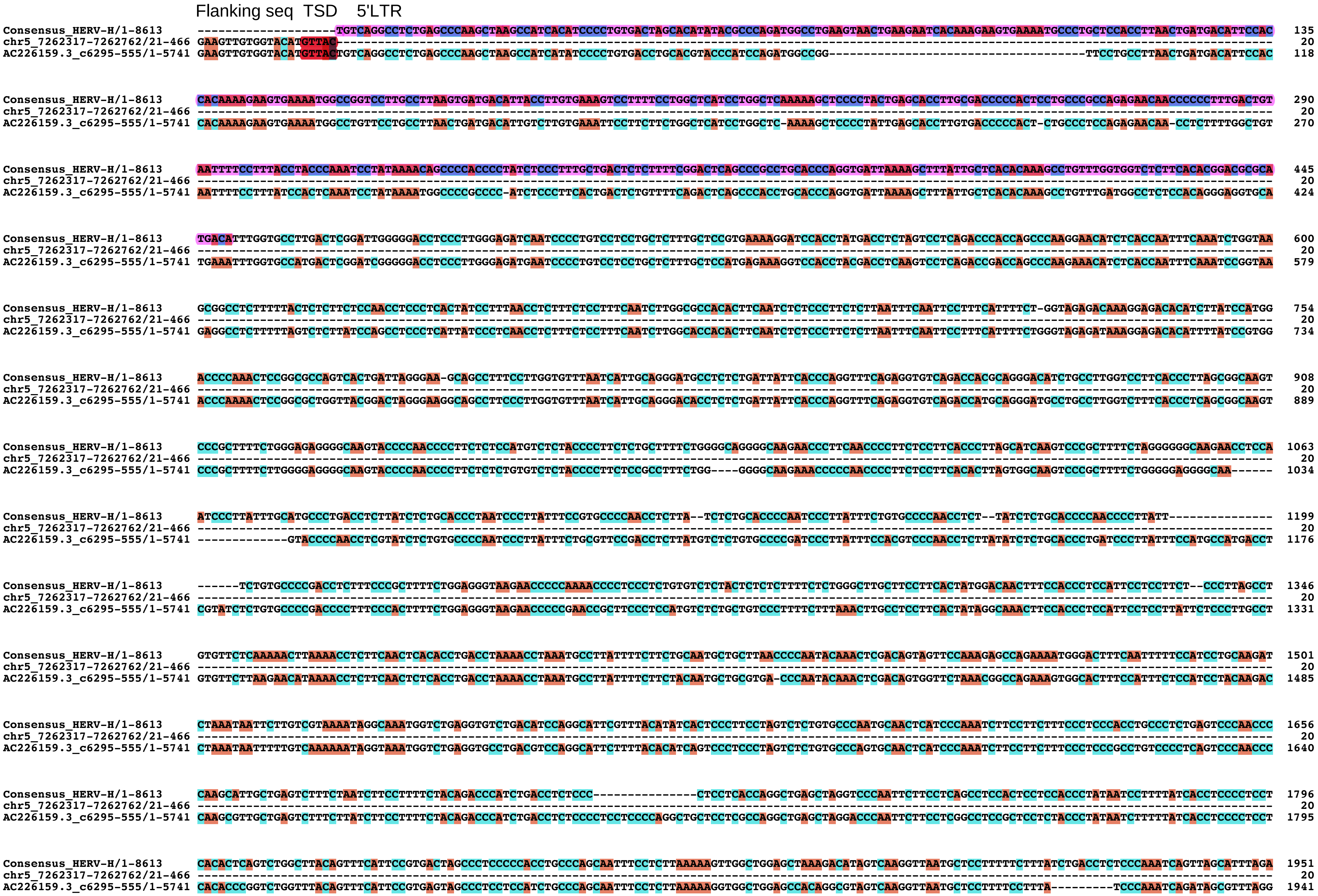

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                            Flanking seq  TSD    5'LTR
Consensus_HERV-H/1-8613     --------------------TGTCAGGCCTCTGAGCCCAAGCTAAGCCATCACATCCCCTGTGACTAGCACATATACGCCCAGATGGCCTGAAGTAACTGAAGAATCACAAAGAAGTGAAAATGCCCTGCTCCACCTTAACTGATGACATTCCAC 135
chr5_7262317-7262762/21-466 GAAGTTGTGGTACATGTTAC--------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 GAAGTTGTGGTACATGTTACTGTCAGGCCTCTGAGCCCAAGCTAAGCCATCATATCCCCTGTGACCTGCACGTACCCATCCAGATGGCCGG-------------------------------------TTCCTGCCTTAACTGATGACATTCCAC 118

Consensus_HERV-H/1-8613     CACAAAAGAAGTGAAAATGGCCGGTCCTTGCCTTAAGTGATGACATTACCTTGTGAAAGTCCTTTTCCTGGCTCATCCTGGCTCAAAAAGCTCCCCTACTGAGCACCTTGCGACCCCCACTCCTGCCCGCCAGAGAACAACCCCCCTTTGACTGT 290
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AC226159.3_c6295-555/1-5741 CACAAAAGAAGTGAAAATGGCCTGTTCCTGCCTTAACTGATGACATTGTCTTGTGAAATTCCTTCTTCTGGCTCATCCTGGCTC-AAAAGCTCCCCTATTGAGCACCTTGTGACCCCCACT-CTGCCCTCCAGAGAACAA-CCTCTTTTGGCTGT 270

