

Flanking seq TSD

5'LTR

Consensus\_HERV-W chr18 50449131-50449934 ACCTAATATTGCTCATGCTA... 135

Consensus\_HERV-W chr18 50449131-50449934 TCACTAAAATGCTAATTAGGC... 290

Consensus\_HERV-W chr18 50449131-50449934 AGCTCTGTTTTCTATTAAAT... 438

Consensus\_HERV-W chr18 50449131-50449934 AAGGTGTCCGCTGTGCTCCT... 593

Consensus\_HERV-W chr18 50449131-50449934 ACGGCTTCTAATAGAGCTATA... 748

Consensus\_HERV-W chr18 50449131-50449934 GGAGCTCTGGGAGCAAGGAA... 898

Consensus\_HERV-W chr18 50449131-50449934 ATGATTAGCGTGTGGGAGGCT... 902

Consensus\_HERV-W chr18 50449131-50449934 AACGATTAGCGTGGCCCGGCA... 1057

Consensus\_HERV-W chr18 50449131-50449934 AGGCAGAAAGCTGTCTCCGAA... 1212

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

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Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171



Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 CCTCAGGCCAAGCGGACTTTGGAGGCTCGGAAAAGGAAAGGCTGGGCAATCGAATGCTAATAGGGCTTGCCTCCAGTGCCTGTACAAAGGACACTTTAAAAAAGATTGTCCAAAGTAGAAATAAGCCGCCCTCGTCCATGCCCTTATGTT 4105  
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Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 AAGGGAATCAC TGGAAGGCCACTGCCCCAGGGGACGAAAGTCTCTGAGTCAAGAGCCACTAACAGATGATCCAGCAGCAGGACTGAGGGTGCCTGGGGCAAGCGCCAGCCATGCCATCACCCTCACAGAGCCCCGGGTATGCTTGACCATT 4260  
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Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 GAGGGCCAGGAGGTTAACTGTCTCTGGGACACTGGCCGGGCCCTTCTCAGTCTTACTCTCTGTCTCCGGACAACTGTCTCCAGATCTGTCTCATATCCGAGGGGTCTAGGACAGCCAGTCACTAGATACCTCTCCAGCCACTAAGTTGTGACTG 4415  
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Pol

Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 GGGAACTTTACTCTTTTCACTGCTTTTCTAATATGCTGAAAGCCCCACTCCCTTGTGAGGGAGACACTTCTAGCAAAGCAGGGGCCATTAACACCTGAAACATAGGAGAAAGAACACCCGTTTGTGTGCCCTGCTTGAGGAAAGGAATTA 4570  
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Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 ATCTCGAAGTCTGGGCAACAGAGGACAAATATGGACGAGCAAAGAAATGCCCTCTGTTCAAGTTAAACTAAAGGATTCGCCCTCTTTCCCTACCAAAGCAGTACCCCCCTTAGACCCGAGGCCAACAGGACTCCAAAAGATTGTTAAGGAC 4725  
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Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 CTAAAAGCCCCAAGGCTAGCCTAGTAAAACCATGCAATAGCCCCGCAATCTCCAATTTTGGAGTACAGAAAACCAATGGACAGTGGAGGTTAGTGCAAGATCTCAGGATTATCAATGAGGCCGTTGTCTCTATACCCAGCTGTACCTAAC 4875  
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Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 CCTTATACCTCTGCTTTCCCAAAATACCAGAGGAAACAGAGTGGTTACAGTCTCGGACCTAAGGATGCTTTTTCTGCATCCCTGTACATCCCTGACTCTCAATTTCTGTTTGCCTTTGAAAGATCCTTCGAAACCCCAACGCTCAACTCACTGGAC 5030  
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TGTTTTACCCCAAGGGTTCAGGGATAGCCCCACTCTATTGGCCAGACTTAGCCCAAGACTTGAGCCAGTTCTCATACCTGGACACTCTTGCTCTTCGGTACGTGGATGATTTACTTTTAGCCGCCCGTTACAGAAACCTTGTCATCAAGCCA 5342  
TGTTTTACCCCAAGGGTTCAGGGATAGCCCCACTCTATTGGCCAGACTTAGCCCAAGACTTGAGCCAGTTCTCATACCTGGACACTCTTGCTCTTCGGTACGTGGATGATTTACTTTTAGCCGCCCGTTACAGAAACCTTGTCATCAAGCCA 5340  
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Consensus\_HERV-W chr18 50449131-50449934 AC241669.2 12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171 CCCAAGCTCTTAAATTTCTCTGCTACCTGTGGCTACAAGGTTTCCAAACCAAGGCTCAGCTCTGCTCAGCAGAGGTTAAATACCTTAGGGCTAAAAATTTCCAAAGGCCACAGGGCCCTCAGTGAGGAAGTATCCAGCCTATACTGGCTTAT 5340  
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Consensus\_HERV-W CCTCATCCCAAAACCCCTAAAGCAACTAAGAGGGTTCTTGGCATAACAGGTTCTGCCGAATATGGAATCCAGGTACGGCGAAATAGCCAGGCCATTATATACACTAATTAAGGAACTCAGAAAGCCAATACCCATTTAGTAAGATGGACACC 5495  
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AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W TGAAGCAGAAGCGGCTTTCCAGGCCCTAAAGAGGCCCTAACCCAAGCCCCAGTGTAAAGTTGCCAACGGGGCAAGACTTTCTTTATATGTACAGAAAAACAGGAATAGCTCTAGGAGTCCTTACACAGGTCAGAGGGACGAGCTTGCAAC 5650  
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AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W CCGTGGCATACCTGAGTAAGGAAATGTATGTAGTGGCAAAGGGTTGGCCCATTTGTTTACGGGTAGTGGCGGAGTAGCAGTCTTAGTATCTGAAAGCAGTTAAAATAATACAGGGAAAGAGATCTTACGTGTGGACATCTCATGATGTGAAACGGC 5805  
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AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W ATACTCATGCTAAAGGAGACTTGTGGCTGTGAGACAACCGTTTACTTAAATATCAGGCTCTATTACTTGAAGGGCCAGTGCAGCAGTGGCACCTTGTGCAACTCTTAACCCAGCCACATTTCTCCAGACAATGAAGAAAAGATAGAACATA 5960  
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AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W CCGTCAACAGTAAATTTGCTCAAACCTACGCCGCTCGAGGGGACCTTTTAGAGGTTCCCTTGTAGTATCCCGACCTCAACTTGTATACTGATGGAAGTTCCTTTGTAGAAAAGGACTTCGAAAAGCGGGGTATGCACTGGTCACTAGTATAATGGAA 6115  
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AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W TACTTTGAAAGTAATCCCCTCACTCCAGGAAGTAGTGTCTAGCTGGCAGAACTAATAGCCCTCACTCGGGCACTAGAATTAGGAGAAGGAAAAAGGGTAAATATATATACAGACTCTAAGTATGCTTACCCTAGTCCCTCCATGCCCAACCGCAGCAATA 6270  
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AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W TGGAGACAAAGGGAATTCCTAACCTCCGAGGGAACCCCTATCAAACTCAGGAAGCCATTAGGAGATTATTATTGGCTGTACAGAAACCATAAGAGGTGGCAGTCTTACACTGCGGGGTCTCAGAAAGGAAAGGAAAGGAAATAGAAAGGAA 6425  
chr18\_50449131-50449934 ----- 260  
AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W CCGCCAAGCGGATATTGAAGCCAAAGAGCCGCAAGGCAGGACCTCCATTAGAAATGCTTATAGAAAGGACCCCTAGTATGGGGTAAATCCCCCTCCGGGAAACCAAGCCCCAGTACTCAGCAGAAGAAATAGAATGGGGAACTCAGCAGGACATA 6580  
chr18\_50449131-50449934 ----- 260  
AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
AC241258.1\_c31008-23012 ----- 5439  
AC013759.6\_36174-44171 ----- 5440

Consensus\_HERV-W GTTCTCTCCCTCAGGATGGCTAGCCACCGAAGAAAGAAAAATACTTTTCCTGCAAGCTAACCAATGGAATTACTTAAAACCTTCACCAAACTTTCTACTTAGGCATTGATAGCAATCAGATGGCCAAATCATTTTTCCTGGAACAGGC 6735  
chr18\_50449131-50449934 ----- 260  
AC241669.2\_12558-20556 ----- 5441  
AC203657.2\_c41170-33172 ----- 5441  
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CTTTTCAAACATCAAGCAGATAGTCAGGGCCGTGTGAAAGTGTGCCAAAGAAATAATCCCCGTCCTTATCGCCAAGCTCCTTCAGGAGAACAAAGAACAGGCCATTACCCAGGAGAACACATGGCAACTAGATTTTACCCACATGCCCAAATCTCA

6890 260 5441 5441 5439 5440

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GGGATTTAGTATCTACTAGTCTGGGTAGATACTTTCACTGGTTGGGCAGAGGCCCTCCCCGTAGGACAGAAAAGGCCAAGAGGTAATAAAGGCATAGTTTCATGAAATAATCCAGATTGGACTTCCCCGAGGCTTACAGAGTGACAATG

