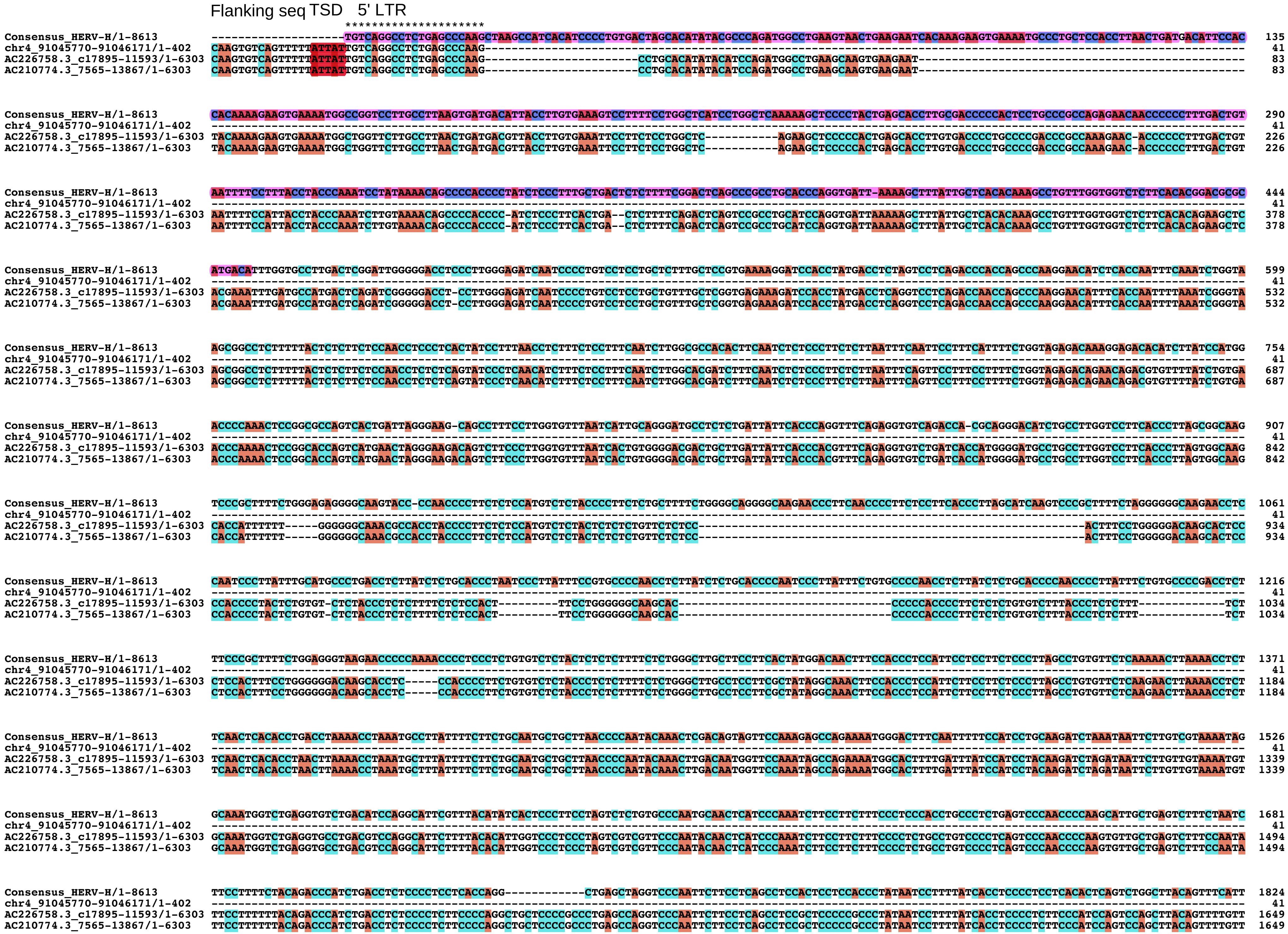

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Consensus_HERV-H/1-8613        --------------------TGTCAGGCCTCTGAGCCCAAGCTAAGCCATCACATCCCCTGTGACTAGCACATATACGCCCAGATGGCCTGAAGTAACTGAAGAATCACAAAGAAGTGAAAATGCCCTGCTCCACCTTAACTGATGACATTCCAC  135
chr4_91045770-91046171/1-402   CAAGTGTCAGTTTTTATTATTGTCAGGCCTCTGAGCCCAAG------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 CAAGTGTCAGTTTTTATTATTGTCAGGCCTCTGAGCCCAAG-----------------------CCTGCACATATACATCCAGATGGCCTGAAGCAAGTGAAGAAT-------------------------------------------------   83
AC210774.3_7565-13867/1-6303   CAAGTGTCAGTTTTTATTATTGTCAGGCCTCTGAGCCCAAG-----------------------CCTGCACATATACATCCAGATGGCCTGAAGCAAGTGAAGAAT-------------------------------------------------   83

Consensus_HERV-H/1-8613        CACAAAAGAAGTGAAAATGGCCGGTCCTTGCCTTAAGTGATGACATTACCTTGTGAAAGTCCTTTTCCTGGCTCATCCTGGCTCAAAAAGCTCCCCTACTGAGCACCTTGCGACCCCCACTCCTGCCCGCCAGAGAACAACCCCCCTTTGACTGT  290
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
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AC210774.3_7565-13867/1-6303   TACAAAAGAAGTGAAAATGGCTGGTTCTTGCCTTAACTGATGACGTTACCTTGTGAAATTCCTTCTCCTGGCTC-----------AGAAGCTCCCCCACTGAGCACCTTGTGACCCCTGCCCCGACCCGCCAAAGAAC-ACCCCCCTTTGACTGT  226

Consensus_HERV-H/1-8613        AATTTTCCTTTACCTACCCAAATCCTATAAAACAGCCCCACCCCTATCTCCCTTTGCTGACTCTCTTTTCGGACTCAGCCCGCCTGCACCCAGGTGATT-AAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGACGCGC  444
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 AATTTTCCATTACCTACCCAAATCTTGTAAAACAGCCCCACCCC-ATCTCCCTTCACTGA--CTCTTTTCAGACTCAGTCCGCCTGCATCCAGGTGATTAAAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACAGAAGCTC  378
AC210774.3_7565-13867/1-6303   AATTTTCCATTACCTACCCAAATCTTGTAAAACAGCCCCACCCC-ATCTCCCTTCACTGA--CTCTTTTCAGACTCAGTCCGCCTGCATCCAGGTGATTAAAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACAGAAGCTC  378

Consensus_HERV-H/1-8613        ATGACATTTGGTGCCTTGACTCGGATTGGGGGACCTCCCTTGGGAGATCAATCCCCTGTCCTCCTGCTCTTTGCTCCGTGAAAAGGATCCACCTATGACCTCTAGTCCTCAGACCCACCAGCCCAAGGAACATCTCACCAATTTCAAATCTGGTA  599
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 ACGAAATTTGATGCCATGACTCAGATCGGGGGACCT-CCTTGGGAGATCAATCCCCTGTCCTCCTGCTGTTTGCTCGGTGAGAAAGATCCACCTATGACCTCAGGTCCTCAGACCAACCAGCCCAAGGAACATTTCACCAATTTTAAATCGGGTA  532
AC210774.3_7565-13867/1-6303   ACGAAATTTGATGCCATGACTCAGATCGGGGGACCT-CCTTGGGAGATCAATCCCCTGTCCTCCTGCTGTTTGCTCGGTGAGAAAGATCCACCTATGACCTCAGGTCCTCAGACCAACCAGCCCAAGGAACATTTCACCAATTTTAAATCGGGTA  532

