC
V13(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V14(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V15(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V16(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V17(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V180(2)         CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V19(1)          CAAACTC-----GGAAGGACAA---------ACCAACCTCAACCGGGAGCACCT------
V20(1)          CAAAG-------GGAAACCTCA------TCCTACAAAGCCCGTCAAAAGTACCTTAATGC
V21(1)          CAAAG-------GACAACCTCAACCTCAGCCTCCAAAGCCCGTCAAAAGTACCTTAATGC
V22(1)          CAAGGCCCCGTGGAACAACCCA-CCTCAACCTCCAAAGCCTGTTAAAAGTACCTTAATTC
V23(1)          CAAAGCCCCGTGGAACAACCCA-CCTCAACCTCCAAAGCCTGTTAAAAGTACCTTAATTC
V24(1)          CAAACTC-----GGAAGGACAA---------ACCAACCTCAACCAGGA------------
V25(1)          CAAACTC-----GGAAGGACAA---------ACCAACCTCAACCAGGAACAGTA------
V26(1)          CAAACTC-----GGAAGGACAA---------ACCAACCTCAACAAGGAGCACCT------
V27(1)          CAAACTC-----AAAAGAACAA---------ACCAACCTCCACCAGGTCCTACT------
V28(1)          CAAACTC-----AAAAGAACAA---------ACCAACCTCCACCAGGTCCTACT------
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TP02_0140       CAGGAAATGAT-GGTCA--AACAG------------GAGCTACTGGAGGTTAT---CCAG
XM_760370       CAGGAAATGAT-GGTCA--AACAG------------GAGCTACTGGAGGTTAT---CCAG
V1(3)           CAGGAAATGAT-GGTCA--AACAG------------GAGCTACTGGAGGTTAT---CCAG
V2(3)           CAGGAAATGAT-GGTCA--AACAG------------GAGCTACTGGACCCTATGGACAAA
V3(2)           CAGAGGGTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTACTGGACCCTATGGACAAG
V4(3)           CAGAGGGTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTACTGGACCCTATGGACAAG
V5(1)           --GGAGG---------------------------TTATCCAGGCGGTTACCCAACTCAAC
V6(2)           --GGTTATGG------------------------TCAACCACAAGG--------------
V7(1)           CAGGTGATGATGTTCCACAAG---------------GAGCCGTTGGACCTTACGG---AG
V8(1)           CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V9(1)           --GGAGG---------------------------CTATGGG-------------------
V10(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V11(1)          CAGGAAATGAT-GGTCA--AACAG------------GAGCTACTGGACCCTATGGACAAA
V12(1)          CAGGAAATGAT-GGTCA--AACAG------------GACCTACTGGACCCTATGGACAAA
V13(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V14(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V15(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V16(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V17(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V180(2)         CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V19(1)          --GGGGCATATCCTCCACCTGCAG------------CAGCTGGCGGATTCGGT-------
V20(1)          CAGAGGCTGGTCAATCAGGAGCAGTTGGAGGTTACGGAGCTGCTGGACCCTATGGACAAA
V21(1)          CAGAATCCGGTCGTCCACAAG---------------GTGCCGCTGCAGGTTAT---CCAG
V22(1)          CAGGTGATGATGTTCCACAAG---------------GAGCCGTTGGACCTTACGG---AG
V23(1)          CAGGTGATGATGTTCCACAAG---------------GAGCCGTTGGACCTTACGG---AG
V24(1)          ------------------------------------------------------------
V25(1)          --GGAGG---------------------------CTATGGG-------------------
V26(1)          --GGAGCATATCCTCCACCTGCAGCCGCTGGACCTTACGGAGGCGGTTACCCAAGTCAAC
V27(1)          --GGGGGCTA------------------------TGGGCAACCTGGTTATCCAAGTCAAC
V28(1)          --GGGGGCTA------------------------TGGGCAACCTGGTTACCCAAGTCAAC


TP02_0140       GTGGTTATCCCACTCAA---GGA---------------------------------CC--
XM_760370       GTGGTTATCCCACTCAA---GGA---------------------------------CC--
V1(3)           GTGGTTATCCCACTCAA---GGA---------------------------------CC--
V2(3)           CTGGTTATCCCACTCAACCTGG----------------T-----------------CC--
V3(2)           CAGGTTATGTCGGTCAACCGGG------------------AGCTGCTGGAAATTATCCAG
V4(3)           CAGGTTATGTCGGTCAACCGGG------------------AGCTGCTGGAAATTATCCAG
V5(1)           CAGGAGCTGCAGGAGGTTATCC--------------------------------------
V6(2)           ------------------------------------------------------------
V7(1)           GCGGTTATCCAAGTCAA---GGA---------------------------------CC--
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V8(1)           CAGGTTATGTCGGTCAACCTGGTCCTTATGGTCAAACTGGAGCTGCTGGAGGTTATCAAG
V9(1)           ------------------------------------------------------------
V10(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V11(1)          CTGGTTATCCCACTCAACCTGG----------------T-----------------CC--
V12(1)          CTGGTTATCCCACTCAACCTGG----------------T-----------------CC--
V13(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V14(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V15(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V16(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V17(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V18(2)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V19(1)          --GGCTATCCGAGTCAATCAGG--------------------------------------
V20(1)          CAGGTTATGTCGGTCAACCTGG----------------T-----------------CC--
V21(1)          CAGGTTATCCCACTCAA---GGA---------------------------------CC--
V22(1)          GCGGTTATCCAAGTCAA---GGA---------------------------------CC--
V23(1)          GCGGTTATCCAACTCAA---GGA---------------------------------CC--
V24(1)          ------------------------------------------------------------
V25(1)          ------------------------------------------------------------
V26(1)          AAGGAGCACCTGGAGCATATCCTCCACCTGCAGCCGCTGGACCTTACGGAGGCGGTTACC
V27(1)          CACAAGCTGCAGGACCTTACGG---------------------------AGGCGGTTACC
V28(1)          CACAAGCTGCAGGACCTTACGG---------------------------AGGCGGTTACC


TP02_0140       ----TTAT---GGTCAACCAGG------------------AGCTACTGGACCCTATGGAC
XM_760370       ----TTAT---GGTCAACCAGG------------------AGCTACTGGACCCTATGGAC
V1(3)           ----TTAT---GGTCAACCAGG------------------AGCTACTGGACCCTATGGAC
V2(3)           ----TTAC---GGTCAACCGGG------------------ACCCGTTGG-----------
V3(2)           GTGGTTATGCTGGTCAACCTGGTCCTTATGGTCAACCAGGAGCTACTGGACCCTATGGAC
V4(3)           GTGGTTATGCTGGTCAACCTGGTCCTTATGGTCAACCAGGAGCTACTGGACCCTATGGAC
V5(1)           ----------------AGGCGGTTACCCAACTCAACCAGGAGCTGCAGGAGGTTATCCA-
V6(2)           -------------AGGACCTGGGGTATATCCTCCACCGGCAGCAGCTGGACCTTACGGA-
V7(1)           ----TTAT---GGTCAACCAGG---------------------AGCTGGACCCTATGGAC
V8(1)           GTGGTTATCCCACTCAACCTGGTCCTTATGGTCAAACAGGAGCCACTGGACCCTATGGAC
V9(1)           --------------------------------------------------------CAA-
V10(1)          ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTCGGACCTTACGGA-
V11(1)          ----TTAC---GGTCAACCGGG------------------AGCCACTGGAGGTTATCAA-
V12(1)          ----TTAC---GGTCAACCGGG------------------AGCCACTGGAGGTTATCAA-
V13(1)          ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGA-
V14(1)          ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGA-
V15(1)          ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTCGGACCTTACGGA-
V16(1)          ----TTAT---GGTCAAACGGGTTACGTT-------------------------------
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V17(1)           ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGA-
V18(2)           ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGA-
V19(1)           ----------------ACAAGG---------------------CGTTTATCCTCCACAA-
V20(1)           ----TTAT---GGTCAAACGGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGA-
V21(1)           ----TTAT---GGTCAACCAGG-------------------AGCTAGTGGAGGTTATCCA-
V22(1)           ----TTAT---GGTCAATCAGG----------------------AGCTGGACCTTATGGAC
V23(1)           ----TTAT---GGTCAACCAGG----------------------AGCTGGACCCTATGGAC
V24(1)           ------------------------------------------------------------
V25(1)           --------------------------------------------------------CAA-
V26(1)           CAAGTCAACAAGGAGCACCTGGAGCATATCCTCCACCTGCAGCCGCTGGACCTTACGGA-
V27(1)           CAAGTCAACCACAAGGACCTGGGGTATATCCTCCACCAGGAGCAGCTGGACCTTACGGA-
V28(1)           CAAGTCAACCACAAGGACCTGGGGTATATCCTCCACCAGGAGCAGCTGGACCTTACGGA-


TP02_0140        AAGCAGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGTCAACCAGGAGCT----
XM_760370        AAGCAGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGTCAACCAGGAGCT----
V1(3)            AAGCAGGTTACGTTGGTCAACCGGGAGCCGTTGGACCTTACGGTCAACCAGGAGCT----
V2(3)            ------------------------------------------------------------
V3(2)            AAGCAGGTTATGTCGGTCAACC---------GGGAGCTGCTGGAAATTATCCAGGT----
V4(3)            AAGCAGGTTATGTCGGTCAACC---------GGGAGCTGCTGGAAATTATCCAGGT----
V5(1)            --GGCGGTTACCCAAGTCAACA---------AGGAGCTGCAGGAGG--------------
V6(2)            --GGTGGTTACCCAAGTCAACC---------AGGAGCATCTGGAGGTTATGGAGGCG---
V7(1)            AAACGGGTTACGTTGGACCTTACGGAGGCGGTTATCCA----------------------
V8(1)            AAGCAGGTTATGTCGGTCAACC---------GGGAGCTGCTGGAGGTTATCCAGGT----
V9(1)            --CCTGGTTATCCATCTCAACC---------ACAAGCAGCTGGAGC--------------
V10(1)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
V11(1)           --GGTGGTTATCCAACTCAACC---------TGGTCCTTATCCTCCACCAGGAGCTA---
V12(1)           --GGTGGTTATCCAACTCAACC---------TGGTCCTTATCCTCCACCAGGAGCTA---
V13(1)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
V14(1)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
V15(1)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
V16(1)           ------------------------------------------------------------
V17(1)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
V18(2)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
19(1)           -----GGTTACGTTGGACAA---------------CC-----------------------
V20(1)           --GGGGGTTATCCAACTCAA------------GGACCTTATGGTCAACCAGGAGCT----
V21(1)           --GCTGGTTATCCCACTCAACC---------TGGTCCTTATGTTCAACCAGGAGCTA---
V22(1)           AAACGGGTTACGTTGGTCAACC---------TGGTCCTTATC------------------
V23(1)           AAACGGGTTACGTTGGACCTTACGGAGGCGGTTATCCAACTCAAGGACCTTATGGTCAAC
V24(1)           -----------------------------------GCATCTGGAGG--------------
V25(1)           --CCTGGTTATCCATCTCAACC---------ACAAGCAGCTGGAGC--------------
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V26(1)         --GGCGGTTACCCAACTCAACA---------AGGAGCACCTGGAGCATATCC--------
V27(1)         --GGCGGTTACCCAAGTCAACC---------ACAAGGACCTGGGGTATATCC--------
V28(1)         --GGCGGTTACCCAAGTCAACC---------ACAAGGACCTGGGGTATATCC--------