7045 260 5441 5441 5439 5440

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

GGCCCCCTTTCAGGCCGACAGTAAACCCAGGGAGTATCCCAGGCGTTAGGTATCAATATCACTTACCTGCGCCTGGAGGCCAACATCCCTCAGGGAAGGTCGAGAAAATGAATGAAACACTCAAAACGACATCTAAAAAGCTAACCCAGGAAACC

7200 260 5441 5441 5439 5440

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

CACCTCGCATGCCCTGCTCTGTTCCTATAGCCCTTACTAAGAATCCGAAACTCTCCCCAAAAGCAGGACTTAGCCCATAGAAATGCTGTAAGGACGGCCCTTCTTAAACATGACCTTTGTGCTTGACCGGAGAGACGGCCAACTTAGTTGCAGA

7355 260 5441 5441 5439 5440

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

CATCACCTCCTTAGCCAAATATCAACAGTTCCTTAAAAATTACAGGGAACTTGTCCCCGAGGAGGGAAAGGAACATATCCACCCCTGGTGACATGGTATTAGTCAAGTCCCTCCCTCTAATCCCCATCCCTAGATACATCCCTGGGAAGGAC

7510 260 5441 5441 5439 5440

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

CCTACCCAGTCAATTTATCTACCCCAACCGGGTAAAGTGGCTGGAGTGGAGTCTGGATACATCACACTCGAGTCAAACCCCTGGATATGCGAAAGAACCCGAAATCCAGGAGACAACGCTAGCTATTCTGTGAACCTCTAGAGGATCTG

ACAAATGCTAGCTATTCTGTCAACCTCTAGAGGATCTG  
ACAAATGCTAGCTATTCTGTCAACCTCTAGAGGATCTG  
ACAAATGCTAGCTATTCTGTCAACCTCTAGAGGATCTG  
ACAAATGCTAGCTATTCTGTCAACCTCTAGAGGATCTG

7665 260 5479 5479 5477 5478

Env

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

CGCCTGCTCTTCAAGCGACAACCGTGAAGGAAAGTAACTAAAACTGTAATCCCCATGGGCCCTCCCTTATCATATTTTTCTTTTACTGTTCTTTTACCCCTTTCACTCTCACTGCAACCCCTCCATGCCGCTGTACNACAGTAGCTCCCTTTA

7820 260 5634 5634 5632 5633

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

CCAAGAGTTCTATGGAGAAATGCGGCTCCCGGAAATATTGATGCCCCATCGTATAGGAGTTTTCTAAGGGAAACCCCACTTCAACCGCCACACCCATATGCCCGCAACTGTATAACTCTGCCACTCTTTGATGATGCAAAATACTCATT

7975 260 5788 5788 5786 5787

Consensus\_HERV-W chr18\_50449131-50449934 AC241669.2\_12558-20556 AC203657.2\_c41170-33172 AC241258.1\_c31008-23012 AC013759.6\_36174-44171

ATTGGACAGGGAAAAATGATTAATCTAGTTGTCTGGAGGACTGGAGCCACTGTTGTTGGACTTACTTACCCTATCGGTATGTTGATGGGGGTGGAGTTCAAGATCAGGCAAGAGAAAAACATGTAAGGAAATTAATCTCCCAACTGACC

8130 260 5943 5943 5941 5942

Consensus\_HERV-W chr18 50449131-50449934 8285  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 6098  
AC241258.1\_c31008-23012 6098  
AC013759.6\_36174-44171 6096  
AC013759.6\_36174-44171 6097

Consensus\_HERV-W chr18 50449131-50449934 8440  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 6253  
AC241258.1\_c31008-23012 6253  
AC013759.6\_36174-44171 6251  
AC013759.6\_36174-44171 6252

Consensus\_HERV-W chr18 50449131-50449934 8595  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 6408  
AC241258.1\_c31008-23012 6408  
AC013759.6\_36174-44171 6406  
AC013759.6\_36174-44171 6407

Consensus\_HERV-W chr18 50449131-50449934 8750  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 6563  
AC241258.1\_c31008-23012 6563  
AC013759.6\_36174-44171 6561  
AC013759.6\_36174-44171 6562

Consensus\_HERV-W chr18 50449131-50449934 8905  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 6718  
AC241258.1\_c31008-23012 6718  
AC013759.6\_36174-44171 6716  
AC013759.6\_36174-44171 6717