Consensus_HERV-H/1-8613        AGCGGCCTCTTTTTACTCTCTTCTCCAACCTCCCTCACTATCCTTTAACCTCTTTCTCCTTTCAATCTTGGCGCCACACTTCAATCTCTCCCTTCTCTTAATTTCAATTCCTTTCATTTTCTGGTAGAGACAAAGGAGACACATCTTATCCATGG  754
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
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AC210774.3_7565-13867/1-6303   AGCGGCCTCTTTTTACTCTCTTCTCCAACCTCTCTCAGTATCCCTCAACATCTTTCTCCTTTCAATCTTGGCACGATCTTTCAATCTCTCCCTTCTCTTAATTTCAGTTCCTTTCCTTTTCTGGTAGAGACAGAACAGACGTGTTTTATCTGTGA  687

Consensus_HERV-H/1-8613        ACCCCAAACTCCGGCGCCAGTCACTGATTAGGGAAG-CAGCCTTTCCTTGGTGTTTAATCATTGCAGGGATGCCTCTCTGATTATTCACCCAGGTTTCAGAGGTGTCAGACCA-CGCAGGGACATCTGCCTTGGTCCTTCACCCTTAGCGGCAAG  907
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 ACCCAAAACTCCGGCACCAGTCATGAACTAGGGAAGACAGTCTTCCCTTGGTGTTTAATCACTGTGGGGACGACTGCTTGATTATTCACCCACGTTTCAGAGGTGTCTGATCACCATGGGGATGCCTGCCTTGGTCCTTCACCCTTAGTGGCAAG  842
AC210774.3_7565-13867/1-6303   ACCCAAAACTCCGGCACCAGTCATGAACTAGGGAAGACAGTCTTCCCTTGGTGTTTAATCACTGTGGGGACGACTGCTTGATTATTCACCCACGTTTCAGAGGTGTCTGATCACCATGGGGATGCCTGCCTTGGTCCTTCACCCTTAGTGGCAAG  842

Consensus_HERV-H/1-8613        TCCCGCTTTTCTGGGAGAGGGGCAAGTACC-CCAACCCCTTCTCTCCATGTCTCTACCCCTTCTCTGCTTTTCTGGGGCAGGGGCAAGAACCCTTCAACCCCTTCTCCTTCACCCTTAGCATCAAGTCCCGCTTTTCTAGGGGGGCAAGAACCTC 1061
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 CACCATTTTTT-----GGGGGGCAAACGCCACCTACCCCTTCTCTCCATGTCTCTACTCTCTCTGTTCTCTCC----------------------------------------------------------ACTTTCCTGGGGGACAAGCACTCC  934
AC210774.3_7565-13867/1-6303   CACCATTTTTT-----GGGGGGCAAACGCCACCTACCCCTTCTCTCCATGTCTCTACTCTCTCTGTTCTCTCC----------------------------------------------------------ACTTTCCTGGGGGACAAGCACTCC  934

Consensus_HERV-H/1-8613        CAATCCCTTATTTGCATGCCCTGACCTCTTATCTCTGCACCCTAATCCCTTATTTCCGTGCCCCAACCTCTTATCTCTGCACCCCAATCCCTTATTTCTGTGCCCCAACCTCTTATCTCTGCACCCCAACCCCTTATTTCTGTGCCCCGACCTCT 1216
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 CCACCCCTACTCTGTGT-CTCTACCCTCTCTTTTCTCTCCACT---------TTCCTGGGGGGCAAGCAC--------------------------------CCCCCACCCCTTCTCTCTGTGTCTTTACCCTCTCTTT-------------TCT 1034
AC210774.3_7565-13867/1-6303   CCACCCCTACTCTGTGT-CTCTACCCTCTCTTTTCTCTCCACT---------TTCCTGGGGGGCAAGCAC--------------------------------CCCCCACCCCTTCTCTCTGTGTCTTTACCCTCTCTTT-------------TCT 1034

Consensus_HERV-H/1-8613        TTCCCGCTTTTCTGGAGGGTAAGAACCCCCAAAACCCCTCCCTCTGTGTCTCTACTCTCTCTTTTCTCTGGGCTTGCTTCCTTCACTATGGACAACTTTCCACCCTCCATTCCTCCTTCTCCCTTAGCCTGTGTTCTCAAAAACTTAAAACCTCT 1371
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 CTCCACTTTCCTGGGGGGACAAGCACCTC-----CCACCCCTTCTGTGTCTCTACCCTCTCTTTTCTCTGGGCTTGCCTCCTTCGCTATAGGCAAACTTCCACCCTCCATTCTTCCTTCTCCCTTAGCCTGTGTTCTCAAGAACTTAAAACCTCT 1184
AC210774.3_7565-13867/1-6303   CTCCACTTTCCTGGGGGGACAAGCACCTC-----CCACCCCTTCTGTGTCTCTACCCTCTCTTTTCTCTGGGCTTGCCTCCTTCGCTATAGGCAAACTTCCACCCTCCATTCTTCCTTCTCCCTTAGCCTGTGTTCTCAAGAACTTAAAACCTCT 1184

Consensus_HERV-H/1-8613        TCAACTCACACCTGACCTAAAACCTAAATGCCTTATTTTCTTCTGCAATGCTGCTTAACCCCAATACAAACTCGACAGTAGTTCCAAAGAGCCAGAAAATGGGACTTTCAATTTTTCCATCCTGCAAGATCTAAATAATTCTTGTCGTAAAATAG 1526
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
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AC210774.3_7565-13867/1-6303   TCAACTCACACCTAACTTAAAACCTAAATGCTTTATTTTCTTCTGCAATGCTGCTTAACCCCAATACAAACTTGACAATGGTTCCAAATAGCCAGAAAATGGCACTTTTGATTTATCCATCCTACAAGATCTAGATAATTCTTGTTGTAAAATGT 1339

Consensus_HERV-H/1-8613        GCAAATGGTCTGAGGTGTCTGACATCCAGGCATTCGTTTACATATCACTCCCTTCCTAGTCTCTGTGCCCAATGCAACTCATCCCAAATCTTCCTTCTTTCCCTCCCACCTGCCCTCTGAGTCCCAACCCCAAGCATTGCTGAGTCTTTCTAATC 1681
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 GCAAATGGTCTGAGGTGCCTGACGTCCAGGCATTCTTTTACACATTGGTCCCTCCCTAGTCGTCGTTCCCAATACAACTCATCCCAAATCTTCCTTCTTTCCCCTCTGCCTGTCCCCTCAGTCCCAACCCCAAGTGTTGCTGAGTCTTTCCAATA 1494
AC210774.3_7565-13867/1-6303   GCAAATGGTCTGAGGTGCCTGACGTCCAGGCATTCTTTTACACATTGGTCCCTCCCTAGTCGTCGTTCCCAATACAACTCATCCCAAATCTTCCTTCTTTCCCCTCTGCCTGTCCCCTCAGTCCCAACCCCAAGTGTTGCTGAGTCTTTCCAATA 1494