TP02_0140      --------GTACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
XM_760370      --------GTACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V1(3)          --------GTACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V2(3)          ------------------------------------------------------------
V3(2)          --------GGTTATGATGGTCAACCTGGTCCTTATGGTCAACCAGGAGCTACTGGACCCT
V4(3)          --------GGTTATGATGGTCAACCTGGTCCTTATGGTCAACCAGGAGCTACTGGACCCT
V5(1)          ----------------------------------------------------------TT
V6(2)          ------------------------------------GTGCATCAGGTGGCGCTGGACCTT
V7(1)          ------------------------------------------------------------
V8(1)          --------GGTTATGCTGGTCAACCTGGTCCTTATGGTCAACCAGGAGCTACTGGACCCT
V9(1)          ----------------------------------------------------------TT
V10(1)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V11(1)         ------CTGGACCCTATGGACAAACTAGTTATCCCACTCAACCAGGAGCTGCTGGAGGTT
V12(1)         ------CTGGACCCTATGGACAAACTAATTATCCCACTCAACCAGGAGCTGCTGGAGGTT
V13(1)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V14(1)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V15(1)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V16(1)         ------------------------------------------------------------
V17(1)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V18(2)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V19(1)         -------------------------------------------AGGAGCACCTGGGGCCT
V20(1)         --------GGACCCTATGGACAAACTGGTTATCCCACTCAACCAGGAGCAGCTGGAAATT
V21(1)         ------CTGGACCCTATCGACAAACGGGTTATCCCACTCAACCAGGAGCTGCTGGAGGTT
V22(1)         ------------------------------------CTCCACCAGGAGCTACTGGACCCT
V23(1)         CAGGAGCTGGACCCTATGGACAAACGGGTTATCCCACTCAACCAGGAGCAGCTGGAGGTT
V24(1)         ----------------------------------------------------------TT
V25(1)         ----------------------------------------------------------TT
V26(1)         -------------------------------------TCCACCTGCAGCCGCTGGACCTT
V27(1)         -------------------------------------TCCACCAGGAGCAGCTGGACCTT
V28(1)         -------------------------------------TCCACCAGGAGCAGCTGGACCTT


TP02_0140      AT---CCAGGTGGTTATGCTGGCCAACCTGGTCCTTATGGT-------------------
XM_760370      AT---CCAGGTGGTTATGCTGGCCAACCTGGTCCTTATGGT-------------------
V1(3)          AT---CCAGGTGGTTATGCTGGCCAACCTGGTCCTTATGGT-------------------
V2(3)          ------------------------------------------------------------
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V3(2)           ATGGACAAGCAGGTTATGTCGGTCAACCGGGAGC--------------------------
V4(3)           ATGGACAAGCAGGTTATGTCGGTCAACCGGGAGC--------------------------
V5(1)           ATC---CAGGCGGTTACCCAAGTCAACAAGGAGGACCTGGAGCAT---------------
V6(2)           ACG---GAGGTGGTTACCCAAGTCAACCAGGAGCATCTGGAGGTT---------------
V7(1)           --------GGTGGTTATGCTGGTCAACCGGGAGC--------------------------
V8(1)           ATGGACAAGCAGGTTATGTCGGTCAACCGGGAGCTGCTGGAGGTTATCCAGGTGGTTATG
V9(1)           ACG---GAGGCGGTTATCCAACTCAACAAGGAGGACCTGGTTATC---------------
V10(1)          AT---CCAGGTGGTTATACTGGTCAACCAGGAGC--------------------------
V11(1)          AT---CCAGGTGGTTATCCCACTCAACCAGGAGC--------------------------
V12(1)          AT---CCAGGTGGTTATCCCACTCAACCAGGAGC--------------------------
V13(1)          AT---CCAGGTGGTTATACTGGCCAACCAGGAGC--------------------------
V14(1)          AT---CCAGGTGGTTATACTGGTCAACCAGGAGC--------------------------
V15(1)          AT---CCAGGTGGTTATACTGGTCAACCAGGAGC--------------------------
V16(1)          ------------------------------------------------------------
V17(1)          AT---CCAGGTGGTTATACTGGTCAACCAGGAGC--------------------------
V18(2)          AT---CCAGGTGGTTATACTGGTCAACCAGGAGC--------------------------
V19(1)          ATG---GAGGCGGTTATCCTAGTCAGCAAGGGGC--------------------------
V20(1)          AT---CCAGGTGGTTATGCTGGTCAACCGGGAGC--------------------------
V21(1)          AT---CCGGCTGGTTATGCTGGTCAACCGGGAGC--------------------------
V22(1)          ATGGACAAACGGGTTACGTTGGTCAACCGGGAGC--------------------------
V23(1)          AT---CCAGGTGGTTATGCTGGTCAACCGGGAGC--------------------------
V24(1)          ACG---GAGGTGGTTACCCAA---------------------------------------
V25(1)          ACG---GAGGCGGTTATCCAACTCAACAAGGAGGACCTGGTTATC---------------
V26(1)          ACG---GAGGCGGTTACCCAAGTCAACAAGGAGCACCTGGAGCAT---------------
V27(1)          ACG---GAGGCGGTTACCCAAGTCAACCACAAGGACCTGGGGTAT---------------
V28(1)          ACG---GAGGCGGTTACCCAAGTCAACCACAAGGACCTGGGGTAT---------------


TP02_0140       ---------------CAACCAGGAGCTACTGGACCCTATGGACAAGC--AGGTTATGTCG
XM_760370       ---------------CAACCAGGAGCTACTGGACCCTATGGACAAGC--AGGTTATGTCG
V1(3)           ---------------CAACCAGGAGCTACTGGACCCTATGGACAAGC--AGGTTATGTCG
V2(3)           ------------------------------------------------------------
V3(2)           ----------------ATCTGGAGGTTACGGAGCCGGTTATTCTGGTCAAGGTGGTTATC
V4(3)           ----------------ATCTGGAGGTTACGGAGCCGGTTATTCTGGTCAAGGTGGTTATC
V5(1)           ---------------ATCC------TCCACCGGCAGCAGCTGGAGGTCAAGGGCCGGCTT
V6(2)           ---------------ATGGAGGCGGTGCATCAGGTGGCGCTGGACCTTACGGAGGTGGTT
V7(1)           ----------------ATCTGGAGGTTACGGAGCCGGTTATTCTGGTCAAGGTGGTTATC
V8(1)           CTGGTCAACCGGGAGCATCTGGAGGTTACGGAGCCGGTTATTCTGGTCAAGGTGGTTATC
V9(1)           ---------------CACC------TCCACCGGCAGCAGCTGGAGCTCAAGGACATGCTT
V10(1)          ----------------TACTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V11(1)          ----------------GGTTGGAGGCTACGGAGGCGGTTATTCAGGTCAAGGTGGTTATC
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V12(1)          ----------------GGTTGGAGGCTACGGACGCGGTTATTCAGGTCAAGGTGGTTATC
V13(1)          ----------------TACTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V14(1)          ----------------TACTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V15(1)          ----------------TACTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V16(1)          ------------------------------------------------------------
V17(1)          ----------------TACTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V180(2)         ----------------TACTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V19(1)          ----------------AACTGGCGGATTCGG---TGGCTATCCGAGTCAATCAGG-----
V20(1)          ----------------ATCTGGAGGTTACGGAGCCGGTTATTCTGGTCAAGGTGGTTATC
V21(1)          ----------------ATCTGGAGGTTACGGAGCCGGTTATTCTGGTCAAGGTGGTTATC
V22(1)          ----------------ATCTGGAGGTTACGGAGCTGGTTATTCAGGTCAAGGTGGTTATC
V23(1)          ----------------ATCTGGAGGTTACGGAGCAGGTTATTCTGGTCAAGGTGGTTATC
V24(1)          ------------------------------------------------------------
V25(1)          ---------------CACC------TCCACCGGCAGCAGCTGGAGCTCAAGGACATGCTT
V26(1)          ---------------ATCC------TCCACCTGCAGCCGCTGGAGCTCAAGGGCCGGCTT
V27(1)          ---------------ATCC------TCCACCAGGAGCAGCTGGACCTTACGGAGGCGGTT
V28(1)          ---------------ATCC------TCCACCAGGAGCAGCTGGACCTTACGGAGGCGGTT