Consensus_HERV-H/1-8613     AATTTTCCTTTACCTACCCAAATCCTATAAAACAGCCCCACCCCTATCTCCCTTTGCTGACTCTCTTTTCGGACTCAGCCCGCCTGCACCCAGGTGATTAAAAGCTTTATTGCTCACACAAAGCCTGTTTGGTGGTCTCTTCACACGGACGCGCA 445
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 AATTTTCCTTTATCCACTCAAATCCTATAAAATGGCCCCGCCCC-ATCTCCCTTCACTGACTCTGTTTTCAGACTCAGCCCACCTGCACCCAGGTGATTAAAAGCTTTATTGCTCACACAAAGCCTGTTTGATGGCCTCTCCACAGGGAGGTGCA 424

Consensus_HERV-H/1-8613     TGACATTTGGTGCCTTGACTCGGATTGGGGGACCTCCCTTGGGAGATCAATCCCCTGTCCTCCTGCTCTTTGCTCCGTGAAAAGGATCCACCTATGACCTCTAGTCCTCAGACCCACCAGCCCAAGGAACATCTCACCAATTTCAAATCTGGTAA 600
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 TGAAATTTGGTGCCATGACTCGGATCGGGGGACCTCCCTTGGGAGATGAATCCCCTGTCCTCCTGCTCTTTGCTCCATGAGAAAGGTCCACCTACGACCTCAAGTCCTCAGACCGACCAGCCCAAGAAACATCTCACCAATTTCAAATCCGGTAA 579

Consensus_HERV-H/1-8613     GCGGCCTCTTTTTACTCTCTTCTCCAACCTCCCTCACTATCCTTTAACCTCTTTCTCCTTTCAATCTTGGCGCCACACTTCAATCTCTCCCTTCTCTTAATTTCAATTCCTTTCATTTTCT-GGTAGAGACAAAGGAGACACATCTTATCCATGG 754
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 GAGGCCTCTTTTTAGTCTCTTATCCAGCCTCCCTCATTATCCCTCAACCTCTTTCTCCTTTCAATCTTGGCACCACACTTCAATCTCTCCCTTCTCTTAATTTCAATTCCTTTCATTTTCTGGGTAGAGATAAAGGAGACACATTTTATCCGTGG 734

Consensus_HERV-H/1-8613     ACCCCAAACTCCGGCGCCAGTCACTGATTAGGGAA-GCAGCCTTTCCTTGGTGTTTAATCATTGCAGGGATGCCTCTCTGATTATTCACCCAGGTTTCAGAGGTGTCAGACCACGCAGGGACATCTGCCTTGGTCCTTCACCCTTAGCGGCAAGT 908
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 ACCCAAAACTCCGGCGCTGGTTACGGACTAGGGAAGGCAGCCTTCCCTTGGTGTTTAATCATTGCAGGGACACCTCTCTGATTATTCACCCAGGTTTCAGAGGTGTCAGACCATGCAGGGATGCCTGCCTTGGTCTTTCACCCTCAGCGGCAAGT 889

Consensus_HERV-H/1-8613     CCCGCTTTTCTGGGAGAGGGGCAAGTACCCCAACCCCTTCTCTCCATGTCTCTACCCCTTCTCTGCTTTTCTGGGGCAGGGGCAAGAACCCTTCAACCCCTTCTCCTTCACCCTTAGCATCAAGTCCCGCTTTTCTAGGGGGGCAAGAACCTCCA 1063
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AC226159.3_c6295-555/1-5741 CCCGCTTTTCTTGGGGAGGGGCAAGTACCCCAACCCCTTCTCTCTGTGTCTCTACCCCTTCTCCGCCTTTCTGG----GGGGCAAGAAACCCCCAACCCCTTCTCCTTCACACTTAGTGGCAAGTCCCGCTTTTCTGGGGGAGGGGCAA------ 1034

Consensus_HERV-H/1-8613     ATCCCTTATTTGCATGCCCTGACCTCTTATCTCTGCACCCTAATCCCTTATTTCCGTGCCCCAACCTCTTA--TCTCTGCACCCCAATCCCTTATTTCTGTGCCCCAACCTCT--TATCTCTGCACCCCAACCCCTTATT--------------- 1199
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 -------------GTACCCCAACCTCGTATCTCTGTGCCCCAATCCCTTATTTCTGCGTTCCGACCTCTTATGTCTCTGTGCCCCGATCCCTTATTTCCACGTCCCAACCTCTTATATCTCTGCACCCTGATCCCTTATTTCCATGCCATGACCT 1176

Consensus_HERV-H/1-8613     ------TCTGTGCCCCGACCTCTTTCCCGCTTTTCTGGAGGGTAAGAACCCCCAAAACCCCTCCCTCTGTGTCTCTACTCTCTCTTTTCTCTGGGCTTGCTTCCTTCACTATGGACAACTTTCCACCCTCCATTCCTCCTTCT--CCCTTAGCCT 1346
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 CGTATCTCTGTGCCCCGACCCCTTTCCCACTTTTCTGGAGGGTAAGAACCCCCGAACCGCTTCCCTCCATGTCTCTGCTGTCCCTTTTCTTTAAACTTGCCTCCTTCACTATAGGCAAACTTCCACCCTCCATTCCTCCTTATTCTCCCTTGCCT 1331