Consensus_HERV-H/1-8613        TTCCTTTTCTACAGACCCATCTGACCTCTCCCCTCCTCACCAGG------------CTGAGCTAGGTCCCAATTCTTCCTCAGCCTCCACTCCTCCACCCTATAATCCTTTTATCACCTCCCCTCCTCACACTCAGTCTGGCTTACAGTTTCATT 1824
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 TTCCTTTTTTACAGACCCATCTGACCTCTCCCCTCTTCCCCAGGCTGCTCCCCGCCCTGAGCCAGGTCCCAATTCTTCCTCAGCCTCCGCTCCCCCGCCCTATAATCCTTTTATCACCTCCCCTCTTCCCATCCAGTCCAGCTTACAGTTTTGTT 1649
AC210774.3_7565-13867/1-6303   TTCCTTTTTTACAGACCCATCTGACCTCTCCCCTCTTCCCCAGGCTGCTCCCCGCCCTGAGCCAGGTCCCAATTCTTCCTCAGCCTCCGCTCCCCCGCCCTATAATCCTTTTATCACCTCCCCTCTTCCCATCCAGTCCAGCTTACAGTTTTGTT 1649
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Consensus_HERV-H/1-8613        CCGTGACTAGCCCTCCCCCACCTGCCCAGCAATTTCCTCTTAAAAAGTTGGCTGGAGCTAAAGACATAGTCAAGGTTAATGCTCCTTTTTCTTTATCTGACCTCTCCCAAATCAGTTAGCATTTAGACTCTTTTTCATCAAATACAAAAAACCCA 1979
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 CTGCAACTAGCCCTCCCCCACCTGCCCAGCAATTTCCTCTTTAAAAGGTGGCTGGAGCTAAAGGCATAGTCAAGGTTACTGCTCCTTTTTCTTTAACCAACCTCTCCCAAATCAGTTAGCATGTAGGCTCTTTTTCATCAAATAT-AAAAACCCA 1803
AC210774.3_7565-13867/1-6303   CTGCAACTAGCCCTCCCCCACCTGCCCAGCAATTTCCTCTTTAAAAGGTGGCTGGAGCTAAAGGCATAGTCAAGGTTACTGCTCCTTTTTCTTTAACCAACCTCTCCCAAATCAGTTAGCATGTAGGCTCTTTTTCATCAAATAT-AAAAACCCA 1803

Consensus_HERV-H/1-8613        GCCCAGTTCATGGCTCATTCGGCAGCAACCCTGAGACGCTTTACAGCCTTAGACCCTAAAAGGTCAAAAGGCCGTCTTATCCTCAATATACATTTTATTACCCAATCTGCTCCAAACATTAAATAAAACTCCAAAAATTAAATTCTGGCCCTCAA 2134
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 GCCCAGTTCATGGCTCATTTGGCAGCAACCCTGAGACGCTTTACGGCCCTAGGCCCTAAAAGGTCAAAAGGCCATCTTATTCTCAATATACATTTTATTACCCAATCTACTCCCAACATTAAATAAAATTCCAAAAATTAAATTCCCACCCTCAA 1958
AC210774.3_7565-13867/1-6303   GCCCAGTTCATGGCTCATTTGGCAGCAACCCTGAGACGCTTTACGGCCCTAGGCCCTAAAAGGTCAAAAGGCCATCTTATTCTCAATATACATTTTATTACCCAATCTACTCCCAACATTAAATAAAATTCCAAAAATTAAATTCCCACCCTCAA 1958

Consensus_HERV-H/1-8613        ACCCCACAACAGGATTTAATTAACCTCACCTTCAAGGTGTACAATAATAGAAAA---------------------------AAGTTGCAATTCCTTGCCTCCACTGTGAGACAAACCCCAGACACATCTCCAGCACACAAGAACTTCGAAATGCC 2262
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
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AC210774.3_7565-13867/1-6303   ACCCCACAATAGGACTTAATTAACCTCAACTTCAAGTTGTATAATAGTAGAGTAGAGGCAGCCAAGTAGCAAGGTATTTCTGAGTTGCAGTTCCTTGCCTCCACTGTGAGAGAAACCCCAGCCACATCTCCAGCACACAAGAACTTCAAAATGCC 2113

Consensus_HERV-H/1-8613        TCAACCTCAGGTGCCAGGGGTTCCTCCAGAACCTTCTCCCCCAGGAGCTTGCTACAAGTGCCAGAAATCTGGCCACTGGGCCAAGGAATGCCCACAGACCAGGATTCCTCCTAAGCTGTATCCCATCTCTGTGGGACCCCACTAAAAATCAGACT 2417
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 TAAGCCACAGTGGTGAGGCATTCCTTCAGGACCTCCTCCCCCAGGATCTTGCTTCAAGTGCCGGAAATCTGGCCACCAGGCCAAGGAATGCCTGCAGCCTGGGATTCCTCCTAAGCTGTGTCCCAGCTGTGTGGGTCCCCACTGGAAATTCAACT 2268
AC210774.3_7565-13867/1-6303   TAAGCCACAGTGGTGAGGCATTCCTTCAGGACCTCCTCCCCCAGGATCTTGCTTCAAGTGCCGGAAATCTGGCCACCAGGCCAAGGAATGCCTGCAGCCTGGGATTCCTCCTAAGCTGTGTCCCAGCTGTGTGGGTCCCCACTGGAAATTCAACT 2268

Consensus_HERV-H/1-8613        GTTCAACTCACCTGGCAGCCACTTCCAGAGCCCCTGGAACTCTAGCCCAAGGCTCTCTGACTGACCCCTTCTGAGATCTTCTTGGCTTAGCAGCTGAAGACTGACACTGCCAGATCGCCTCGGAAGCCTACAGGACCATCACAGATGCTCCAGGT 2572
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 GTCCAA-----------------------------------CTAGCCCAAGG--CTCTGACTTACTTCTTCCCAGATCTTCTCAGCTTAGTGGCTGAAGACTGGCGCTGCCTGTGTGCCTTGGAAGCCTCCTGGACCATCACAGATGCTTTGGGT 2386
AC210774.3_7565-13867/1-6303   GTCCAA-----------------------------------CTAGCCCAAGG--CTCTGACTTACTTCTTCCCAGATCTTCTCAGCTTAGTGGCTGAAGACTGGCGCTGCCTGTGTGCCTTGGAAGCCTCCTGGACCATCACAGATGCTTTGGGT 2386

Consensus_HERV-H/1-8613        AACTCTCACAGTAGAGGGTAAGTCTGTCCCCTTCTTAATCAATATGGAGGCTACCCACTGCACATTACCTTCTTTTCAAGGGCCTGTTTCCTTTGCCTCCATAACTGTTGTGGGTATTGACGGCCAGGCTTCTAAACCTCTTAAAACTCCCCAAC 2727
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
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AC210774.3_7565-13867/1-6303   AACTCTTACAGTGGAGGGTAAGTCCATCCCCTTCTTAATCAATACAGAGGCTACCCACTCCACATTACCTTCTTTTCAAGGGCCTGTTTCCCTTGCCTCCATAACTGTTGTGCGTATTGATGGCCAGGCTTCTAAACCTCTTCAAACTCCCCAAC 2541