TP02_0140       GTCAACCGGGAGCTGCTGGGGGTTATCCAGGTGGTTATCCTCCACCAGGAGCA-------
XM_760370       GTCAACCGGGAGCTGCTGGGGGTTATCCAGGTGGTTATCCTCCACCAGGAGCA-------
V1(3)           GTCAACCGGGAGCTGCTGGGGGTTATCCAGGTGGTTATCCTCCACCAGGAGCA-------
V2(3)           ------------------------------------------------------------
V3(2)           CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGAGCA-------
V4(3)           CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGAGCA-------
V5(1)           ATCCTCCAGGCTATGGTCAACCGGGAGCAGCTGGAGGTTATGGAGGCGGTGCATCAGGTG
V6(2)           ACCCA---------AGTCAACCAGGAGCATCTGGAGGTTATGGAGGCGGTGCATCAGGTG
V7(1)           CTCCACAAGGTTACGTACAACCCGGGCAAGGTCCTTATCCTCCGTCAGGACCATCTGGAG
V8(1)           CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGAGCA-------
V9(1)           ATCCTCCAGGCTATGGTCAACCGGTAGCAGCTGGAGGTTATGGAGGCGGTGCATCAGGTG
V10(1)          CTCCACAAGGCTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGACCATCTGGGG
V11(1)          CACCACAAGGCTATGGACAACCCGGGAAAGGTCCTTATCCTCCGCCAGGACCATCTGGGG
V12(1)          CACCACAAGGCTATGGACAACCCGGGAAAGGTCCTTATCCTCCGCCAGGACCATCTGGGG
V13(1)          CTCCACAAGGCTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGACCATCTGGGG
V14(1)          CTCCACAAGGCTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGACCATCTGGGG
V15(1)          CTCCACAAGGCTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGACCATCTGGGG
V16(1)          ------------------------------------------------------------
V17(1)          CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGTCAGGACCATCTGGAG
V180(2)         CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGTCAGGACCATCTGGAG
V19(1)          ----ACAAGGC---GTTTATCCTCCACAAGGTCCTTATGCTCCACCCGGAGCAGCCGGAG
V20(1)          CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGAGCA-------
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V21(1)          CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGTCAGGACCATCTGGAG
V22(1)          CTCCACAAGGTTATGGACAACCCGGGCAAGGTCCTTATCCTCCGCCAGGAGCA-------
V23(1)          CTCCACAAGGTTACGTACAACCCGGGCAAGGTCCTTATCCTCCGTCAGGACCATCTGGAG
V24(1)          ---------------GTCAACCAGGAGCATCTGGAGGTTATGGAGGCGGTGCATCAGGTG
V25(1)          ATCCTCCAGGCTATGGTCAACCGGTAGCAGCTGGAGGTTATGGAGGCGGTGCATCAGGTG
V26(1)          ATCCTCCAGGCTATGGTCAACCGGTAGCATCTGGAGGTTATGGAGGCGGTGCATCAGGTG
V27(1)          ACCCA---------AGTCAACCACAAGGACCTGGGGTATATCC------TCCACCAGGAG
V28(1)          ACCCA---------AGTCAACCACAAGGACCTGGGGTATATCC------TCCACCAGGAG


TP02_0140       --------------GCTGGAGGCTATGGAGGCGGCCCACCCGGTC---CAGGTCAGCCAA
XM_760370       --------------GCTGGAGGCTATGGAGGCGGCCCACCCGGTC---CAGGTCAGCCAA
V1(3)           --------------GCTGGAGGCTATGGAGGCGGCCCACCCGGTC---CAGGTCAGCCAA
V2(3)           ------------------------------------------------------------
V3(2)           --------------GCTGGAGGCTATGGAGGTGGCCCACCCGGTC---CAGGTCAGCCAA
V4(3)           --------------GCTGGAGGCTATGGAGGTGGCCCACCCGGTC---CAGGTCAGCCAA
V5(1)           GC------------GCTGGAGGCTACGGAGGTGGTTATCCAGGTCAACAAGGTGGTCCAC
V6(2)           GC------------GCTGGAGGTTACGGAGGCGGTTATCCAAGTCAACCAGGTGGTCCAC
V7(1)           GCCATGGAGCAGGTGCTGGAGGCTATGGAGGCGGCGCACCCGGTC---CAGGTCAGCCAA
V8(1)           --------------GCTGGAGGCTATGGAGGTGGCCCACCCGGTC---CAGGTCAGCCAA
V9(1)           GC------------GCTGGAGGTTACGGAGGTGGTTATCCAAGTCAACCAGGTGGTCCAC
V10(1)          GCTATGGAGCAGGTGCTGGAGGCTATGGAGGTAGTGCACCCGGTC---CAGGTCACCCAA
V11(1)          GCTATGGATCAGGTGCTGGAGGCTATGGAGGCGGCGAACCGGGTT---CAGGTCACCCAA
V12(1)          GCTATGGATCACGTGCTGGAGGCTATGGAGGCGGCAAACCGGGTT---CAGGTCACCCAA
V13(1)          GCTATGGAGCAGGTGCTGGAGGCTATGGAGGTAGTGCACCCGGTC---CAGGTCACCCAA
V14(1)          GCTATGGAGCAGGTGCTGGAGGCTATGGAGGCGGCGAACCGGGTC---CAGGTCACCCAA
V15(1)          GCTATGGAGCAGGTGCTGGAGGCTATGGAGGTAGTGCACCCGGTC---CAGGTCACCCAA
V16(1)          ------------------------------------------------------------
V17(1)          GCCATGGAGCAGGTGCTGGAGGCTATGGAGGCGGCGCCTGGTC---CAGGTCAGCCAA
V180(2)         GCCATGGAGCAGGTGCTGGAGGCTATGGAGGCGGCGCCTGGTC---CAGGTCAGCCAA
V19(1)          GCTATGGTGGCGGTGCTGGCGGTTATGGCGGTGGCGCATCAGGTC---CAGGTCAGCCGA
V20(1)          --------------GCTGGAGGCTATGGAGGTGGCCCACCCGGTC---CAGGTCAGCCAA
V21(1)          GCCCTGGAGCAGGTGCTGGAGGTTATGGAGGTGGCGCACCCGGTC---CAGGTCAGCCAA
V22(1)          --------------GCTGGAGGATATGGAGGTGGCCCACCCGGTC---CAGGTCAGCCAA
V23(1)          GCCATGGAGCAGGTGCTGGAGGCTATGGAGGCGGCGCACCCGGTC---CAGGTCAGCCAA
V24(1)          GC------------GCTGGACCTTACGGAGGTGGTTACCCAAGTCAACCAGGTGGTCCAC
V25(1)          GC------------GCTGGAGGTTACGGAGGTGGTTATCCAAGTCAACCAGGTGGTCCAC
V26(1)          GC------------GCTGGAGGTTACGGAGGTGGTTATCCAAGTCAACCAGGTGGTCCAC
V27(1)          CA------------GCTGGACCTTACGGAGGCGGTTACCCAAGTCAACCAGGTGGTCCAC
V28(1)          CA------------GCTGGACCTTACGGAGGCGGTTACCCAAGTCAACCAGGTGGTCCAC
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TP02_0140       GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAAAAAAT
XM_760370       GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAAAAAAT
V1(3)           GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAAAAAAT
V2(3)           ------------------------------------------------------------
V3(2)           GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAA-----
V4(3)           GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAAAAAAT
V5(1)           AAGGAGCGGCTGGAC---CTCCTGGCGAGCCGATTATGGTGAAAA-TGGATGCAAAAAGC
V6(2)           AAGGAGCAGCTGGAC---CTCCCGGCCAGCCGATTATGATGAGAA-TTGATGGGAAGAAC
V7(1)           GTGGCCCACCTGGTCAAGCCCCTGGAGGGA---ATATGTTGAAAA-TAGATGCAAAAAGT
V8(1)           GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAAAAAAT
V9(1)           AAGGAGCAGCTGGAC---CTCCTGGCCAGCCGATTATGATGAAAA-TTGATGTGAAGAAC
V10(1)          GCGGTCCCACTGGCCATGCTTCTGGCGGGA---ATTTGTTGAAAA-TAGATGTAAAAAAT
V11(1)          GCGGTCCCACTGGCCATGCTTCTGGCGGGA---ATTTGTTGAAAA-TAGATGTAAAAAAT
V12(1)          TCGATCCCACTGGCCATGCTTCTGGCGGGA---ATTTGTTGAAGA-TAGATGTAAAAAAT
V13(1)          GCGGTCCCACTGGCCATGCTTCTGGCGGGA---ATTTGTTGAAAA-TAGATGTAAAAAAT
V14(1)          GCGGTCCCACTGGCCATGCTTCTGGCGGGA---ATTTGTTGAAAAATAGATGTAAAAAAT
V15(1)          GCGGTCCCACTGGCCATGCTTCTGGCGGGA---ATTTGTTGAAAA-TAGATGTAAAAAAT
V16(1)          ------------------------------------------------------------
V17(1)          GTGGCCCAACTGGTCAAACCCATGGAGGGA---ATATGTTGACAA-TAGATGCAAAAACT
V18(2)          GTGGCCCAACTGGTCAAACCCATGGAGGGA---ATATGTTGACAA-TAGATGCAAAAACT
V19(1)          CCGGTCCTCCTGGCCATACTCCTGGGGTGA---ATTTGTTGACAA-TAGATGCAAAAACT
V20(1)          GCGGTCCCCCTGGTCAAGCTCCTGGCAATATGCAATTGTTGAAAA-TAGATGTAAAAAAT
V21(1)          GTGGCCCACCTAGTCAATCTCCTGATGGGAAAAATTTAGGCCCTG-TAGATGGAAAAACA
V22(1)          GCGGTCCCCCTGGTCAAGCCCCTGGCAATATGCAATTGTTGACAA-TAGATGCAAAAACT
V23(1)          GTGGCCCACCTGGTCAAGCCCCTGGAGGGA---ATATGTTGAAAA-TAGATGCAAAAAGT
V24(1)          AAGGAGCGGCTGGAC---CTCCTGGAGAGCCGATTATGCTGAAAA-TGGATGCAAAGAAC
V25(1)          AAGGAGCAGCTGGAC---CTCCTGGCCAGCCGATTATGATGAAAA-TTGATGTGAAGAAC
V26(1)          AAGGAGCAGCTGGAC---ATCCTGGCCAGCCGATTATGATGAAAA-TTGATGCGAAGAAC
V27(1)          AAGGAGCAACTGGAC---CTCCTGGCCAGCCGATTATGATGAAAA-TTGATGCGAAGAAC
V28(1)          AGGGAGCAACTGGAC---CTCCTGGCCAGCCGATTATGATGAAAA-TTGATGCGAAGAAC