Consensus_HERV-H/1-8613     GTGTTCTCAAAAACTTAAAACCTCTTCAACTCACACCTGACCTAAAACCTAAATGCCTTATTTTCTTCTGCAATGCTGCTTAACCCCAATACAAACTCGACAGTAGTTCCAAAGAGCCAGAAAATGGGACTTTCAATTTTTCCATCCTGCAAGAT 1501
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Consensus_HERV-H/1-8613     CTAAATAATTCTTGTCGTAAAATAGGCAAATGGTCTGAGGTGTCTGACATCCAGGCATTCGTTTACATATCACTCCCTTCCTAGTCTCTGTGCCCAATGCAACTCATCCCAAATCTTCCTTCTTTCCCTCCCACCTGCCCTCTGAGTCCCAACCC 1656
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 CTAAATAATTTTTGTCAAAAAATAGGTAAATGGTCTGAGGTGCCTGACGTCCAGGCATTCTTTTACACATCAGTCCCTCCCTAGTCTCTGTGCCCAGTGCAACTCATCCCAAATCTTCCTTCTTTCCCTCCCGCCTGTCCCCTCAGTCCCAACCC 1640

Consensus_HERV-H/1-8613     CAAGCATTGCTGAGTCTTTCTAATCTTCCTTTTCTACAGACCCATCTGACCTCTCCC---------------CTCCTCACCAGGCTGAGCTAGGTCCCAATTCTTCCTCAGCCTCCACTCCTCCACCCTATAATCCTTTTATCACCTCCCCTCCT 1796
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 CAAGCGTTGCTGAGTCTTTCTTATCTTCCTTTTCTACAGACCCATCTGACCTCTCCCCTCCTCCCCAGGCTGCTCCTCGCCAGGCTGAGCTAGGACCCAATTCTTCCTCGGCCTCCGCTCCTCTACCCTATAATCTTTTTATCACCTCCCCTCCT 1795

Consensus_HERV-H/1-8613     CACACTCAGTCTGGCTTACAGTTTCATTCCGTGACTAGCCCTCCCCCACCTGCCCAGCAATTTCCTCTTAAAAAGTTGGCTGGAGCTAAAGACATAGTCAAGGTTAATGCTCCTTTTTCTTTATCTGACCTCTCCCAAATCAGTTAGCATTTAGA 1951
chr5_7262317-7262762/21-466 ----------------------------------------------------------------------------------------------------------------------------------------------------------- 20
AC226159.3_c6295-555/1-5741 CACACCCGGTCTGGTTTACAGTTTCATTCCGTGAGTAGCCCTCCTCCATCTGCCCAGCAATTTCCTCTTAAAAAGGTGGCTGGAGCCACAGGCGTAGTCAAGGTTAATGCTCCTTTTCCTTTA---------TCCCAAATCAGATAGCGTTTAGG 1941
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Consensus_HERV-H/1-8613     CTCTTTTTCATCAAATACAAAAAACCCAGCCCAGTTCATGGCTCATTCGGCAGCAACCCTGAGACGCTTTACAGCCTTAGACCCTAAAAGGTCAAAAGGCCGTCTTATCCTCAATATACATTTTATTACCCAATCTGCTCCAAACATTAAATAAA  2106
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CTCTTTTTCATCAAATATGAAAAACCCAACCCAGTTCATGGCTCGTTCGGCAGCAACCCTGAGACGCTTTACAGCCCTAGACCCTAAAAGGTCAAAAGGTCGTCTTATTCTCAATATACATTTTATTACCCAATCTGCTCCCAACATTAAATAAA  2096


Consensus_HERV-H/1-8613     ACTCCAAAAATTAAATTCTGGCCCTCAAACCCCACAACAGGATTTAATTAACCTCACCTTCAAGGTGTACAA-TAATAGAAAA---------------------------AAGTTGCAATTCCTTGCCTCCACTGTGAGACAAACCCCAGACACA  2233
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 ACTCCAAAAATTAAATTCTGGCCCTCAAACCCCACAACAGGACTTAATTAACCTCACCTTCAAGGTGTACAATTAATAGAGTAGAGGCAGCCAAGTAGCAACATATTTCTGAGTTGCGATTCTTTGCCTCTACTGTGAGACAAACCCCAGCTACA  2251


Consensus_HERV-H/1-8613     TCTCCAGCACACAAGAACTTCGAAATGCCTCAACCTCAGGTGCCAGGGGTTCCTCCAGAACCTTCTCCCCCAGGAGCTTGCTACAAGTGCCAGAAATCTGGCCACTGGGCCAAGGAATGCCCACAGACCAGGATTCCTCCTAAGCTGTATCCCAT  2388
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
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Consensus_HERV-H/1-8613     CTCTGTGGGACCCCACTAAAAATCAGACTGTTCAACTCACCTGGCAGCCACTTCCAGAGCCCCTGGAACTCTAGCCCAAGGCTCTCTGACTGACCCCTTCTGAGATCTTCTTGGCTTAGCAGCTGAAGACTGACACTGCCAGATCGCCTCGGAAG  2543
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CTGTGTGGGACCCCACTGAAAATTGGACTGTTCAACTCACCTGGCAGCCACTTCCAGAGGCCCTGGAACTCTGGCCCAAGGCTCTCTGACTGACTTCTCCCCAGATCTTCTTGGCTTAACAGCTGAAGACTGACACTGCCCGATTGCCTCAGAAG  2560