Consensus_HERV-H/1-8613        TCTAGTACCAACTTAGACAATACTCTTTTAAGCACTCCTTTTTAGTTATCCCCACTTGCCCAGTTCCCTTATGAGGCCGAGACACTTCAACTAAATTATCTGCTTCCCTGACTATTCCTGGACTACAGCTACATCTCATTGCTGCCCTTCTTCCC 2882
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 TCTGGTGCCAACTTGGACAGTATTCTTTTATGCACTCCTTTTTAGTTATCCCCACCTGCCCAGTTCCCTTATTAGGCCAAGATATTTTAACTAAATTATCTGCTTCCCTGACCATTCCTAGGCTACAGCCACACCTCATTGCCACCCATTTCCCC 2696
AC210774.3_7565-13867/1-6303   TCTGGTGCCAACTTGGACAGTATTCTTTTATGCACTCCTTTTTAGTTATCCCCACCTGCCCAGTTCCCTTATTAGGCCAAGATATTTTAACTAAATTATCTGCTTCCCTGACCATTCCTAGGCTACAGCCACACCTCATTGCCACCCATTTCCCC 2696

Consensus_HERV-H/1-8613        AATCCAAAGCCTCCTTTGCATCTT---CTTGTATCCCCCAACCTTAACCCACAAGTATAAGATACCTCTATTCCCTCCTTGGTGACCAATCATGCACCCCTTACCATCTCATTAAAACCTAATCACTCTTACCCGGCTCAATGCCAAGATCCCAT 3034
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
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AC210774.3_7565-13867/1-6303   AGTTCAAAGCCTCCTTCACATCCTCCCCTTGTATCTCCCCACCTTAATCCACAAGTATAGGACATCTCTACTCCATCCTTGGCGACCAATCATGCACCCCTTACCATCCCATTAAAACCTAATCACCCTTACCCCACTCAACGCCAATATCCCAT 2851

Consensus_HERV-H/1-8613        CCCACAGCATGCTTTAAAAGGATTAAAACCTGTTATCACTCGCCTGCTAGAGCATGGCCTTTTAAAGCCTATAAACTCTCCTTACAATTCCCCCATTTTACCTGTCCTAGAACCAGACAAGCCTTACAG----GTTCAGGATCTGTGTCTTATCA 3185
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 CCCACAGCAGGCTGTAAAAGGAATAAAGCCTGTTATCACTTGCCTGTTACAGCATGGCCTTTTAAAGCCTATAAACTCTCCTTAC-ATTCCCCCATTTTACCTGTCCAAAAACGAGACAAGTCTTACAGGTTAGTTCAGGATCTGCACCTTATCA 3005
AC210774.3_7565-13867/1-6303   CCCACAGCAGGCTGTAAAAGGAATAAAGCCTGTTATCACTTGCCTGTTACAGCATGGCCTTTTAAAGCCTATAAACTCTCCTTAC-ATTCCCCCATTTTACCTGTCCAAAAACGAGACAAGTCTTACAGGTTAGTTCAGGATCTGCACCTTATCA 3005

Consensus_HERV-H/1-8613        ATGAAATTGTTTTCCCTATCCACCCTGTGGTGCTGAACCCATATACTCTCCTATCCTCAATACCTC-----------CCTCTACAACCCATTATTCTGTTCTAGATCTCAAACATGCTTTCTTTACTATCCCTTTACACCCTTCAACCCAGCCTC 3329
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 ACCAAATTGTTTTGCCTATCCACCCCATGGTGCCAAACCCATATACTCTCCTATCCTCGATACCTCCCCCGACAACACCTCCACAACCCATTATTCTGTTCTGGATCTCAAACATGCTTTCTTTACTATTCCTTTGCAGCCTTCATCCCAGCCTG 3160
AC210774.3_7565-13867/1-6303   ACCAAATTGTTTTGCCTATCCACCCCATGGTGCCAAACCCATATACTCTCCTATCCTCGATACCTCCCCCGACAACACCTCCACAACCCATTATTCTGTTCTGGATCTCAAACATGCTTTCTTTACTATTCCTTTGCAGCCTTCATCCCAGCCTG 3160

Consensus_HERV-H/1-8613        TCTTCGTTTTCACCTGGACTGACCCTGACACCCATCAGTCCCAGCAGCTTACCTGGGCTGTAATGCTGCAAGGTTTCAGGGGCAGCCCTTATTATTTCAGCCAAGCTCTTTCTCATGATTTACTTTCTTTCCACCCCTCCACTTCTCACCTTATT 3484
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 TCTTCACTTTCACTTGGACTGACCCTGATACCCATCAGCCTCAGCAAATTACCTGGGTTGTACTGCCACAAGGCTTCACGGACAGCCCCCATTACTTCAGTC----------------------------------------------------- 3262
AC210774.3_7565-13867/1-6303   TCTTCACTTTCACTTGGACTGACCCTGATACCCATCAGCCTCAGCAAATTACCTGGGTTGTACTGCCACAAGGCTTCACGGACAGCCCCCATTACTTCAGTC----------------------------------------------------- 3262

Consensus_HERV-H/1-8613        CAATATATTGGTGATGTTCTTCTTTGTAGCCCCTCCTTTGAATCTTCTCAACAAGACACACTTCTGCTCCTTCAGCATTTATTCTCCAAAGGATATCCCCCTCCAAAGCTCAAATGTCTTCTCCATCCGTTACCTACCTTGGCATAATTCTTCAT 3639
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------   41
AC226758.3_c17895-11593/1-6303 ---------------------------------------------------------------------------------------------------------AAGCTCAAATTTCTTCCTCATCCATTACCTATCTTGGCATAATTCTTCAT 3312
AC210774.3_7565-13867/1-6303   ---------------------------------------------------------------------------------------------------------AAGCTCAAATTTCTTCCTCATCCATTACCTATCTTGGCATAATTCTTCAT 3312
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Consensus_HERV-H/1-8613          AAAAACACACGTGCCCTCCCTGCTGATAGTGTCTGACTGATCTCTCAAACCCCAACCCCTTCTACAAAACAACAACTCTTTTCCATCCTAGGCATGGTTGGATACTTTCGTGTTAGGATACCTGGTTTTGCCATCCTAACAAAACCATTATATAA 3794
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 GAAAACACATGTGCTCTGCCTCCTGATCGTGTCTGACTGATATCTCAAACCCCAATACCTTCTACAAAACAACAACTC-TTTCCTTCCTAGTCATGGTTAGGTACTTCCACCTTTGGATACCTAGTTTTACCATCCTAACAAAACCATTATATAA 3466
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Consensus_HERV-H/1-8613          ACTCACAAAAGGAAACCTAGTTGACCCCATAGATCCTAAATCGTTTCCCCACTCCTCTTTCCATTCCTTGAAGACAGCTTTAGAGACTGTCTCCACTCTAGCTCTCCCTGACTCATCCCAACACTTTTCATTACACACAGCTGAAGTGCAGGGCT 3949
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 ACTCACAAAAGGAAACCTAGCTGACCCCATAGATCCTAAATCCTTT-CCCACTCCTTTTTCTGTTCCTTGAAGACAGCTTTAGAGACTGCCCCCACACTATCTCTCCCTGACTCATCCCAACCCTTTTCATTACACACAGCCAAAGTACAGGACT 3620
AC210774.3_7565-13867/1-6303     ACTCACAAAAGGAAACCTAGCTGACCCCATAGATCCTAAATCCTTT-CCCACTCCTTTTTCTGTTCCTTGAAGACAGCTTTAGAGACTGCCCCCACACTATCTCTCCCTGACTCATCCCAACCCTTTTCATTACACACAGCCAAAGTACAGGACT 3620