TP02_0140       CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAAAGCCAGAACGTCGT
XM_760370       CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAAAGCCAGAACGTCGT
V1(3)           CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAAAGCCAGAACGTCGT
V2(3)           ------------------------------------------------------------
V3(2)           ------------------------------------------------------------
V4(3)           CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAA--------------
V5(1)           AGAGTAAAT---AGAGATATTAATCTTACTAAATTTACACT---GACAAATGGTAAAACT
V6(2)           AGAAGAAAT---CCAAATACTAGACTTGATAGATTTACACT---ACCAGATGGTAGAACT
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V7(1)           CCAAACAATGGCAAAAATATTATTGTTGAAGAATTTAGAGCGGGTAGACCAGAACGTACT
V8(1)           CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAAAGCCAGAACGTCGT
V9(1)           AGAAGAAAC---CCAAATACTAAACTTGATAGATTTACACT---AACAGATGGTAGAACT
V10(1)          CCAAACAATGGTCCAAA-------------------------------------------
V11(1)          CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAAAGCCAGAACGTCGT
V12(1)          CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATACCCA-----------------
V13(1)          CCAAACAATGGTCCAAA-------------------------------------------
V14(1)          CCAAACAATGGTCCAAA-------------------------------------------
V15(1)          CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCC------------------
V16(1)          ------------------------------------------------------------
V17(1)          AAACACAATGGCCCAAA-------------------------------------------
V18(2)          AAACACAATGGCCCAAATATTATTGTTGACGAATATAGAGCCGGACCACAGGATCGTCGT
V19(1)          AAACACAATGGCGCAAATATTATTGTTGACGAATATAGAGCCGGTCGACCAGAACGTATT
V20(1)          CCAAACAATGGTCCAAATATTATTTTTGAAGAATATATAGCCGGAAAGCCAGAACGTCGT
V21(1)          GGAAAAAACGATCCATTTGTTATTTTCGAAAGATTTAGGGCAGGACCACAAAATCGTGTT
V22(1)          AAACACAATGGCGCAAATATTATTGTTGACGAATATAGAGCCGGTCGACCAGAACGTATT
V23(1)          CCAAACAATGGCAAAAATATTATTGTTGAAGAATTTAGAGCGGGTAGACCAGAACGTACT
V24(1)          AGAACAAAT---CGAAATATTAATCTTACTAAATTTACACT---ACCAAATGGTAAAACT
V25(1)          AGAAGAAAC---CCAAATACTAAACTTGATAGATTTACACT---AACAGATGGTAGAACT
V26(1)          AGAAGAAAT---CCAAATACTAAACTTGATAGATTTACACT---ATCAAATGGTGGAACT
V27(1)          AGAAGAAAT---CCAAATACTAAACTTGATAGATTTACGCT---ATCAAATGGTGGAACT
V28(1)          AGAAGAGAT---CCAAATACTAAACTTGATAGATTTACGCT---ATCAAATGGTGGAACT


TP02_0140       CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGCGAA
XM_760370       CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGCGAA
V1(3)           CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGCGAA
V2(3)           ------------------------------------------------------------
V3(2)           ------------------------------------------------------------
V4(3)           ------------------------------------------------------------
V5(1)           CAACATGTGTTTAGAGCTAATCCTGGACATGGAATTAAACAAGTAAATTATGACGGTGAT
V6(2)           CAACATGTGTTTAGACCTAATCTTGGATATGCAATTAAACAAGTAAATTATGACGGTGAT
V7(1)           CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTA----------
V8(1)           CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGCGAA
V9(1)           CAACATGCGTTTAGAGCTAATCCTGGATATGCAATTAAACAAGTAAATTATGACGGTGAT
V10(1)          ------------------------------------------------------------
V11(1)          CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGCGAA
V12(1)          ------------------------------------------------------------
V13(1)          ------------------------------------------------------------
V14(1)          ------------------------------------------------------------
V15(1)          ------------------------------------------------------------
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V16(1)          ------------------------------------------------------------
V17(1)          ------------------------------------------------------------
V18(2)          CACCGTCAGTTTGATCCTGTTCCTGGATGTGGAATTATTCAAGTAAATTATGACGGTCGC
V19(1)          CACCGTCAGTTTGATCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATAATGGTAAA
V20(1)          CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGTGGT
V21(1)          CACCATCAGTATACTCCCCGTAGTGGTTGTGGGTTCAATATGGTAAAATATTCAGGTGGA
V22(1)          CACCGTCAGTTTGATCCCGTTCCTGGATGTGGAATTAATCAAGTAAATTATAATGGTCAA
V23(1)          CACCGTCAGTTTACCCCTGTTCCTGGATGTGGAATTAATCAAGTAAATTATGACGGTCGC
V24(1)          CAACATGTGTTTAGAGCTAATCCTGGACATGGAATTAAACAAGTAAATTATGACGGTGAT
V25(1)          CAACATGCGTTTAGAGCTAATCCTGGATATGCAATTAAACAAGTAAATTATGACGGTGAT
V26(1)          CAACATGTGTTTAGACCTGATCCTGGACATGGAATTAAACAAGTAAATTATGACGGTGAT
V27(1)          CAACATGTGTTTAGACCTGATCCTGGACATGGAATTAAACAAGTAAATTATGACGGTGAT
V28(1)          CAACATGTGTTTAGACCTGATCCTGGACATGGAATTAAACAAGTAAATTATGACGGTGAT


TP02_0140       AAAGTTTGGTCATTAGAAGTGGGTG---GCGATTATGCAGTAAAAGTTCTTGTTTTTCCT
XM_760370       AAAGTTTGGTCATTAGAAGTGGGTG---GCGATTATGCAGTAAAAGTTCTTGTTTTTCCT
V1(3)           AAAGTTTGGTCATTAGAAGTGGGTG---GCGATTATGCAGTAAAAGTTCTTGTTTTTCCT
V2(3)           ------------------------------------------------------------
V3(2)           ------------------------------------------------------------
V4(3)           ------------------------------------------------------------
V5(1)           CCTGTTTGGTCAATGGATGGTAAT------AATTTTGGAACAGAAGTTCTTCTGGATCCT
V6(2)           CGTGTTTGGTCAATGGATGAT---------------------------------------
V7(1)           ------------------------------------------------------------
V8(1)           AAAGTTTGGTCATTAGAAGTGGGT------GGCGATTATGCAGTAAAAGTTCTTGTTTTT
V9(1)           CGTGTTTGGTCAATGGATGGTGGT------AATTTTGGAACAGAAGTTCTTGTGGATCCT
V10(1)          ------------------------------------------------------------
V11(1)          AAAGTTTGGT--------------------------------------------------
V12(1)          ------------------------------------------------------------
V13(1)          ------------------------------------------------------------
V14(1)          ------------------------------------------------------------
V15(1)          ------------------------------------------------------------
V16(1)          ------------------------------------------------------------
V17(1)          ------------------------------------------------------------
V18(2)          AAAGTTTGGACAGCGAGTGGTCCC------GAACATGCAGTAAAAGTAGTTGTGTTTCCT
V19(1)          CCAGTTTGGAAAATGATAGGTGAA------AAATATGCAGTAAAAGTAGTTCTGTTTCCT
V20(1)          AACGTTTGGACAATGAACGATGAC------ATTCATGCATTAAAAGTAGTTGTGTTTCCT
V21(1)          ATCGTTTGGATATTAGGGGGTGACGGTAGTAATTATGCAACAAAGGTTATTGTGCATCCT
V22(1)          CCAGTTTGGAAAATGATAGGTGAA------AAATATGCAGTAACAGTAGTTTTGTTTCCT
V23(1)          AAAGTTTGGTCATTAGAAGTGGGTGGCGATCATGCAGTAAAAGTTCTTGTGTTTCCTATA
V24(1)          TTTGTTTGGTCAATGGATGGTGGT------AATTTTGGAACAGAAGTTCTTGTGGATCCT
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V25(1)	CGTGTTTGGTCAATGGATGGTGGT------AATTTTGGAACAGAAGTTCTTGTGGATCCT
V26(1)	CGTGTTTGGTCAATGGATCGTGAT------AATTTTGGCACAGAAGTTCTTGTAGATCCT
V27(1)	CCTGTTTGGTCAATGGATGGTAAT------AATTTTGGAACAGAAGTTCTTCTGGATCCT
V28(1)	CCTGTTTGGTCAATGGATGGTAAT------AATTTTGGAACAGAAGTTCTTCTGGATCCT

TP02_0140	ATAGGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAAATCTAT
XM_760370	ATAGGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAAATCTAT
V1(3)	ATAGGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAAATCTAT
V2(3)	--
V3(2)	--
V4(3)	--
V5(1)	ATAGGGTCTCCAGCAAAAAATATGACAATCAAACTGGCAAACGGTGATAAGGTTACTTTT
V6(2)	--
V7(1)	--
V8(1)	CCTATAGGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAAATC
V9(1)	ATAGGGTCTGGAGCAAAAACTATGACAATCAAACTGGCAAACGG----------------
V10(1)	--
V11(1)	--
V12(1)	--
V13(1)	--
V14(1)	--
V15(1)	--
V16(1)	--
V17(1)	--
V18(2)	CTAGGATTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGCGATCTAT
V19(1)	ATAGGATTTGAAGAAAAAACTATTGTAATCACAATGATAGGTGGTGAAAACGAGATCTAT
V20(1)	ATAGGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAAATCTAT
V21(1)	GTAGGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAGATCTAT
V22(1)	ATAGGGTTTGAAGAAAAAACTATTGTAATCACAATGATAGGTGGTGAAAAGGAGATCTAT
V23(1)	GGGTTTAAAGAAAAAACTATTGAAATCACATTTATTGGCGGTGAAAAGGAGATCTATAAA
V24(1)	ATAGGGTCTGGAGCAAAAACTATGACAATCAAATTGGCAAACGGTGATAAGGTTATTCAT
V25(1)	ATAGGGTCTGGAGCAAAAACTATGACAATCAAACTGGCAAACGGTGATAATGTTATTTAT
V26(1)	ATAGGGTCTGGAGCAAAAACTATGACAATCAAAATGGTAAACGGTGATGAGGTTACTTTT
V27(1)	ATAGGGTCTCCAGCAAAAAATATGACAATCAAAATGGTAAACGGTGATAAGGAAATCTAT
V28(1)	ATAGG-TCTCCAGCAAAAA-TATGACA-TCAAATTTATTGGCGGTGAAAAGGAAATCTAT

TP02_0140	AAAAAGAAAGGG***CGTAATAAACCATGGACAAAACAATAA***
XM_760370	AAAAAGAAAGGGCGTAATAAACCATGGACAAAACAATAA
V1(3)	AAAAAGAAAGGG---------------------------