Consensus_HERV-H/1-8613     CCTACAGGACCATCACAGATGCTCCAGGTAACTCTCACAGTAGAGGGTAAGTCTGTCCCCTTCTTAATCAATATGGAGGCTACCCACTGCACATTACCTTCTTTTCAAGGGCCTGTTTCCTTTGCCTCCATAACTGTTGTGGGTATTGACGGCCA  2698
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CCTACAGGACCATCACAGACGCTCTAGGAAACTCTCACAGTGGAAGGTAAGTCCGTCCCCTTCTT----AATACAGAGGCTACTCACTCCACATTACCTTATTTTCAAGGGCCTGTCTCCCTTGCTTCCATAATTGTTGTGCATATTGATGGCCA  2711


Consensus_HERV-H/1-8613     GGCTTCTAAACCTCTTAAAACTCCCCAACTCTAGTACCAACTTAGACAATACTCTTTTAAGCACTCCTTTTTAGTTATCCCCACTTGCCCAGTTCCCTTATGAGGCCGAGACACTTCAACTAAATTATCTGCTTCCCTGACTATTCCTGGACTAC  2853
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 GGCTTCTAAACCTCTTTAAACTCCCCAACTCTGGTGCCAACTTAGACAATACTCTTTTAAGTACTCCTTTTTAATTATCCCCACCTGCCCAGTTCCCTTATTAGGCCGAGACACTT----TAAATTATCTGCTTCCCTGACTGTTCCTAGGCTAC  2862


Consensus_HERV-H/1-8613     AGCTACATCTCATTGCTGCCCTTCTTCCCAATCCAAAGCCTCCTTTGCATCTT---CTTGTATCCCCCAACCTTAACCCACAAGTATAAGATACCTCTATTCCCTCCTTGGTGACCAATCATGCACCCCTTACCATCTCATTAAAACCTAATCAC  3005
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AC226159.3_c6295-555/1-5741 AGCCACACCTCATTGCCACCTTTTCCCGCCGTTTAAAGCTTCCTTCACGTCCTCCCCTTGTATCTCCCCACCTTAACCCACAAGTATAAGACACCTCTACTCCCCCCTTAGTGACCAATCATGCACCCCTTACCATCCCATTAAAACCTAATCAC  3017


Consensus_HERV-H/1-8613     TCTTACCCGGCTCAATGCCAAGATCCCATCCCACAGCATGCTTTAAAAGGATTAAAACCTGTTATCACTCGCCTGCTAGAGCATGGCCTTTTAAAGCCTATAAACTCTCCTTACAATTCCCCCATTTTACCTGTCCTAGAACCAGACAAGCCTTA  3160
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
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Consensus_HERV-H/1-8613     CAG----GTTCAGGATCTGTGTCTTATCAATGAAATTGTTTTCCCTATCCACCCTGTGGTGCTGAACCCATATACTCTCCTATCCTCAATACCTCCCTCTACAACCCATTATTCTGTTCTAGATCTCAAACATGCTTTCTTTACTATCCCTTTAC  3311
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CAGGTTAGTTCAGAATCTACGCCTTATCAACCAAATTGTTTTGCCTATCCACCCCGTGTTGCCAAAACCATATACTCTCTTATCCTCAATACCTCCCTCTACAACCCATTATTCTGTTCTGGATCTCAAACATGCTTTCTTTA--------TTGC  3317


Consensus_HERV-H/1-8613     ACCCTTCAACCCAGCCTCTCTTCGTTTTCACCTGGACTGACCCTGACACCCATCAGTCCCAGCAGCTTACCTGGGCTGTAATGCTGCAAGGTTTCAGGGGCAGCCCTTATTATTTCAGCCAAGCTCTTTCTCATGATTTACTTTCTTTCCACCCC  3466
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
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Consensus_HERV-H/1-8613     TCCACTTCTCACCTTATTCAATATATTGGTGATGTTCTTCTTTGTAGCCCCTCCTTTGAATCTTCTCAACAAGACACACTTCTGCTCCTTCAGCATTTATTCTCCAAAGGATATCCCCCTCCAAAGCTCAAATGTCTTCTCCATCCGTTACCTAC  3621
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 ---------------------------------------------------------------------------------------------------------------------------AAGCCCAAATTTCATCCTCATCTGTTACCTAT  3469


Consensus_HERV-H/1-8613     CTTGGCATAATTCTTCATAAAAACACACGTGCCCTCCCTGCTGATAGTGTCTGACTGATCTCTCAAACCCCAACCCCTTCTACAAAACAACAACTCTTTTCCATCCTAGGCATGGTTGGATACTTTCGTGTTAGGATACCTGGTTTTGCCATCCT  3776
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CTCGGCATAATTC-TCATAAAAACACACGTGCTCTCCCTGCTGATCGTGTCCATTTCATCTCCCAAACCTCAATCCCT--TACAAAACAACAACTCCTTTCCTTCCTAGGCATGGT---------------------------------------  3582