Consensus\_HERV-W chr18 50449131-50449934 9060  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 6869  
AC241258.1\_c31008-23012 6869  
AC013759.6\_36174-44171 6867  
AC013759.6\_36174-44171 6868

Consensus\_HERV-W chr18 50449131-50449934 9215  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 7024  
AC241258.1\_c31008-23012 7024  
AC013759.6\_36174-44171 7022  
AC013759.6\_36174-44171 7023

Consensus\_HERV-W chr18 50449131-50449934 9370  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 7179  
AC241258.1\_c31008-23012 7179  
AC013759.6\_36174-44171 7177  
AC013759.6\_36174-44171 7178

3'LTR

Consensus\_HERV-W chr18 50449131-50449934 9525  
AC241669.2 12558-20556 260  
AC203657.2\_c41170-33172 7333  
AC241258.1\_c31008-23012 7333  
AC013759.6\_36174-44171 7331  
AC013759.6\_36174-44171 7332

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Consensus_HERV-W      AAGTAGTAAAGAGAGCTCACTAAAAATGCTAATTAGGCAAAAACAGGAGGTAAGAAATAGCCAAATCATCTATCGCCTGAGAGCCACAGCGGAGGGACAATGATCGGATATAAAACCCAGGCATTTCGAGCCGGCAACGGGTACCCCTCTTTGGGTCC 9680
chr18_50449131-50449934  -----TTCAAGCCGGCAATGGCTACCCCTCTTTGGGTCC 293
AC241669.2_12558-20556  AAGTAATAAAGAGAGCTCACTAAAAATGCTAATCAGGCAAAAACAGCAGGTAAAAAAATAGCCAAATCATCTTTTCGCCTGAGAGCCACAGTGGGCAGGCAATGATCAGGATATAAAACCCAGGCATTCAAGCCAGCAATGGGTACCCCTCTTTGGGTCC 7488
AC203657.2_c41170-33172  AAGTAATAAAGAGAGCTCACTAAAAATGCTAATCAGGCAAAAACAGCAGGTAAAAAAATAGCCAAATCATCTTTTCGCCTGAGAGCCACAGTGGGCAGGCAATGATCAGGATATAAAACCCAGGCATTCAAGCCAGCAATGGGTACCCCTCTTTGGGTCC 7488
AC241258.1_c31008-23012  AAGTAATAAAGAGAGCTCACTAAAAATGCTAATCAGGCAAAAACAGCAGGTAAAAAAATAGCCAAATCATCTTTTCGCCTGAGAGCCACAGTGGGCAGGCAATGATCAGGATATAAAACCCAGGCATTCAAGCCAGCAATGGGTACCCCTCTTTGGGTCC 7486
AC013759.6_36174-44171  AAGTAATAAAGAGAGCTCACTAAAAATGCTAATCAGGCAAAAACAGCAGGTAAAAAAATAGCCAAATCATCTTTTCGCCTGAGAGCCACAGTGGGCAGGCAATGATCAGGATATAAAACCCAGGCATTCAAGCCAGCAATGGGTACCCCTCTTTGGGTCC 7487

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Consensus_HERV-W      CTTCCCTTTGTTATGGGAGCTCTGTTTTCACTCTATTAATACTTTGCAACTGCA--CTCTTCGGTCCGGTGTGTTAGGGTCG---AGCTGAGTTTTCGTTACCGTCCACCCTGCTGTTTGGCCGGTCCGACACCCGGCCGGTGAATTCCA 9828
chr18_50449131-50449934  CTTCCCTTTGTTATGGGAGCTCTGTTTTCGCTCTATTAATACTTTGCAACTGCGCTCTCTTCTGGTGCATGTTTGTCTATGGCTCGGCTTAGCTGAGCTTTTGTTCCTGTCACCCTGCTGTTTGTGTCGCCGCCGACAGCCTGCCACTGACTTCCA 448
AC241669.2_12558-20556  CTTCCCTTTGTTATGGGAGCTCTGTTTTCGCTCTATTAATACTTTGCAACTGCGCTCTCTTCTGGTGCATGTTTGTCTATGGCTCGGCTTAGCTGAGCTTTTGTTCCTGTCACCCTGCTGTTTGTGTCGCCGCCGACAGCCTGCCACTGACTTCCA 7643
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AC013759.6_36174-44171  CTTCCCTTTGTTATGGGAGCTCTGTTTTCGCTCTATTAATACTTTGCAACTGCGCTCTCTTCTGGTGCATGTTTGTCTATGGCTCGGCTTAGCTGAGCTTTTGTTCCTGTCACCCTGCTGTTTGTGTCGCCGCCGACAGCCTGCCACTGACTTCCA 7642