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V2(3)          ---------------------------------------
V3(2)          ---------------------------------------
V4(3)          ---------------------------------------
V5(1)          ATAAAGAAAGGG---------------------------
V6(2)          ---------------------------------------
V7(1)          ---------------------------------------
V8(1)          TATAAAAAGAAAGGG------------------------
V9(1)          ---------------------------------------
V10(1)         ---------------------------------------
V11(1)         ---------------------------------------
V12(1)         ---------------------------------------
V13(1)         ---------------------------------------
V14(1)         ---------------------------------------
V15(1)         ---------------------------------------
V16(1)         ---------------------------------------
V17(1)         ---------------------------------------
V18(2)         AAAAAGCCAGGGCGTAATAAACCATGGACAAAACAATAA
V19(1)         AAAAAGAAAGGG---------------------------
V20(1)         AAAAAGAAAGGGCGTAATAAACCATGGACAAAACAATAA
V21(1)         AAAAAGAAAGGG---------------------------
V22(1)         AAAAAGAAAGGGCGTAATAAACCATGGACAAAACAATAA
V23(1)         AAGAAAGGG------------------------------
V24(1)         ACAAAGCCAGGA---------------------------
V25(1)         ACAAAGCCAGGA---------------------------
V26(1)         ACAAAGTCAGGA---------------------------
V27(1)         AAAAAGAAAGGG---------------------------
V28(1)         AAAAAGAAAGGGCGTAATAAACCATGGACAAAACAATAA
```

Primer regions are in bold, underlined and italicized text.

Table S11b: Tp9 protein variant Clustal alignment

```
TP02_0895       MNVLTTGIILYSFYLSICMDP---DDDVFGFDPDDDGDGSMLPPHQRSSMFRDDLGSSFT
V1(3)           MNVLTTGIILYSFYLSICMDP---DDDVFGFDPDDDGDGSMLPPHQRSSMFRDDLGSSFT
V2(1)           ----------------ICMDSGEEEDDVFGAE-----GGSMLPPRQRSSMFGEPLGSLLT
V3(1)           --------------------------DVFGAE-----GGSMLPPRQRSSMFGEPLGSLHT
V4(3)           ----------------ICMDSGEEEDDVFGAE-----GGSMLPPRQRSSMFGEPLGSLHT
V5(2)           ----------------TSKDSGDDDDDVFGAA-----GGSMQPPRQRSPMFSGGLGSSFT
V6(2)           MNVLTTGIILYSFYMSICMDP-DDNDDVFGDD-----EGSMLPKHQRSSMLGSGLGSTFT
V7(1)           MNVLTTGIILYSFYMSICMDTDEEDDDVFGDP-----GGSMLPPRQRSSVFSGGLGSTFT
V8(1)           ----------------LAVDSDDDDDDVFGAA-----GGSMLPPRQRSSMFSEPLGSTFT
V9(1)           MNVLTTGIILFSFYTCLCMDS---DDDVFGAD-----DGSMLPPHQRSSMFSEPLGSLHT
V10(1)          -------IILYSFYTCLCMDPDDDD--AFGDD-----GGSMLPEHKPFSMISGGLGSSHT
V11(1)          MNVLTTGIILYSFYTCLCMNSDDDDDDAFGAE-----GGSMLPRHKRSSMFSEPLGSTFT
V12(1)          MNVLTTGIILYSFYTCLCMNSDDDDDDAFGAE-----GGSMLPRHKRSSMFSEPLGSTFT
V13(1)          MNVLTTGIILYSFYLSICMDTGDDDD-VFGAD-----GGSMLPRHQRSSVFSGGLGETFT
V14(1)          MNVLTTGIILYSFYLSICMDTGDDDD-VFGAD-----GGSMLPRHQRSSVFSGGLGETFT
V15(2)          ----------------AAEDPGEEEDDVFGAE-----GGSMQPPHQRSSMLGSGLGSTFT
V16(1)          ----------------AAEDPGEEEDDVFGAE-----GGSMQPPHQRSSMLGSGLGSTIT
V17(2)          ----------------VCKDTGDDDD-VFGDD-----GGSMLTPHQRSSMFRDDLGSSFT
V18(1)          ----------------VTVDP-DDNDDVFGDD-----EGSMLPKHQRSSMLGSGLGSTFT
V19(1)          ----------------LAVDSDDDDDDVFGAA-----GGSMLPPRQRSPMFSGGLGSSFT
V20(1)          MNVLTTGIILYSFYQCICMDSGDDDDDVFGAA-----GGSMLPPRQRSPMFSGGLGSSFT
V21(1)          MNVLTTGIILYSFYLSICMDTGDD-DDVFGAP-----GGSMLPPRQRSSVFSGGIGSTFT
V22(3)          MNVLTTGIILYSFYQCICMDSGDDDDDVFGAA-----GGSMLPPRQRSPMFSGGLGSSFT
V23(1)          ----------------FSVDPGEEEDDVFGAE-----GGSMLPPHQRSSMLGSGLGSTFT
V24(1)          -------------------------------------------SHQRSSMLGSGLGSTFT
V25(1)          MNVLTTGIILYSFYQCICMDSGDDDDDVFGAA-----GGSMLPPRQRSPMFSGGLGSSFT
V26(1)          MNVLTTGIILYSFYLSICMD---PDDDVFGFDPDDDGDGSMLPPHQRSSIFSSDLGSTFT
V27(1)          ---------VRLVVRCICLDSGEEEDDVFGAE-----GGSMLPKHQRSSMLGSGLGSTFT
                                                                           *

TP02_0895       SGYTKQDLDAKFPGMKKSKGPKDKG----KPH--PTKPVKSTLMPG-----NDGQTGATG
V1(3)           SGYTKQDLDAKFPGMKKSKGPKDKG----KPH--PTKPVKSTLMPG-----NDGQTGATG
V2(1)           GGYGDEEFENKFKSMGIGKKPKDKG----KPH--PTKPVKSTLMP--------GNDGQTG
V3(1)           GGYGDEEFENKFKSMGIGKKPKDKG----KPH--PTKPVKSTLMP--------GNDGQTG
V4(3)           GGYGDEEFENKFKSMGIGKKPKDKG----KPH--PTKPVKSTLMP--------GNDGQTG
V5(2)           SGYTRQELDAKFPGMKKGKGSKDKG----QPK--LPKPVKSTLMP------EGGQSGAVG
V6(2)           SGYSDQEFDEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V7(1)           SGYSDQEFDEKFKHMRIGKKPKDK--------------LGRTNQPQQGAPGAYPPPAAAG
```

```
V8(1)           SGYSDDEFEEKFKRMGMKKKPKDK--------------LGRTNQPQ---------PGTVG
V9(1)           GGYGDEEFENKFKHMRIGKKPKDK--------------LGRTNQP---------QPGAPG
V10(1)          GGYDDDEFQRKFQRMGIGKKPKDK--------------LGRTNQPQ---------PGAAG
V11(1)          SGYSDDEFEEKFKRMGMKKKPKDK--------------LGRTNQPQ---------PGTVG
V12(1)          SGYSDDEFEEKFKRMGMKKKPKDK--------------LGRTNQPQ---------PGASG
V13(1)          SGYSDQEFDEKFKHMGIGKKPKDK--------------LKRTNQPP---------PGPTG
V14(1)          SGYSDQEFDEKFKHMGIGKKPKDK--------------LKRTNQPP---------PGPTG
V15(2)          SGYSDQEFDEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V16(1)          SGYSDQEFDEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V17(2)          SGYTRQELDAKFPNLKARRGPIGK--------------P--RGQPQ--------THQAAG
V18(1)          SGYSDQEFDEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V19(1)          SGYTRQELDAKFPGMKKGKGSKDKAPWNNPPQ--PPKPVKSTLIP--------GDDVPQG
V20(1)          SGYTRQELDAKFPGMKKGKGSKDKAPWNNPPQ--PPKPVKSTLIP--------GDDVPQG
V21(1)          SGYSDKEFEEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V22(3)          SGYTRQELDAKFPGMKKGKGSKDKG----QPK--LPKPVKSTLMP------EGGQSGAVG
V23(1)          SGYSDQEFDEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V24(1)          SGYSDQEFDEKFQRMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
V25(1)          SGYTRQELDAKFPGMKKGKGSKDKAPWNNPPQ--PPKPVKSTLIP--------GDDVPQG
V26(1)          TGYTCWDLENKFPGMKKGKGHKDKG----QPQPQPPKPVKSTLMP------ESGRPQ---
V27(2)          SGYSDQEFDEKFKHMGIGKKPKDKG----KPH--PTKPVKSTLMP------EAGQSGAVG
                 **   ::: **  :   :   .*                    *

TP02_0895       GYPGGYPTQGPYGQPGATGPYGQAGYVGQ-----------PGAVGPYGQPGAV-PYGQTG
V1(3)           GYPGGYPTQGPYGQPGATGPYGQAGYVGQ-----------PGAVGPYGQPGAV-PYGQTG
V2(1)           ---PTGP-YGQTGYPTQPGPYGQPGATGG------YQGGYPTQPGPYPPPGATGPYGQTN
V3(1)           ---ATGP-YGQTGYPTQPGPYGQPGATGG------YQGGYPTQPGPYPPPGATGPYGQTS
V4(3)           ---ATGP-YGQTGYPTQPGPYGQPGPV---------------------------------
V5(2)           GYGATGP-YGQAGYVGQPGAAGN------------YPGGYAGQPGPYGQPGATGPYGQAG
V6(2)           GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
V7(1)           PYGGGYP--SQQGAPGAYPPPAAAGPYGGGYPSQQGAPGAYPPPAAAGPYGGGYPTQQGA
V8(1)           GYG-----------------------------------------------QPGYPSQPQA
V9(1)           AYPPPAAAGGFGGYPSQSGQG---------------------------------VYPPQG
V10(1)          GYPGGYP--TQPGAAGGYPGGYPT------------------QPGAAGGYPGGYPSQQGA
V11(1)          GYG-----------------------------------------------QPGYPSQPQA
V12(1)          GYG---------------------------------------------------------
V13(1)          GYGQPGY--PS-------------------------------QPQAAGPYGGGYPSQPQG
V14(1)          GYGQPGY--PS-------------------------------QPQAAGPYGGGYPSQPQG
V15(2)          GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
V16(1)          GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
V17(2)          GYGQPQG--GPGVYP---------------------------PPAAAGPYGGGYPSQPGA
V18(1)          GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
```