Consensus_HERV-H/1-8613     AACAAAACCATTATATAAACTCACAAAAGGAAACCTAGTTGACCCCATAGATCCTAAATCGTTTCCCCACTCCTCTTTCCATTCCTTGAAGACAGCTTTAGAGACTGTCTCCACTCTAGCTCTCCCTGACTCATCCCAACACTTTTCATTACACA  3931
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------  3582
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Consensus_HERV-H/1-8613     CAGCTGAAGTGCAGGGCTGTGCAGTCAGAATTCTTACACAAGGACCGGGATCGCATCCTGTAGCCTTTTTGTCCAAACAACTTGACCTTACTGTTTTAGGCTGGCCATCATGTCTCCATGCAGCGTCTGCTGCCACCCTAATACTTTTAGAGGCC  4086
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
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Consensus_HERV-H/1-8613     CTCAAAATCACAAACTATGCTCAACTCATTCTCTACAGCTCTCATAATTTCCAAAATCTATTTTCTTCCTCACACCTGACACATATACTTTCTGCTCCCCGGCTCCTTCAGATATACTCACTCCATTTATTCTCCCACAATTACCATTATTCCTG  4241
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CTAAAAATCACAAACTACGCTCAACTCA--ATCTACATTTCTCATAACTTCCAAAATCCATTTTCTTCCTCATACCTGATGCATATACTTTCTGCTCCCCGGCTCCTTCAGCTGTAATCACTCTTTCTTAAGTCCCACAATTACCATTGTTCCTG  3874

Consensus_HERV-H/1-8613     GCCTGGACTTCAATCCGGCCTCCCACATTATTCTGGATACCATACCTGACCCTCATGACTGCATCTCTCTGATCCACCTGACGTTCACCCCATTTCCCCACATTTCCTTCTGCCCTGTTTCTCACCCTGATCACACTTGGTTTATTGATGGCAGT  4396
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 GCCCAGACTTCAATCCGGCCTCCTACATTATTCTGGATACCACACCTGACCCTCATGACTGTCTCTCTCTGATCCACCTGACATTCACCCCATTTCCCCATATTTCCTTCTTTCCTGTTCCTCACCCTGATCACACTTGATTTATTGATGTCAGT  4029

Consensus_HERV-H/1-8613     TCCACCAGGCCTAATCGCCACTCACCAGCAAAGGCAGGATATGCTATGAACTAGTTGCCTTAATTCAAGCCCTCACTCTTGCAAAAGGACTACGTGTCAATATCTATACTGATTCTAAATATGCCTTTCATATTCTGCACCACCATGCGGTCATA  4551
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 TCCACTAGGCCTAATCGCCACACACCAGCAAAGGCAGGCTATGCTATAG----------------------------------------------------------------------------------------------------------  4078

Consensus_HERV-H/1-8613     TGGGCTGAAAGAGGTTTCCTCACTACACAAGTGTCCTCCATCATTAATGCCTCTTTAAGAAAACTCTGCTCAAGGCTGCTTTACTTCCAAAGGAAGCTGGGGTCATTCACTGCAAGGGGCATCAAAAGACTTCAGATCCCATTGCTCTAGGCAAT  4706
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------  4078

Consensus_HERV-H/1-8613     GCTTATGCTGATAAGGTGGCTAGACAAGCAGCTAGCTCTCCAACTTTTGTCCCTCATGGCCAGTTTTTCTCCTTCACATCCGTCACTCCCACCTACTCCACAGCTGAAACTTCCACCTATCAAGCTCTTCCCCCGCAAGGTAAATGGTTCTTAGA  4861
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------  4078

Consensus_HERV-H/1-8613     CCAAGGAAAATATCTCCTTCCAGCCTCACAGGCCCATTCTATTCTGTCGTCATTTCATAACCTTTTCCATGTAGGTTACAAGCCACTAGCCTGTCTCTTAGGACCTCTCATTTCCTTTCCATCATGGAAATCTATCCTCAAGGAGATCACTTCTC  5016
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Consensus_HERV-H/1-8613     AGTGTTCCATCTGCTATTCTGCTACCCCTCAGGGATTGTTCAGGCCTCCTCCCTTTCCTACACATAAAGCTCGGGGATTTGCCCCTGCCCAGGACTGGCAAATTGACTTTACTC-ACATGCCTCGGGTCAGAAAACTAAAATATCTCTTAGTCTG  5170
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 AGTGTTCCATCTGCTATTCTACTACTCCTCAGGGATTATTCAGGCCCCCTCCCTTCCATACACATCAAGCTTGAAGATTTGCCCCCACCCAGGACTGGCAAATTAGCTTTACTCAACATGCCCTGAGTCAGATAGCTAAAATACCTCTTAGTCTA  4312

Consensus_HERV-H/1-8613     GGTAGACACTTTCACTGGGTGGGTAGAGGCCTTTCCCATAGAGTCTGAGAAGGCCACCGCGGTCATTTCTTCCCTTCTGTCAGACATAATTCCTTGGTTTGGCCTTCCCTTCTCTATACAGTCTGATAACGGACCAGCCTTTACTAGTTAAATCA  5325
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 GGTAGACACTTCCACTGGATAGGTACAGG-------------GTCTGAGAAGGCCACCACAGTCATTTCTTCCCTTCTGTCAGACATAATTCCTCAGTTTAGCCTTCCCACCTCTATACAGTCTGATAACAGACCAGCCTTCATTAGTCAAATCA  4454