Consensus_HERV-H/1-8613          GTGCAGTCAGAATTCTTACACAAGGACCGGGATCGCATCCTGTAGCCTTTTTGTCCAAACAACTTGACCTTACTGTTTTAGGCTGGCCATCATGTCTCCATGCAGCGTCTGCTGCCACCCTAATACTTTTAGAGGCCCTCAAAATCACAAACTAT 4104
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 GTGCAGTCAGAATTCTTACACAAGGACTGGGACTGCACCCTGTAGCCTTTTTGTCCAAACAACTTGACCTTACTGTTTTAGGCTGGCCATCATGTATCCGTGCAGCGGCTGCCGCCATCCTAATACTTTGAGAGGCCCTCAAACTCACAAACTAT 3775
AC210774.3_7565-13867/1-6303     GTGCAGTCAGAATTCTTACACAAGGACTGGGACTGCACCCTGTAGCCTTTTTGTCCAAACAACTTGACCTTACTGTTTTAGGCTGGCCATCATGTATCCGTGCAGCGGCTGCCGCCATCCTAATACTTTGAGAGGCCCTCAAACTCACAAACTAT 3775

Consensus_HERV-H/1-8613          GCTCAACTCATTCTCTACAGCTCTCATAATTTCCAAAATCTATTTTCTTCCTCACACCTGACACATATACTTTCTGCTCCCCGGCTCCTTCAGATATACTCACTC--CATTTATTCTCCCACAATTACCATTATTCCTGGCCTGGACTTCAATCC 4257
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 GCTCAACTCACTCTCTACAGCTCTCATAACTTCCAAAATTTATTTTCTTCCTCACATCTGACACATATACTTTCTGCTCCCTGGCTCCTTCAGCTATACTCACTCTTTGTTGAGTCTCCCACAGGTATCATT-------GGCCGGACTTCAATCC 3923
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Consensus_HERV-H/1-8613          GGCCTCCCACATTATTCTGGATACCATACCTGACCCTCATGACTGCATCTCTCTGATCCACCTGACGTTCACCCCATTTCCCCACATTTCCTTCTGCCCTGTTTCTCACCCTGATCACACTTGGTTTATTGATGGCAGTTCCACCAGGCCTAATC 4412
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 GGCCTCCGACATTATTCCGGATACCACACCTGACCCCCAAGACTGTATCTCTCTGATCCACCTGACATTTGCCCCATTTCCCCATATTTCCTTCTTTCCTGTTCCTCACCCTGATTACATTTGGTTTACTGATGGCAGTTCCACCAGGCCTAATC 4078
AC210774.3_7565-13867/1-6303     GGCCTCCGACATTATTCCGGATACCACACCTGACCCCCAAGACTGTATCTCTCTGATCCACCTGACATTTGCCCCATTTCCCCATATTTCCTTCTTTCCTGTTCCTCACCCTGATTACATTTGGTTTACTGATGGCAGTTCCACCAGGCCTAATC 4078

Consensus_HERV-H/1-8613          GCCACTCACCAGCAAAGGCAGGATATGCTA------------------------------------------------------------------TGAACTAGTTGCCTTAATTCAAGCCCTCACTCTTGCAAAAGGACTACGTGTCAATATCT 4501
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
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AC210774.3_7565-13867/1-6303     ACCACTCACCAGCAAAGGCAGGCTATGCTATATAGTATCTTCCACATCTATAATTGAGGCTACTGCTCTGCCCCGCTCCACTACCTCTCAGCAAGCTGAACTCATTGCCTTAACTCGGGACCTCACTCTTGCAAAGGGACTACACATCAATACTT 4233

Consensus_HERV-H/1-8613          ATACTGATTCTAAATATGCCTTTCATATTCTGCACCACCATGCGGTCATATGGGCTGAAAGAGGTTTCCTCACTACAC-AAGTGTCCTCCATCATTAATGCCTCTTTAA-GAAAACTCTGCTCAAGGCTGCTTTACTTCCAAAGGAAGCTGGGGT 4654
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 ATACTGACTCTAAATATGCCTTCCATATCCTGCACCACCATGCTGTTACATGGGCAGAAAGAGGTTTCCTTACTACACAAAAGGTCCTCCATCATTAATGCCTCTTTAATAAAAACTCTTCTCAAGGCCTCTTTGCTTCCAAAGGAAGCTGGAGT 4388
AC210774.3_7565-13867/1-6303     ATACTGACTCTAAATATGCCTTCCATATCCTGCACCACCATGCTGTTACATGGGCAGAAAGAGGTTTCCTTACTACACAAAAGGTCCTCCATCATTAATGCCTCTTTAATAAAAACTCTTCTCAAGGCCTCTTTGCTTCCAAAGGAAGCTGGAGT 4388

Consensus_HERV-H/1-8613          CATTCACTGCAAGGGGCATCAAAAGACTTCAGATCCCATTGCTCTAGGCAATGCTTATGCTGATAAGGTGGCTAGACAAGCAGCTAGCTCTCCAACTTTTGTCCCTCATGGCCAGTTTTTCTCCTTCACATCCG----TCACTCCCACCTACTCC 4805
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 CATTCACTGCAAGGGCCATCAAAAGGCGTCATATCCCATTGCTCTAGGCAGTGCTTATGCTGATAACGTAGCTAAAGAAGCAGCTAACATTCCAACTTCTGTCCCTCACGGCCAGTTTTTCTTCTTCTCATCCATCGTTCACTCTCACCTACTCC 4543
AC210774.3_7565-13867/1-6303     CATTCACTGCAAGGGCCATCAAAAGGCGTCATATCCCATTGCTCTAGGCAGTGCTTATGCTGATAACGTAGCTAAAGAAGCAGCTAACATTCCAACTTCTGTCCCTCACGGCCAGTTTTTCTTCTTCTCATCCATCGTTCACTCTCACCTACTCC 4543

Consensus_HERV-H/1-8613          ACAGCTGAAACTTCCACCTATCAAGCTCTTCCCCCGCAAGGTAAATGGTTCTTAGACCAAGGAAAATATCTCCTTCCAGCCTCACAGGCCCATTCTATTCTGTCGTCATTTCATAACCTTTTCCATGTAGGTTACAAGCCACTAGCCTGTCTCTT 4960
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 CCAGCTGAAACTGCCACCTATCAATCTCTTCCCACACAAGGCAAATGGTTCTTGGACCAAGGAAAATATCTCCTTCCGGCCTCACAGGCCTATTGCATTGTGTCGTCATTTCATAAACTCTTCCATGTAAGTTACAAGCCACTAGCCCATCTCTT 4698
AC210774.3_7565-13867/1-6303     CCAGCTGAAACTGCCACCTATCAATCTCTTCCCACACAAGGCAAATGGTTCTTGGACCAAGGAAAATATCTCCTTCCGGCCTCACAGGCCTATTGCATTGTGTCGTCATTTCATAAACTCTTCCATGTAAGTTACAAGCCACTAGCCCATCTCTT 4698