```
V19(1)          ---AVGP-YGG-GYPSQ-GPYGQPG------------------AGPYGQTGYVGPYGG--
V20(1)          ---AVGP-YGG-GYPSQ-GPYGQSG------------------AGPYGQTGYVGQPGPYP
V21(1)          GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
V22(3)          GYGATGP-YGQAGYVGQPGAAGN------------YPGGYAGQPGPYGQPGATGPYGQAG
V23(1)          GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
V24(1)          GYGAAGP-YGQTGYVGQPGPYGQTGYVGQPGAVGPYGGGYPTQ-GPYGQPGAG-PYGQTG
V25(1)          ---AVGP-YGG-GYPTQ-GPYGQPG------------------AGPYGQTGYVGPYGGGY
V26(1)          --GAAAG-Y-PAGYPTQ-GPYGQPGASGG------YPAGYPTQPGPYVQPGATGPYRQTG
V27(2)          GYGAAGP-YGQTGYVGQPGPYGQTGYV---------------------------------


TP02_0895       YPTQP----------------------GAAGGYPG---------------------GYAG
V1(3)           YPTQP----------------------GAAGGYPG---------------------GYAG
V2(1)           YPTQP----------------------GAAGGYPG---------------------GYPT
V3(1)           YPTQP----------------------GAAGGYPG---------------------GYPT
V4(3)           ------------------------------------------------------------
V5(2)           YVGQP----------------------GAAGNYPGGYDGQPGPYGQPGATGPYGQAGYVG
V6(2)           YPTQP----------------------GAAGGYPG---------------------GYTG
V7(1)           PGAYP--------------------PPAAAGPYGG---------------------GYPS
V8(1)           -----------------------------AGAYGG---------------------GYPT
V9(1)           YVGQP----------------------GAPGAYGG---------------------GYPS
V10(1)          -----------------------------AGGYPG---------------------GYPS
V11(1)          -----------------------------AGAYGG---------------------GYPT
V12(1)          ----------------------------------G---------------------GYPS
V13(1)          PGVYP--------------------PPGAAGPYGG---------------------GYPS
V14(1)          PGVYP--------------------PPGAAGPYGG---------------------GYPS
V15(2)          YPTQP----------------------GAAGGYPG---------------------GYTG
V16(1)          YPTQP----------------------GAAGGYPG---------------------GYTG
V17(2)          SGGYGGG------------------ASGGAGPYGG---------------------GYPS
V18(1)          YPTQP----------------------GAAGGYPG---------------------GYTG
V19(1)          ---------------------------GYPG-------------------------GYAG
V20(1)          PP-------------------------GATGPYGQ--------------------TGYVG
V21(1)          YPTQP----------------------GAAGNYPG---------------------GYAG
V22(3)          YVGQP----------------------GAAGNYPGGYDGQPGPYGQPGATGPYGQAGYVG
V23(1)          YPTQP----------------------GAAGGYPG---------------------GYTG
V24(1)          YPTQP----------------------GAAGGYPG---------------------GYTG
V25(1)          PTQGPYGQPGAGPYGQTGYPTQPGAAGGYPG-------------------------GYAG
V26(1)          YPTQP----------------------GAAGGYPA---------------------GYAG
V27(2)          ------------------------------------------------------------
```

```
TP02_0895       QPGPYGQPG---AT-GPYGQAGYVGQP----GAAGGYPGGYPPPG---------------
V1(3)           QPGPYGQPG---AT-GPYGQAGYVGQP----GAAGGYPGGYPPPG---------------
V2(1)           QPGAVGGYG---R--GYSGQGGYPPQ-----GYGQPGKGPYPPPG--------PSGGYGS
V3(1)           QPGAVGGYG---G--GYSGQGGYPPQ-----GYGQPGKGPYPPPG--------PSGGYGS
V4(3)           ------------------------------------------------------------
V5(2)           QPGASGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG---------------
V6(2)           QPGATGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPSG--------PSGGHGA
V7(1)           QQGAPGAYP--PPAAAGAQGPAYPPG------YGQPVASGGYGGG------------ASG
V8(1)           QQGGPGYPP--PPAAAGAQGHAYPPG------YGQPVAAGGYGGG------------ASG
V9(1)           QQGATGGFG---GYPSQSGQGVYPPQ------------GPYAPPG--------AAGGYGG
V10(1)          QQGGPGAYP--PPAAAGGQGPAYPPG------YGQPGAAGGYGGG------------ASG
V11(1)          QQGGPGYPP--PPAAAGAQGHAYPPG------YGQPVAAGGYGGG------------ASG
V12(1)          QPG----------------------------------ASGGYGGG------------ASG
V13(1)          QPQGPGVYP--PPGAAGPYGGGYPSQPQGPGVYPPPGAAGPYGGGYPSQPQGPGVYPPPG
V14(1)          QPQGPGVYP--PPGAAGPYGGGYPSQPQGPGVYPPPGAAGPYGGGYPSQPQGPGVYPPPG
V15(2)          QPGATGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG--------PSGGYGA
V16(1)          QPGATGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG--------PSGGYGA
V17(2)          QPGASGGYGGGASGGAGPYGGGYPSQ---------PGASGGYGGG------------ASG
V18(1)          QPGATGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPSG--------PSGGHGA
V19(1)          QPGASGGYG---A--GYSGQGGYPPQ-----GYVQPGQGPYPPSG--------PSGGHGA
V20(1)          QPGASGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG---------------
V21(1)          QPGASGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG---------------
V22(3)          QPGASGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG---------------
V23(1)          QPGATGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG--------PSGGYGA
V24(1)          QPGATGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPPG--------PSGGYGA
V25(1)          QPGASGGYG---A--GYSGQGGYPPQ-----GYVQPGQGPYPPSG--------PSGGHGA
V26(1)          QPGASGGYG---A--GYSGQGGYPPQ-----GYGQPGQGPYPPSG--------PSGGPGA
V27(2)          ------------------------------------------------------------


TP02_0895       AAGGYGGGPPG-PGQPSGPPGQAPGNMQLLKIDVKNPNNGPNIIFEEYIAGKPERRHRQF
V1(3)           AAGGYGGGPPG-PGQPSGPPGQAPGNMQLLKIDVKNPNNGPNIIFEEYIAGKPERRHRQF
V2(1)           RAGGYGGGKPG-SGHPIDPTGHASG-GNLLKIDVKNPNNGPNIIFEEYIP----------
V3(1)           GAGGYGGGEPG-SGHPSGPTGHASG-GNLLKIDVKNPNNGPNIIFEEYIAGKPERRHRQF
V4(3)           ------------------------------------------------------------
V5(2)           AAGGYGGGPPG-PGQPSGPPGQAPGNMQLLKIDV--------------------------
V6(2)           GAGGYGGGAPG-PGQPSGPTGQTHG-GNMLTIDAKTKHNGPNIIVDEYRAGPQDRRHRQF
V7(1)           GAGGYGGGYPSQPGGPQGAAG-HPGQPIMMKIDAKNRRN-PNTKLDRFTLSN-GGTQHVF
V8(1)           GAGGYGGGYPSQPGGPQGAAG-PPGQPIMMKIDVKNRRN-PNTKLDRFTLTD-GRTQHAF
V9(1)           GAGGYGGGASG-PGQPTGPPGHTPG-VNLLTIDAKTKHNGANIIVDEYRAGRPERIHRQF
V10(1)          GAGGYGGGYPGQQGGPQGAAG-PPGEPIMVKMDAKSRVN-RDINLTKFTLTN-GKTQHVF
```

```
V11(1)          GAGGYGGGYPSQPGGPQGAAG-PPGQPIMMKIDVKNRRN-PNTKLDRFTLTD-GRTQHAF
V12(1)          GAGPYGGGYPSQPGGPQGAAG-PPGEPIMLKMDAKNRTN-RNINLTKFTLPN-GKTQHVF
V13(1)          AAGPYGGGYPSQPGGPQGATG-PPGQPIMMKIDAKNRRN-PNTKLDRFTLSN-GGTQHVF
V14(1)          AAGPYGGGYPSQPGGPQGATG-PPGQPIMMKIDAKNRRD-PNTKLDRFTLSN-GGTQHVF
V15(2)          GAGGYGGSAPG-PGHPSGPTGHASG-GNLLKIDVKNPNNGP-------------------
V16(1)          GAGGYGGSAPG-PGHPSGPTGHASG-GNLLKIDVKNPNNGP-------------------
V17(2)          GAGGYGGGYPSQPGGPQGAAG-PPGQPIMMRIDGKNRRN-PNTRLDRFTLPD-GRTQHVF
V18(1)          GAGGYGGGAPG-PGQPSGPTGQTHG-GNMLTIDAKTKHNGP-------------------
V19(1)          GAGGYGGGAPG-PGQPSGPPGQAPG-GNMLKIDAKSPNNGKNIIVEEFRAGRPERTHRQF
V20(1)          AAGGYGGGPPG-PGQPSGPPGQAPGNMQLLTIDAKTKHNGANIIVDEYRAGRPERIHRQF
V21(1)          AAGGYGGGPPG-PGQPSGPPGQAPGNMQLLKIDVKNPNNGPNIIFEEYIAGKPERRHRQF
V22(3)          AAGGYGGGPPG-PGQPSGPPGQAPGNMQLLKIDVKNPNNGPNIIFEEYIAGKPERRHRQF
V23(1)          GAGGYGGGEPG-PGHPSGPTGHASG-GNLLKNRCKKSKQWSK------------------
V24(1)          GAGGYGGSAPG-PGHPSGPTGHASG-GNLLKIDVKNPNNGPNIIFEEYIA----------
V25(1)          GAGGYGGGAPG-PGQPSGPPGQAPG-GNMLKIDAKSPNNGKNIIVEEFRAGRPERTHRQF
V26(1)          GAGGYGGGAPG-PGQPSGPPSQSPDGKNLGPVDGKTGKNDPFVIFERFRAGPQNRVHHQY
V27(2)          ------------------------------------------------------------