Consensus_HERV-H/1-8613     CCCAAGCAGTTTCTCAGGCTCTTGGTATTCAGTGGAACCTTCATATCCCTTAACATCCTCAATCTTCAGGAAAGGTAAAACCGACTAATGGTCTTTTAAAGACACACCTCACCAAGCTCAGCCTCCAACTTAAAAAGGATTGGACAGTACTTTTA  5480
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 GCCAAGCAGTTTTTCAGGCTCTTAGTATTCAGTGAAACCTTTATATCCCTTACGGTCCTCCGTCTTCAGGAAAAGTAGAACGGACTAAAGGTCTTTTAAAAACACACCTCCCCAAGCTCAGCCACCAACTTAAAAAGGACTGGACAATACTTTTA  4609

Consensus_HERV-H/1-8613     CCTCTCGCCCTTCTCAGAATTAGAACCTGTCCTCGAGATGCTACAGGGTACAGTCCATTTGAACTTTTATATGGACGCACTTTCTTGCTTGGTCCCAACCTCATCCCAGACACCAGCCCTCTAGGCGACTATCTTCCAGTCCTCCAACAGGCTAG  5635
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 CCACTTTCCCTTCTCAGAAGTCAGACCTGCCCTCAGAATGCTACAGGATACAGCCCATTTGAGCTCCTGTATAGATGCTCCTTTTTATTAGGCCCCAGTCTCATTCCAGACACCAGAC-------------------------------------  4727

Consensus_HERV-H/1-8613     GCAGGAAAGTCACCAGGCTGCTAATCTTCTCTTGCCTACTCCAGATCCCCAGCCATATGAAGACACTCTAGCTGGACGATCAGTTCTTGTTAAGAATCTGACCCCTCAAACTCTACAACCTCGATGGACTGGACCCTACTTAGTCATCTATAGTA  5790
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------  4727

Consensus_HERV-H/1-8613     CCCTGACTGCCGTCCGCCTGCAGGATCCTCCCCACTGGGTTCACCATTCCAGAATAAAGCTGTGTCCATTGGACAGCCAGCCTAATCCCTCCTCTTCCTCCTGGAAGTCGCAATTACTCTCCCCTACTTCCCTTAAACTCACTCGTATTTCTGAA  5945
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------  4727
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Consensus_HERV-H/1-8613     GAACAGTAATAACCCTTATGAGCCTAATACATCCCTTCATTCTATTAGGTCTGTTTGTCCTTACCCTACTTTTTGCAACAGGGCTTTATGAACTCACCCCCACCACTTAGGCTGAGCCCAAAAAATCTTGTCATCCCTACTATTTTCTGTCCAGT   6100
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 ------------------------------------------------------------------------------------------------------CAACTTAGACTGTGCCCCAAAAAAATTGTCATCCCTACTATCTTCTGTCTAGT   4780

Consensus_HERV-H/1-8613     CATACTCCTATTCTCTGCTCTCAACTACTTATAAATGCCGTACTCTTGTTTACACTGCTGGTTTACACTGTTTCTTCAAGCCATCACAGCTGATATCTCTTGGTGCTATCCCCAAACCGCCACTCTTAATTCCCTCTTAGAGTGGGTAGATGATC   6255
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 CATACTCCTATTCACCATTCTCAACTACTCATACATGCCCTGCTCTTGTTTACACTGCCGGTTTACACTGTTTTTCCAAGCCATCACAGCTGATATCTCCTGGTGCTATCCCCAAACTGCCACTCTTAA----CTCTTGAAGTAAATAAATAATC   4931