Consensus_HERV-H/1-8613          AGGACCTCTCATTTCCTTTCCATCATGGAAATCTATCCTCAAGGAGATCACTTCTCAGTGTTCCATCTGCTATTCTGCTACCCCTCAGGGATTGTTCAGG-CCTCCTCCCTTTCCTACACATAAAGCTCGGGGATTTGCCCCTGCCCAGGACTGG 5114
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 AGAACCTCTCATTTCCTTTCCATCGTGGAAATCTATCCTTAAGGAAATCACTTCTCAGTATTCCATCTGCTATTCTACTACTCCTCAGGAATTTCTCAGGCCCCCCTCCCTTCCCTACACATCAAGCTTGGGGATTTGCTTCTGCCCAGGACTGG 4853
AC210774.3_7565-13867/1-6303     AGAACCTCTCATTTCCTTTCCATCGTGGAAATCTATCCTTAAGGAAATCACTTCTCAGTATTCCATCTGCTATTCTACTACTCCTCAGGAATTTCTCAGGCCCCCCTCCCTTCCCTACACATCAAGCTTGGGGATTTGCTTCTGCCCAGGACTGG 4853

Consensus_HERV-H/1-8613          CAAATTGACTTTACTCACATGCCTCGGGTCAGAAAACTAAAATATCTCTTAGTCTGGGTAGACACTTTCACTGGGTGGGTAGAGGCCTTTCCCATAGAGTCTGAGAAGGCCACCGCGGTCATTTCTTCCCTTCTGTCAGACATAATTCCTTGGTT 5269
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
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AC210774.3_7565-13867/1-6303     CAAATTGACTTTACTCACATGCCCCGAGTCAGGAAACTAAAATACCTCTTGGTCTGGGTAGACACTTTCACTGGATGGGTAGAGACCTTTCCTGCAGGGTCTGAGAAGGCCACTGCGATCATTTATTCCCTTCTGTCAGACATAA---------- 4998

Consensus_HERV-H/1-8613          TGGCCTTCCCTTCTCTATACAGTCTGATAACGGACCAGCCTTTACTAGTTAAATCACCCAAGCAGTTTCTCAGGCTCTTGGTATTCAGTGGAACCTTCATATCCCTTAACATCCTCAATCTTCAGGAAAGGTAAAACCGACTAATGGTCTTTTAA 5424
chr4_91045770-91046171/1-402     ----------------------------------------------------------------------------------------------------------------------------------------------------------- 41
AC226758.3_c17895-11593/1-6303 -----TTCCCACCTCTATACAGTCTAATAACAGACCGGCCTTTACTATTCAAATCACCCAAGCAGTTTCTCAGGCTCTTGATATTCAATGAAACCTTCATACCCCTTACTGTCCTCAATCTTCAAAAAAGGTAGAACAGACAAATGGTCTTTTAA 5148
AC210774.3_7565-13867/1-6303     -----TTCCCACCTCTATACAGTCTAATAACAGACCGGCCTTTACTATTCAAATCACCCAAGCAGTTTCTCAGGCTCTTGATATTCAATGAAACCTTCATACCCCTTACTGTCCTCAATCTTCAAAAAAGGTAGAACAGACAAATGGTCTTTTAA 5148
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chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 AAACACACCTCACCAAGCTCAGCCACAAACTTAAAAAGGACTGGACAATACTTTTACCACTTTCCCTTCTCAGAATTCGGGCCTGTCCTCAGAATGCTACAGGCTACAGCCCATTTGAGCTCCTGTATGGACACTCCTTTTTACTAGGCCCCAGC  5303
AC210774.3_7565-13867/1-6303   AAACACACCTCACCAAGCTCAGCCACAAACTTAAAAAGGACTGGACAATACTTTTACCACTTTCCCTTCTCAGAATTCGGGCCTGTCCTCAGAATGCTACAGGCTACAGCCCATTTGAGCTCCTGTATGGACACTCCTTTTTACTAGGCCCCAGC  5303

Consensus_HERV-H/1-8613        CTCATCCCAGACACCAGCCCTCTAGGCGACTATCTTCCAGTCCTCCAACAGGCTAGGCAGGAAAGTCACCAGGCTGCTAATCTTCTCTTGCCTACTCCAGATCCCCAGCCATATGAAGACACTCTAGCTGGACGATCAGTTCTTGTTAAGAATCT  5734
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 CTCATTCCAGACACCAGCC----------------------------------------------------------------------------------------------------------------------------------------  5322
AC210774.3_7565-13867/1-6303   CTCATTCCAGACACCAGCC----------------------------------------------------------------------------------------------------------------------------------------  5322

Consensus_HERV-H/1-8613        GACCCCTCAAACTCTACAACCTCGATGGACTGGACCCTACTTAGTCATCTATAGTACCCTGACTGCCGTCCGCCTGCAGGATCCTCCCCACTGGGTTCACCATTCCAGAATAAAGCTGTGTCCATTGGACAGCCAGCCTAATCCCTCCTCTTCCT  5889
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5322
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5322

Consensus_HERV-H/1-8613        CCTGGAAGTCGCAATTACTCTCCCCTACTTCCCTTAAACTCACTCGTATTTCTGAAGAACAGTAATAACCCTTATGAGCCTAATACATCCCTTCATTCTATTAGGTCTGTTTGTCCTTACCCTACTTTTTGCAACAGGGCTTTATGAACTCACCC  6044
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5322
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5322

Consensus_HERV-H/1-8613        CCACCACTTAGGCTGAGCCCAAAAAATCTTGTCATCCCTACTATTTTCTGTCCAGTCATACTCCTATTCTCTGCTCTCAACTACTTATAAATGCCGTACTCTT-------------GTTTACACTGCTGGTTTACACTGTTTCTTCAAGCCATCA  6186
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 ---CAACTTGGACAGTGCCCCAAAAA-CCTGTCATCCCTACTATCTTCTGTCTAGTCATACTCCCATTCACCGTTCTCAATTACTCATAAATGCCCTGCTCTTGTTTACACTGCTGGTTTACACTGCTGGTTTACACTGTTTCTCCAAGCCATCA  5473
AC210774.3_7565-13867/1-6303   ---CAACTTGGACAGTGCCCCAAAAA-CCTGTCATCCCTACTATCTTCTGTCTAGTCATACTCCCATTCACCGTTCTCAATTACTCATAAATGCCCTGCTCTTGTTTACACTGCTGGTTTACACTGCTGGTTTACACTGTTTCTCCAAGCCATCA  5473