TP02_0895       TPVPGCGINQVNYDGEKVWSLEVGG-DYAVKVLVFPIGFKEKTIEITFIGGEKEIYKKKG
V1(3)           TPVPGCGINQVNYDGEKVWSLEVGG-DYAVKVLVFPIGFKEKTIEITFIGGEKEIYKKKG
V2(1)           ------------------------------------------------------------
V3(1)           TPVPGCGINQVNYDGEKVW-----------------------------------------
V4(3)           ------------------------------------------------------------
V5(2)           ------------------------------------------------------------
V6(2)           DPVPGCGIIQVNYDGRKVWTA--SGPEHAVKVVVFPLGFKEKTIEITFIGGEKAIYKKPG
V7(1)           RPDPGHGIKQVNYDGDRVWSMDRD--NFGTEVLVDPIGSGAKTMTIKMVNGDEVTFTKSG
V8(1)           RANPGYAIKQVNYDGDRVWSMDGG--NFGTEVLVDPIGSGAKTMTIKLAN----------
V9(1)           DPVPGCGINQVNYNGKPVWKMIG--EKYAVKVVLFPIGFEEKTIVITMIGGENEIYKKKG
V10(1)          RANPGHGIKQVNYDGDPVWSMDGN--NFGTEVLLDPIGSPAKNMTIKLANGDKVTFIKKG
V11(1)          RANPGYAIKQVNYDGDRVWSMDGG--NFGTEVLVDPIGSGAKTMTIKLANGDNVIYTKPG
V12(1)          RANPGHGIKQVNYDGDFVWSMDGG--NFGTEVLVDPIGSGAKTMTIKLANGDKVIHTKPG
V13(1)          RPDPGHGIKQVNYDGDPVWSMDGN--NFGTEVLLDPIGSPAKNMTIKMVNGDKEIYKKKG
V14(1)          RPDPGHGIKQVNYDGDPVWSMDGN--NFGTEVLLDPIGLQQK-YDIKFIGGEKEIYKKKG
V15(2)          ------------------------------------------------------------
V16(1)          ------------------------------------------------------------
V17(2)          RPNLGYAIKQVNYDGDRVWSMDDD--NFATEVLV--------------------------
V18(1)          ------------------------------------------------------------
V19(1)          TPVPGCGINQVN------------------------------------------------
V20(1)          DPVPGCGINQVNYNGQPVWK-MIG-EKYAVTVVLFPIGFEEKTIVITMIGGEKEIYKKKG
V21(1)          TPVPGCGINQVNYDGGNVWTM--NDDIHALKVVVFPIGFKEKTIEITFIGGEKEIYKKKG
```

```
V22(3)         TPVPGCGINQVN------------------------------------------------
V23(1)         ------------------------------------------------------------
V24(1)         ------------------------------------------------------------
V25(1)         TPVPGCGINQVNYDGRKVWS-LEVGGDHAVKVLVFPIGFKEKTIEITFIGGEKEIYKKKG
V26(1)         TPRSGCGFNMVKYSGGIVWILGGDGSNYATKVIVHPVGFKEKTIEITFIGGEKEIYKKKG
V27(2)         ------------------------------------------------------------


TP02_0895      RNKPWTKQ
V1(3)          RNKPWTKQ
V2(1)          --------
V3(1)          --------
V4(3)          --------
V5(2)          --------
V6(2)          RNKPWTKQ
V7(1)          RNKPWTKQ
V8(1)          --------
V9(1)          RNKPWTKQ
V10(1)         --------
V11(1)         RNKPWTKQ
V12(1)         RNKPWTKQ
V13(1)         RNKPWTKQ
V14(1)         RNKPWTKQ
V15(2)         --------
V16(1)         --------
V17(2)         --------
V18(2)         --------
V19(1)         --------
V20(1)         RNKPWTKQ
V21(1)         RNKPWTKQ
V22(3)         --------
V23(1)         --------
V24(1)         --------
V25(1)         RNKPWTKQ
V26(1)         RNKPWTKQ
V27(2)         --------
```

Eptiope region highlighted in grey.

Table S12a: Tp10 nucleotide variant Clustal alignment

```
Tp04_0772(genomic)      ATGAAGGTCACAAATCTCAAGTGGAATCCAACTGTTGACTACGCTCTTCTTACCACTTCT        60
XP_764408(mRNA)         ATGAAGGTCACAAATCTCAAGTGGAATCCAACTGTTGACTACGCTCTTCTTACCACTTCT        60
V1(3)                   ------------------------------------------------------------        0
V2(1)                   ------------------------------------------------------------        0
V3(1)                   ------------------------------------------------------------        0
V4(1)                   ------------------------------------------------------------        0
V5(1)*                  ------------------------------------------------------------        0
V6(2)                   ------------------------------------------------------------        0
V7(1)                   ------------------------------------------------------------        0
V8(1)                   ------------------------------------------------------------        0
V9(1)*                  ------------------------------------------------------------        0
V10(5)                  ------------------------------------------------------------        0
V11(3)                  ------------------------------------------------------------        0
V12(1)                  ------------------------------------------------------------        0
V13(1)*                 ------------------------------------------------------------        0


Tp04_0772(genomic)      TTCGACTGTACAGCTAAAGTCTGGTAAGAAAAAAAATTTTCTAAAAAATTTAGGGACGCG        120
XP_764408(mRNA)         TTCGACTGTACAGCTAAAGTCTG------------------------------GGACGCG        90
V1(3)                   ----------------------------------------------------GGGACGCG        8
V2(1)                   ----------------------------------------------------GGGACGCT        8
V3(1)                   ----------------------------------------------------GGGACGCG        8
V4(1)                   ------------------------------------------------------------        0
V5(1)*                  ----------------------------------------------------GGGACGCG        8
V6(2)                   ----------------------------------------------------GGGACGCG        8
V7(1)                   ----------------------------------------------------GGGACGCG        8
V8(1)                   ----------------------------------------------------GGGACGCG        8
V9(1)*                  ----------------------------------------------------GGGACGCG        8
V10(5)                  ----------------------------------------------------GGGACGCG        8
V11(3)                  ----------------------------------------------------GGGACGCG        8
V12(1)                  ----------------------------------------------------GGGACGCG        8
V13(1)*                 ------------------------------------------------------------        0


Tp04_0772(genomic)      TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        180
XP_764408(mRNA)         TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        150
V1(3)                   TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
```

```
V2(1)                   TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V3(1)                   TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCACCCTTCTTCATGCTCCTGG        68
V4(1)                   ---------------------TCAACCTCAATTGGTGAGCACCCTTCTTCATGCTCCTGG        39
V5(1)*                  TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCACCCTTCTTCATGCTCCTGG        68
V6(2)                   TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCACCCTTCTTCATGCTCCTGG        68
V7(1)                   TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V8(1)                   TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V9(1)*                  TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V10(5)                  TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V11(3)                  TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V12(1)                  TCAAATGGCAAAGAACTATTTTCAACCTCAATTGGTGAGCATCCTTCTTCATGCTCCTGG        68
V13(1)*                 ------------------------------------------------------------        0


Tp04_0772(genomic)      ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        240
XP_764408(mRNA)         ACACCTAACGG--------------------------------AGACAAGATTTTAGTTT        178
V1(3)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V2(1)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V3(1)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V4(1)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        99
V5(1)*                  ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V6(2)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V7(1)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V8(1)                   ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V9(1)*                  ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAAAGACAAAATTTTAGTTT        128
V10(5)                  ACACCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V11(3)                  ACACCTAACGGGTACTTTATGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V12(1)                  ACACCTAACGGGTACTTTATGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        128
V13(1)*                 ---CCTAACGGGTACTTTAAGTTTGGAAATTAATGTAATTTAGAGACAAGATTTTAGTTT        57
                           ********                                ***************** 

Tp04_0772(genomic)      CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        300
XP_764408(mRNA)         CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        238
V1(3)                   CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V2(1)                   CAACCAAAGAAGCAAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V3(1)                   CAACCAAAGAAGCTAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V4(1)                   CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        159
V5(1)*                  CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V6(2)                   CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V7(1)                   CAACCAAAGAAGCGAATGTATCATTAATCGACCCGAGATCAGGAAATTGTTGTATCAAGT        188
V8(1)                   CAACCAAAGAAGCGAATGTATCATTAATCGACCCGAGATCAGGAAATTGTTGTATCAAGT        188
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V9(1)*                  CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V10(5)                  CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V11(3)                  CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V12(1)                  CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        188
V13(1)*                 CAACCAAAGAAGCGAATGTATCATTAATTGACCCGAGATCAGGAAATTGTTGTAGCAAGT        117
                        ************* ************** ************************* *****