Consensus_HERV-H/1-8613     TTTGCTGGCAGGGCACCCTCCAATACTTCCACCCTGATGAAGTTCTATTCTTTACTTTTATACTCTCTCTTATTCTCATTCCCATTCTTATGCCACCTTTTGCCTCTCCCCAGCTATCTCCACCACACTATCAACCTTACCCATTCTCTCCTAGC   6410
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 TTTGCTGAAAGGAC---------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     TGCTTCTAATCCCTCCTTAGTGAACAACTGCTGGCTTTGCATTTCCCTTTCTTCCAGTGCCTACATAGCTGTCCCTGCCTTACAGACAGACTGGGCTACATCTCCTGTCTCCTTACACCTCTGAACTTCCTTTAACAGCCCTCACCTTTACCCTC   6565
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     CTAAGGAACTCATTTACTTTCTAGACAGGTCCAGCAAGACTTTCCCAGACATTTCACATCAGCAAGCTGCCGCCCTCCTCCGCACTTATTTAAAAAACCTTTCTCCTTATATTAACTCTACTCCCCCCATATTTGGACCTCTCACAACACAAACT   6720
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     ATTATTCCTGTTGCTGCTCCTTTATGTATCTCTTGGCAAAGACCCACTGGAATTCCCCTAGGTAATATTTCACCTTCTTGATGTTCCTTTACTCTTTATCTCCAAAGCCCAACTACACACATCACTGAAACAATTGGAGCCTTCCAGCTCCATAT   6875
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     TACAGACAAGCCCTCTGTCAATACTGACAAACTCAAAAACATTAGCAGTAATTGTTGCTTAGGAAGACACTTACCCTGTATTTCACTCCATCCTTGGCTACCTTCCCCTTGCTCATCAGACTCTCCTCCCAGGCCCTCTTCTTGTTTACTTATAC   7030
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     CCAGCCCCCAAAATAACAGTGAAAGGTTGCTCATAGATAATCAACGTTTTCTCGTACATCATGAAAATTGAACATCCTCCTCTATGCAGTTACCCCATCAGTCCCCATTACAACCTCTGACAGCTGCCGCCCTAGCTGGATCCCTAGGAGTCTGG   7185
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     GTACAAGACACCCCTTTCAGCACTCCTTTTCACTTTTTTACTTTACATCTCCAGTTTTGCCTCACACAAGGTCTCTTCTTCCTCTGTGGATCCTCTACCTACATGTGTCTACCTGCTAATTGGACAGGCACATGCACACTAGTTTTCCTTACCCC   7340
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     CAAAATTCAATTTGCCAGTGGGACTGAAGAGCTCCCTGTTCCCCTCATGACACTGACATGACAAAAAAGGGTTATTCCACTAATTACCTTGATGGTTGGTTTAGGACTTTCTGCCTCCACTGTTGCTCTCGGTACTGGAATAGCAGTCATTTCAA   7495
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     CCTCTGTCACGACCTTCCGTAGCCTGTCTAATGACTTCTCTGCTAGCATCACAGATGTGCCACAAACTTTATCAGTCCTCCAGGCTAAAGTTGACTCTTTAGCTGCAGTTGTCCTCCAAAACCGCTGAGGCCTTGACTTACTCACTGCTGAAAAA   7650
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 -----------------------------------------------------------------------------------------------------------------------------------------------------------   4945

Consensus_HERV-H/1-8613     GGAGGACTGTGTATATTCTTAAATGAAGACTGTTGTTTTTACCTAAAACAACCTGGCCTGGTGTATGACAACATAAAAAAACTCAAGGAAAGAGACCAAAAACTTGCCAACCAAGCAAGTAATTATGCTGAATCCCCTTGGGCACTCTCTAATTG   7805
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 ---------------------------------------------------------------------------------------------------------------------------TATGCTGAATCTCCTTAGGCA--CTCTAATTA   4975

Consensus_HERV-H/1-8613     CATGTCCTGGGTCCTCCCAATTCTTAGTCCTTTAATACCCATTTTTCTCCTTCTTTTATTCGGACCTTGTATCTTCCATTTAGTTTCTCAATTCATCCAAAACTGTATCCAGGCCATCACCAATCATTTTATACGACAAATGTTTCTTCTAACAA   7960
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------     20
AC226159.3_c6295-555/1-5741 GATGTCCTGGGTCCTCCCAAATCTTAGACCTTTTATACCTGTTTTTCTCCTTCTGTTA---------------TTCCATTTAGTTTTTCAATTCATGCAAAACCATATCCAGGCCATCACCAATCATTCTAAATGACAAATGTCTCTTCTAACAG   5115
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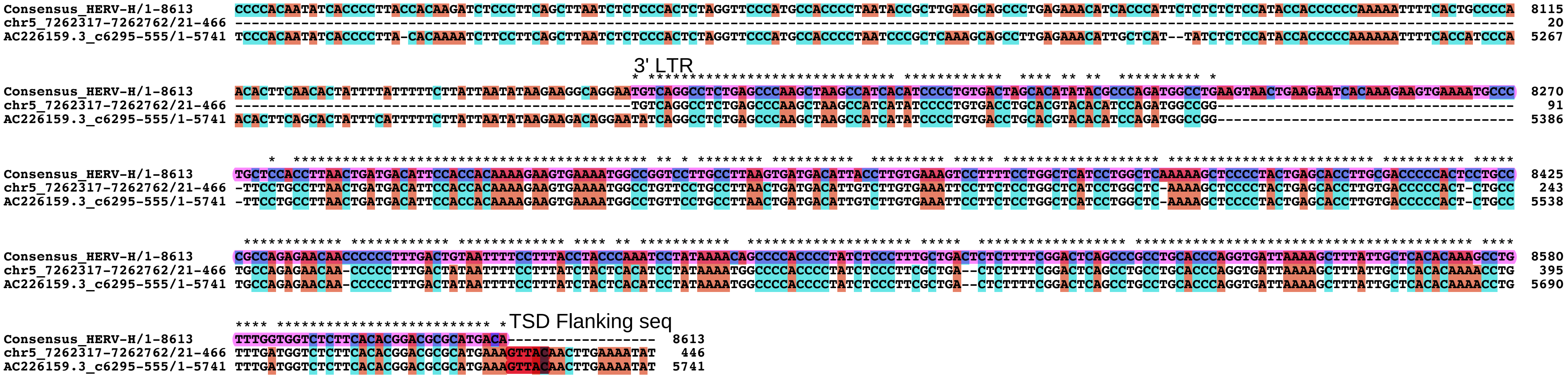