Consensus_HERV-H/1-8613        CAGCTGATATCTCTTGGTGCTATCCCCAAACCGCCACTCTTAATTCCCTCTTAGAGTGGGTAGATGATCTTTGCTGGCAGGGCACCCTCCAATACTTCCACCCTGATGAAGTTCTATTCTTTACTTTTATACTCTCTCTTATTCTCATTCCCATT  6341
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 CAGCTGAGATCTCCTGGTGCTAACCCCAGACTGCCACTCTTAACTCCCTCTTAAA----GTAAATAATCTTTGCTGGCAGGGC------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   CAGCTGAGATCTCCTGGTGCTAACCCCAGACTGCCACTCTTAACTCCCTCTTAAA----GTAAATAATCTTTGCTGGCAGGGC------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        CTTATGCCACCTTTTGCCTCTCCCCAGCTATCTCCACCACACTATCAACCTTACCCATTCTCTCCTAGCTGCTTCTAATCCCTCCTTAGTGAACAACTGCTGGCTTTGCATTTCCCTTTCTTCCAGTGCCTACATAGCTGTCCCTGCCTTACAGA  6496
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        CAGACTGGGCTACATCTCCTGTCTCCTTACACCTCTGAACTTCCTTTAACAGCCCTCACCTTTACCCTCCTAAGGAACTCATTTACTTTCTAGACAGGTCCAGCAAGACTTTCCCAGACATTTCACATCAGCAAGCTGCCGCCCTCCTCCGCACT  6651
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        TATTTAAAAAACCTTTCTCCTTATATTAACTCTACTCCCCCCATATTTGGACCTCTCACAACACAAACTATTATTCCTGTTGCTGCTCCTTTATGTATCTCTTGGCAAAGACCCACTGGAATTCCCCTAGGTAATATTTCACCTTCTTGATGTTC  6806
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        CTTTACTCTTTATCTCCAAAGCCCAACTACACACATCACTGAAACAATTGGAGCCTTCCAGCTCCATATTACAGACAAGCCCTCTGTCAATACTGACAAACTCAAAAACATTAGCAGTAATTGTTGCTTAGGAAGACACTTACCCTGTATTTCAC  6961
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        TCCATCCTTGGCTACCTTCCCCTTGCTCATCAGACTCTCCTCCCAGGCCCTCTTCTTGTTTACTTATACCCAGCCCCCAAAATAACAGTGAAAGGTTGCTCATAGATAATCAACGTTTTCTCGTACATCATGAAAATTGAACATCCTCCTCTATG  7116
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        CAGTTACCCCATCAGTCCCCATTACAACCTCTGACAGCTGCCGCCCTAGCTGGATCCCTAGGAGTCTGGGTACAAGACACCCCTTTCAGCACTCCTTTTCACTTTTTTACTTTACATCTCCAGTTTTGCCTCACACAAGGTCTCTTCTTCCTCTG  7271
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
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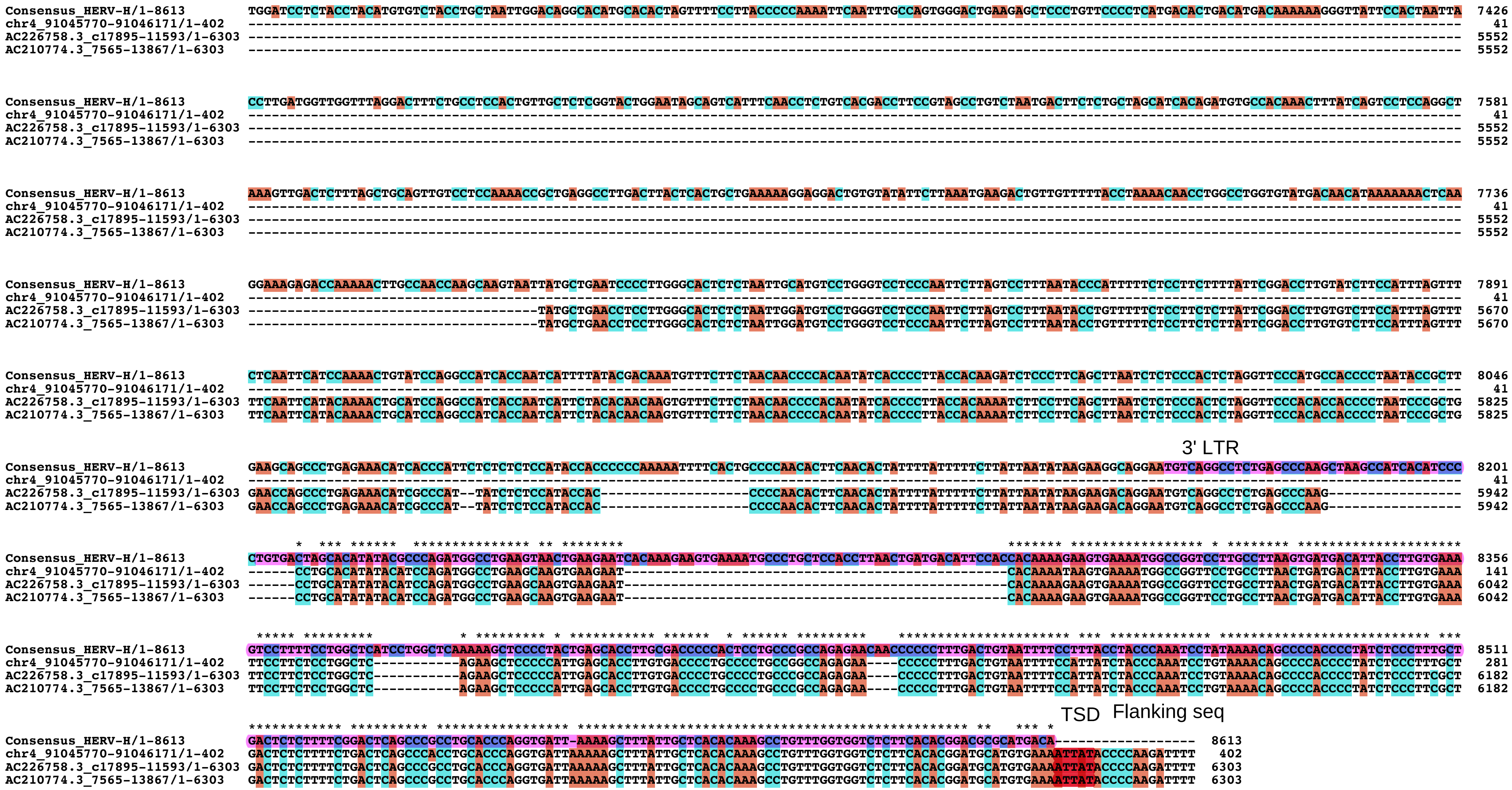

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Consensus_HERV-H/1-8613        TGGATCCTCTACCTACATGTGTCTACCTGCTAATTGGACAGGCACATGCACACTAGTTTTCCTTACCCCCAAAATTCAATTTGCCAGTGGGACTGAAGAGCTCCCTGTTCCCCTCATGACACTGACATGACAAAAAAGGGTTATTCCACTAATTA  7426
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        CCTTGATGGTTGGTTTAGGACTTTCTGCCTCCACTGTTGCTCTCGGTACTGGAATAGCAGTCATTTCAACCTCTGTCACGACCTTCCGTAGCCTGTCTAATGACTTCTCTGCTAGCATCACAGATGTGCCACAAACTTTATCAGTCCTCCAGGCT  7581
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        AAAGTTGACTCTTTAGCTGCAGTTGTCCTCCAAAACCGCTGAGGCCTTGACTTACTCACTGCTGAAAAAGGAGGACTGTGTATATTCTTAAATGAAGACTGTTGTTTTTACCTAAAACAACCTGGCCTGGTGTATGACAACATAAAAAAACTCAA  7736
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552
AC210774.3_7565-13867/1-6303   -----------------------------------------------------------------------------------------------------------------------------------------------------------  5552