Tp04_0772(genomic)      ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        360
XP_764408(mRNA)         ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        298
V1(3)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V2(1)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V3(1)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V4(1)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGGCATTACGGAG        219
V5(1)*                  ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V6(2)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V7(1)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V8(1)                   ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V9(1)*                  ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V10(5)                  ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V11(3)                  ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V12(1)                  ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        248
V13(1)*                 ATAAGGCTCACGACTCTAATAAGTTGACAAGTGCTTTATGGCTTGGAGGACATTACGGAG        177
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Tp04_0772(genomic)      GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        420
XP_764408(mRNA)         GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        358
V1(3)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V2(1)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V3(1)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V4(1)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        279
V5(1)*                  GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V6(2)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V7(1)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAGATAAGGGTTTGGG        308
V8(1)                   GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAGATAAGGGTTTGGG        308
V9(1)*                  GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V10(5)                  GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V11(3)                  GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V12(1)                  GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        308
V13(1)*                 GTGACCACATATTTACAAGTGGTTTTGTTGATAACAAGACTAGACAAATAAGGGTTTGGG        237
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Tp04_0772(genomic)      ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     480
XP_764408(mRNA)         ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     418
V1(3)                   ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     368
V2(1)                   ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     368
V3(1)                   ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     368
V4(1)                   ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     339
V5(1)*                  ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCC     368
V6(2)                   ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGCTCGCCTTCTCCCT     368
V7(1)                   ACACGAGGAAACTCGAGAAACACTTTATTTCCAATGATATTGACAGCTCGCCTTCTCCCT     368
V8(1)                   ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGCTCGCCTTCTCCCT     368
V9(1)*                  ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     368
V10(5)                  ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGTTCGCCTTCTCCCT     368
V11(3)                  ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGCTCGCCTTCTCCCT     368
V12(1)                  ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGCTCGCCTTCTCCCT     368
V13(1)*                 ACACGAGGAAACTCGAGAAACACTTGATTTCCAATGATATTGACAGCTCGCCTTCTCCCT     297
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Tp04_0772(genomic)      TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     540
XP_764408(mRNA)         TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGG---------     469
V1(3)                   TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V2(1)                   TGATTCCACACTGGGATCCCCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V3(1)                   TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCGAAGGTTAATTTCT     428
V4(1)                   TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     399
V5(1)*                  TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V6(2)                   TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V7(1)                   TGATTCCACACTGGGATCCCCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V8(1)                   TGATTCCACACTGGGATCCCCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V9(1)*                  TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V10(5)                  TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V11(3)                  TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V12(1)                  TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCAAAGGTTAATTTCT     428
V13(1)*                 TGATTCCACACTGGGATCCTCAAATTGGGTTGGTTGTCCTCGCTTCGAAGGTTAATTTCT     357
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Tp04_0772(genomic)      TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     599
XP_764408(mRNA)         ----------------------GAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     507
V1(3)                   TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     487
V2(1)                   TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     487
V3(1)                   TTATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     487
V4(1)                   TCATTAAAA-ATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     457
V5(1)*                  TCATTAACAAATT-TTTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG     487
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V6(2)                   TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V7(1)                   TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V8(1)                   TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V9(1)*                  TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V10(5)                  TCATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V11(3)                  TCATTAACAAATT-TTTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V12(1)                  TCATTAACAAATT-TTTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        487
V13(1)*                 TTATTAACAAATT-TCTTTAGGGAGACTTAACAGTCAGAATCTTCCAATACATTGATAAG        416
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Tp04_0772(genomic)      GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        659
XP_764408(mRNA)         GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        567
V1(3)                   GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V2(1)                   GAGCTAAACAGGGCGGGAGAATTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V3(1)                   GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V4(1)                   GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACGGGTTCCATGAAGTCCTTCTGTTTAGTA        517
V5(1)*                  GAGCTAAACAGGGCGGGA------------------------------------------        505
V6(2)                   GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V7(1)                   GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACGGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V8(1)                   GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACGGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V9(1)*                  GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V10(5)                  GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V11(3)                  GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V12(1)                  GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        547
V13(1)*                 GAGCTAAACAGGGCGGGAGAGTTCAAAGCCACAGGTTCCATGAAGTCCTTCTGTTTAGTA        476
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Tp04_0772(genomic)      CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        719
XP_764408(mRNA)         CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        627
V1(3)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V2(1)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V3(1)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V4(1)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        577
V5(1)*                  ------------------------------------------------------------        505
V6(2)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V7(1)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V8(1)                   CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V9(1)*                  CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V10(5)                  CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAACACTGAT        607
V11(3)                  CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
V12(1)                  CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        607
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V13(1)*                 CCCACTGATATCTGTGATAAATCGAAGTGTGAATTAGGAAGGTTCTTGTTCAATACTGAT        536


Tp04_0772(genomic)      TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        779
XP_764408(mRNA)         TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        687
V1(3)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V2(1)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V3(1)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V4(1)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        637
V5(1)*                  ------------------------------------------------------------        505
V6(2)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V7(1)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V8(1)                   TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V9(1)*                  TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V10(5)                  TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V11(3)                  TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V12(1)                  TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        667
V13(1)*                 TGCAAGCAGATAAATCTTACATCCATGTTCATCATAAGGAGGAATTCTGCAACAACAATG        596


Tp04_0772(genomic)      AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        839
XP_764408(mRNA)         AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        747
V1(3)                   AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V2(1)                   AACGAACTTTACGGAGAGGAGTATGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V3(1)                   AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V4(1)                   AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        697
V5(1)*                  ------------------------------------------------------------        505
V6(2)                   AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V7(1)                   AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V8(1)                   AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V9(1)*                  AACGAACTTTA-------------------------------------------------        678
V10(5)                  AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V11(3)                  AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V12(1)                  AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        727
V13(1)*                 AACGAACTTTACGGAGAGGAGTACGATACTGCAAGGTATTCAGTCCGTGACTGGGAAGCA        656


Tp04_0772(genomic)      GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC        899
XP_764408(mRNA)         GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC        807
V1(3)                   GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC        787
V2(1)                   GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC        787
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V3(1)                     GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC    787
V4(1)                     GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAGAACAAATGCGCCCAAATCATC    757
V5(1)*                    ------------------------------------------------------------    505
V6(2)                     GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC    787
V7(1)                     GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCGCAAATCATC    787
V8(1)                     GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCGCAAATCATC    787
V9(1)*                    ------------------------------------------------------------    678
V10(5)                    GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC    787
V11(3)                    GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC    787
V12(1)                    GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC    787
V13(1)*                   GGACTTGAGAAGAACTTGGGTCGTCTGACAATAACCAAAAACAAATGCGCCCAAATCATC    716


Tp04_0772(genomic)        AAAGATAAGGTTTGTGCAGAATCTTTATATTACTTTAGGATGCTGGATGCAAGTTCAGGG    959
XP_764408(mRNA)           AAAGATAAGGTTTGTGCAGAATCTTTATATTACTTTAGGATGCTGGATGCAAGTTCAGGG    867
V1(3)                     AAAGATAAGGTTTGTGCAGAATC-------------------------------------    810
V2(1)                     AAAGATAAGGTTTGTGCAGA----------------------------------------    807
V3(1)                     AAAGATAAGGTTTGTGCAGTATCGTTATATTACTT-------------------------    822
V4(1)                     AAAGATAAGGTTTGTG--------------------------------------------    773
V5(1)*                    ------------------------------------------------------------    505
V6(2)                     AAAGATAAGGTTTGTGCCGAATCGTTATATTACTTA------------------------    823
V7(1)                     AAAGATAAGGTTTGTGCAGAATCGTTATATT-----------------------------    818
V8(1)                     AAAGATAAGGTTTGTGCAGAATCGTTATATTACTTTA-----------------------    824
V9(1)*                    ------------------------------------------------------------    678
V10(5)                    AAAGATAAGGTTTGTGCAGAATCGTTATATTACTTTA-----------------------    824
V11(3)                    AAAGATAAGGTTTGTGCAGAATCCTTATATTACTTTA-----------------------    824
V12(1)                    AAAGATAAGGTTTGTGCAGAATCCTTATATTACTTAG-----------------------    824
V13(1)*                   AAAGATAAGGTTTGTGCAG-----------------------------------------    735


Tp04_0772(genomic)        AGATTTCCAAAACCATCCAGGAGTGTAATGCCAAATACGGAACCAACTTTAACAATCCAG    1019
XP_764408(mRNA)           AGATTTCCAAAACCATCCAGGAGTGTAATGCCAAATACGGAACCAACTTTAACAATCCAG    927
V1(3)                     ------------------------------------------------------------    810
V2(1)                     ------------------------------------------------------------    807
V3(1)                     ------------------------------------------------------------    822
V4(1)                     ------------------------------------------------------------    773
V5(1)*                    ------------------------------------------------------------    505
V6(2)                     ------------------------------------------------------------    823
V7(1)                     ------------------------------------------------------------    818
V8(1)                     ------------------------------------------------------------    824
V9(1)*                    ------------------------------------------------------------    678
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V10(5)                  ------------------------------------------------------------        824
V11(3)                  ------------------------------------------------------------        824
V12(1)                  ------------------------------------------------------------        824
V13(1)*                 ------------------------------------------------------------        735
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Primer regions are in bold, underlined and italicized text.

* Partial sequence as defined by only having either the forward or reverse sequence of the allele available for analysis. This sequence is its own variant due to unique nucleotides.

Table S12b: Tp10 protein variant Clustal alignment

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XP_764408        MKVTNLKWNPTVDYALLTTSFDCTAKVWDASNGKELFSTSIGEHPSSCSWTPNGDKILVS      60
V1(16)           ----------------------------DASNGKELFSTSIGEHPSSCSWTPNGDKILVS      32
V2(1)            --------------------------FRDASNGKELFSTSIGEHPSSCSWTPNGDKILVS      34
V3(1)            ----------------------------DASNGKELFSTSIGEHPSSCSWTPNGDKILVS      32
V4(1)            --------------------------FRDASNGKELFSTSIGEHPSSCSWTPNGDKILVS      34
V5(2)            ----------------------------DASNGKELFSTSIGEHPSSCSWTPNGDKILVS      32
V6(1)            --------------------------FRDASNGKELFSTSIGEHPSSCSWTPNGDKILVS      34
                                             ********************************

XP_764408        TKEANVSLIDPRSGNCCSKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      120
V1(16)           TKEANVSLIDPRSGNCCSKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      92
V2(1)            TKEANVSLIDPRSGNCCIKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      94
V3(1)            TKEANVSLIDPRSGNCCIKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      92
V4(1)            TKEANVSLIDPRSGNCCSKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      94
V5(2)            TKEANVSLIDPRSGNCCSKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      92
V6(1)            TKEANVSLIDPRSGNCCSKYKAHDSNKLTSALWLGGHYGGDHIFTSGFVDNKTRQIRVWD      94
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XP_764408        TRKLEKHLISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      180
V1(16)           TRKLEKHLISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      152
V2(1)            TRKLEKHFISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      154
V3(1)            TRKLEKHLISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      152
V4(1)            TRKLEKHLISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      154
V5(2)            TRKLEKHLISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      152
V6(1)            TRKLEKHLISNDIDSSPSPLIPHWDPQIGLVVLASKGDLTVRIFQYIDKELNRAGEFKAT      154
                 *******:****************************************************

XP_764408        GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      240
V1(16)           GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      212
V2(1)            GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      214
V3(1)            GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      212
V4(1)            GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      214
V5(2)            GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      212
V6(1)            GSMKSFCLVPTDICDKSKCELGRFLFNTDCKQINLTSMFIIRRNSATTMNELYGEEYDTA      214
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XP_764408        RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAESLYYFRMLDASSGRFPKPSRSVMP         300
V1(16)           RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAESLYYFR------------------         254
V2(1)            RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAESLY---------------------         253
V3(1)            RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAESLYYF-------------------         253
V4(1)            RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAVSLYY--------------------         254
V5(2)            RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAESLYYL-------------------         253
V6(1)            RYSVRDWEAGLEKNLGRLTITKNKCAQIIKDKVCAEP------------------------         251
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Eptiope region lies outside of sequenced region.