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Consensus_HERV-H/1-8613     CCCCACAATATCACCCCTTACCACAAGATCTCCCTTCAGCTTAATCTCTCCCACTCTAGGTTCCCATGCCACCCCTAATACCGCTTGAAGCAGCCCTGAGAAACATCACCCATTCTCTCTCTCCATACCACCCCCCAAAAATTTTCACTGCCCCA  8115
chr5_7262317-7262762/21-466 -----------------------------------------------------------------------------------------------------------------------------------------------------------    20
AC226159.3_c6295-555/1-5741 TCCCACAATATCACCCCTTA-CACAAAATCTTCCTTCAGCTTAATCTCTCCCACTCTAGGTTCCCATGCCACCCCTAATCCCGCTCAAAGCAGCCTTGAGAAACATTGCTCAT--TATCTCTCCATACCACCCCCAAAAAATTTTCACCATCCCA  5267

                                                                           3' LTR
                                                                            * ****************************** ************  **** ** **  ********** *
Consensus_HERV-H/1-8613     ACACTTCAACACTATTTTATTTTTCTTATTAATATAAGAAGGCAGGAATGTCAGGCCTCTGAGCCCAAGCTAAGCCATCACATCCCCTGTGACTAGCACATATACGCCCAGATGGCCTGAAGTAACTGAAGAATCACAAAGAAGTGAAAATGCCC  8270
chr5_7262317-7262762/21-466 ------------------------------------------------TGTCAGGCCTCTGAGCCCAAGCTAAGCCATCATATCCCCTGTGACCTGCACGTACACATCCAGATGGCCGG------------------------------------    91
AC226159.3_c6295-555/1-5741 ACACTTCAGCACTATTTCATTTTTCTTATTAATATAAGAAGACAGGAATATCAGGCCTCTGAGCCCAAGCTAAGCCATCATATCCCCTGTGACCTGCACGTACACATCCAGATGGCCGG------------------------------------  5386

                                *  ******************************************* ** * ******** **********  ********* ***** ******************* ************************* ********** *****
Consensus_HERV-H/1-8613     TGCTCCACCTTAACTGATGACATTCCACCACAAAAGAAGTGAAAATGGCCGGTCCTTGCCTTAAGTGATGACATTACCTTGTGAAAGTCCTTTTCCTGGCTCATCCTGGCTCAAAAAGCTCCCCTACTGAGCACCTTGCGACCCCCACTCCTGCC  8425
chr5_7262317-7262762/21-466 -TTCCTGCCTTAACTGATGACATTCCACCACAAAAGAAGTGAAAATGGCCTGTTCCTGCCTTAACTGATGACATTGTCTTGTGAAATTCCTTCTCCTGGCTCATCCTGGCTC-AAAAGCTCCCCTACTGAGCACCTTGTGACCCCCACT-CTGCC   243
AC226159.3_c6295-555/1-5741 -TTCCTGCCTTAACTGATGACATTCCACCACAAAAGAAGTGAAAATGGCCTGTTCCTGCCTTAACTGATGACATTGTCTTGTGAAATTCCTTCTCCTGGCTCATCCTGGCTC-AAAAGCTCCCCTACTGAGCACCTTGTGACCCCCACT-CTGCC  5538

                             ************ ************ ************* **** ** ***********  ******************** *****  ****************** ***************************************** ****
Consensus_HERV-H/1-8613     CGCCAGAGAACAACCCCCCTTTGACTGTAATTTTCCTTTACCTACCCAAATCCTATAAAACAGCCCCACCCCTATCTCCCTTTGCTGACTCTCTTTTCGGACTCAGCCCGCCTGCACCCAGGTGATTAAAAGCTTTATTGCTCACACAAAGCCTG  8580
chr5_7262317-7262762/21-466 TGCCAGAGAACAA-CCCCCTTTGACTATAATTTTCCTTTATCTACTCACATCCTATAAAATGGCCCCACCCCTATCTCCCTTCGCTGA--CTCTTTTCGGACTCAGCCTGCCTGCACCCAGGTGATTAAAAGCTTTATTGCTCACACAAAACCTG   395
AC226159.3_c6295-555/1-5741 TGCCAGAGAACAA-CCCCCTTTGACTATAATTTTCCTTTATCTACTCACATCCTATAAAATGGCCCCACCCCTATCTCCCTTCGCTGA--CTCTTTTCGGACTCAGCCTGCCTGCACCCAGGTGATTAAAAGCTTTATTGCTCACACAAAACCTG  5690

                            **** ************************** *TSD Flanking seq
Consensus_HERV-H/1-8613     TTTGGTGGTCTCTTCACACGGACGCGCATGACA------------------  8613
chr5_7262317-7262762/21-466 TTTGATGGTCTCTTCACACGGACGCGCATGAAAGTTACAACTTGAAAATAT   446
AC226159.3_c6295-555/1-5741 TTTGATGGTCTCTTCACACGGACGCGCATGAAAGTTACAACTTGAAAATAT  5741
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Additional file 7: Alignment of HERV-H consensus with 5p15.31_H2 solo LTR and provirus. The target site duplications (TSD) are marked in red. The 5' and 3'LTRs are highlighted in pink. The HERV-H consensus sequence is from Repbase (LTR7 and HERVH).