Consensus_HERV-H/1-8613        GGAAAGAGACCAAAAACTTGCCAACCAAGCAAGTAATTATGCTGAATCCCCTTGGGCACTCTCTAATTGCATGTCCTGGGTCCTCCCAATTCTTAGTCCTTTAATACCCATTTTTCTCCTTCTTTTATTCGGACCTTGTATCTTCCATTTAGTTT  7891
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
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AC210774.3_7565-13867/1-6303   -------------------------------------TATGCTGAACCTCCTTGGGCACTCTCTAATTGGATGTCCTGGGTCCTCCCAATTCTTAGTCCTTTAATACCTGTTTTTCTCCTTCTCTTATTCGGACCTTGTGTCTTCCATTTAGTTT  5670

Consensus_HERV-H/1-8613        CTCAATTCATCCAAAACTGTATCCAGGCCATCACCAATCATTTTATACGACAAATGTTTCTTCTAACAACCCCACAATATCACCCCTTACCACAAGATCTCCCTTCAGCTTAATCTCTCCCACTCTAGGTTCCCATGCCACCCCTAATACCGCTT  8046
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 TTCAATTCATACAAAACTGCATCCAGGCCATCACCAATCATTCTACACAACAAGTGTTTCTTCTAACAACCCCACAATATCACCCCTTACCACAAAATCTTCCTTCAGCTTAATCTCTCCCACTCTAGGTTCCCACACCACCCCTAATCCCGCTG  5825
AC210774.3_7565-13867/1-6303   TTCAATTCATACAAAACTGCATCCAGGCCATCACCAATCATTCTACACAACAAGTGTTTCTTCTAACAACCCCACAATATCACCCCTTACCACAAAATCTTCCTTCAGCTTAATCTCTCCCACTCTAGGTTCCCACACCACCCCTAATCCCGCTG  5825

                                                                                                                                                      3' LTR
Consensus_HERV-H/1-8613        GAAGCAGCCCTGAGAAACATCACCCATTCTCTCTCTCCATACCACCCCCCAAAAATTTTCACTGCCCCAACACTTCAACACTATTTTATTTTTCTTATTAATATAAGAAGGCAGGAATGTCAGGCCTCTGAGCCCAAGCTAAGCCATCACATCCC  8201
chr4_91045770-91046171/1-402   -----------------------------------------------------------------------------------------------------------------------------------------------------------    41
AC226758.3_c17895-11593/1-6303 GAACCAGCCCTGAGAAACATCGCCCAT--TATCTCTCCATACCAC-------------------CCCCAACACTTCAACACTATTTTATTTTTCTTATTAATATAAGAAGACAGGAATGTCAGGCCTCTGAGCCCAAG-----------------  5942
AC210774.3_7565-13867/1-6303   GAACCAGCCCTGAGAAACATCGCCCAT--TATCTCTCCATACCAC-------------------CCCCAACACTTCAACACTATTTTATTTTTCTTATTAATATAAGAAGACAGGAATGTCAGGCCTCTGAGCCCAAG-----------------  5942

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Consensus_HERV-H/1-8613        CTGTGACTAGCACATATACGCCCAGATGGCCTGAAGTAACTGAAGAATCACAAAGAAGTGAAAATGCCCTGCTCCACCTTAACTGATGACATTCCACCACAAAAGAAGTGAAAATGGCCGGTCCTTGCCTTAAGTGATGACATTACCTTGTGAAA  8356
chr4_91045770-91046171/1-402   ------CCTGCACATATACATCCAGATGGCCTGAAGCAAGTGAAGAAT-------------------------------------------------CACAAAATAAGTGAAAATGGCCGGTTCCTGCCTTAACTGATGACATTACCTTGTGAAA   141
AC226758.3_c17895-11593/1-6303 ------CCTGCATATATACATCCAGATGGCCTGAAGCAAGTGAAGAAT-------------------------------------------------CACAAAAGAAGTGAAAATGGCCGGTTCCTGCCTTAACTGATGACATTACCTTGTGAAA  6042
AC210774.3_7565-13867/1-6303   ------CCTGCATATATACATCCAGATGGCCTGAAGCAAGTGAAGAAT-------------------------------------------------CACAAAAGAAGTGAAAATGGCCGGTTCCTGCCTTAACTGATGACATTACCTTGTGAAA  6042

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Consensus_HERV-H/1-8613        GTCCTTTTCCTGGCTCATCCTGGCTCAAAAAGCTCCCCTACTGAGCACCTTGCGACCCCCACTCCTGCCCGCCAGAGAACAACCCCCCTTTGACTGTAATTTTCCTTTACCTACCCAAATCCTATAAAACAGCCCCACCCCTATCTCCCTTTGCT  8511
chr4_91045770-91046171/1-402   TTCCTTCTCCTGGCTC-----------AGAAGCTCCCCCATTGAGCACCTTGTGACCCCTGCCCCTGCCGGCCAGAGAA----CCCCCTTTGACTGTAATTTTCCATTATCTACCCAAATCCTGTAAAACAGCCCCACCCCTATCTCCCTTTGCT   281
AC226758.3_c17895-11593/1-6303 TTCCTTCTCCTGGCTC-----------AGAAGCTCCCCCATTGAGCACCTTGTGACCCCTGCCCCTGCCCGCCAGAGAA----CCCCCTTTGACTGTAATTTTCCATTATCTACCCAAATCCTGTAAAACAGCCCCACCCCTATCTCCCTTCGCT  6182
AC210774.3_7565-13867/1-6303   TTCCTTCTCCTGGCTC-----------AGAAGCTCCCCCATTGAGCACCTTGTGACCCCTGCCCCTGCCCGCCAGAGAA----CCCCCTTTGACTGTAATTTTCCATTATCTACCCAAATCCTGTAAAACAGCCCCACCCCTATCTCCCTTCGCT  6182

                                                                                                                                        TSD   Flanking seq
                               ************ ********** ***************** ************************************************** **   *** *
Consensus_HERV-H/1-8613        GACTCTCTTTTCGGACTCAGCCCGCCTGCACCCAGGTGATT-AAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGACGCGCATGACA------------------  8613
chr4_91045770-91046171/1-402   GACTCTCTTTTCTGACTCAGCCCACCTGCACCCAGGTGATTAAAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGATGCATGTGAAAATTATACCCCAAGATTTT   402
AC226758.3_c17895-11593/1-6303 GACTCTCTTTTCTGACTCAGCCCGCCTGCACCCAGGTGATTAAAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGATGCATGTGAAAATTATACCCCAAGATTTT  6303
AC210774.3_7565-13867/1-6303   GACTCTCTTTTCTGACTCAGCCCGCCTGCACCCAGGTGATTAAAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGATGCATGTGAAAATTATACCCCAAGATTTT  6303
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Additional file 6: Alignment of HERV-H consensus with 4q22.1_H8 solo LTR and provirus. The target site duplications (TSD) is marked in red. The 5' and 3'LTRs are highlighted in pink. The HERV-H consensus sequence is from Repbase (LTR7 and HERVH).