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Consensus_HERV-W      TCCCTCCGGATCCGGCAGGGTGTCCGCTGTGCTCCTGATCCAGCAGGCGCCCATTCGCCGTCGCCGATCGGGCTAAAGGCTTGCCATTGTTCTGTGACGGCTAAGTGCCCTGGGTTCCGCTTAATCGAGCTGAACACTAGTCACTGGGTTCCACGG 9983
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AC241669.2_12558-20556  TCCCTCCGGATCCGGCAGGGTGTCCCTCTGTGCCCTGATCCAGCAAGGCACCCATTGCTGCTCCGATCGAGGCTAAAGGCTTGCCATTGTTCTGTGACGGCTAAGTGCCCAAGGTTCCCTAAATTGAGCTGAACACTAGTCACTGGGTT-CACAG 7797
AC203657.2_c41170-33172  TCCCTCCGGATCCGGCAGGGTGTCCCTCTGTGCCCTGATCCAGCAAGGCACCCATTGCTGCTCCGATCGAGGCTAAAGGCTTGCCATTGTTCTGTGACGGCTAAGTGCCCAAGGTTCCCTAAATTGAGCTGAACACTAGTCACTGGGTT-CACAG 7797
AC241258.1_c31008-23012  TCCCTCCGGATCCGGCAGGGTGTCCCTCTGTGCCCTGATCCAGCAAGGCACCCATTGCTGCTCCGATCGAGGCTAAAGGCTTGCCATTGTTCTGTGACGGCTAAGTGCCCAAGGTTCCCTAAATTGAGCTGAACACTAGTCACTGGGTT-CACAG 7795
AC013759.6_36174-44171  TCCCTCCGGATCCGGCAGGGTGTCCCTCTGTGCCCTGATCCAGCAAGGCACCCATTGCTGCTCCGATCGAGGCTAAAGGCTTGCCATTGTTCTGTGACGGCTAAGTGCCCAAGGTTCCCTAAATTGAGCTGAACACTAGTCACTGGGTT-CACAG 7796

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Consensus_HERV-W      TTCTCTCCGTGACCCACGGCTTCTAATAGAGCTATAAACACTCACCAGTGGCCCAAGATTCCATTCTTGGAAATCCGTGAGGCCAAGAACCCCAAGGTCAGAGAACACGAGGCTTGCCACCATTCTGGAAAGTGGCCCGCCGCAATTTTGGAAAGCG 10138
chr18_50449131-50449934  TTCTCTCCGTGACCCATGGCTTCTAATAGAGCTATAAACACTCACCAGTGGCCCAAGATTCCATTCTTGGAAATCCATGAGGCCAAGAACCCCAAGGTCAGAGAACACGAGGCTTGCCACCATTCTGGAAAGTGGCCCTGCCG----- 743
AC241669.2_12558-20556  TTCTCTCCGTGACCCATGGCTTCTAATAGAGCTATAAACACTCACCAGTGGCCCAAGATTCCATTCTTGGAAATCCATGAGGCCAAGAACCCCAAGGTCAGAGAACACGAGGCTTGCCACCATTCTGGAAAGTGGCCCTGCCG----- 7938
AC203657.2_c41170-33172  TTCTCTCCGTGACCCACGGCTTCTAATAGAGCTATAAACACTCACCAGTGGCCCAAGATTCCATTCTTGGAAATCCATGAGGCCAAGAACCCCAAGGTCAGAGAACACGAGGCTTGCCACCATTCTGGAAAGTGGCCCTGCCG----- 7938
AC241258.1_c31008-23012  TTCTCTCCGTGACCCATGGCTTCTAATAGAGCTATAAACACTCACCAGTGGCCCAAGATTCCATTCTTGGAAATCCATGAGGCCAAGAACCCCAAGGTCAGAGAACACGAGGCTTGCCACCATTCTGGAAAGTGGCCCTGCTG----- 7936
AC013759.6_36174-44171  TTCTCTCCGTGACCCATGGCTTCTAATAGAGCTATAAACACTCACCAGTGGCCCAAGATTCCATTCTTGGAAATCCATGAGGCCAAGAACCCCAAGGTCAGAGAACACGAGGCTTGCCACCATTCTGGAAAGTGGCCCTGCTG----- 7937

TSD Flanking seq
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Consensus_HERV-W      GCCCCCAACCTTTGGGAGCTCTGGGAGCAAGGAA-CCCCCGGTAAACA----- 10186
chr18_50449131-50449934  -----CACTCTGGGAGCTCTGGGAGCAAGGACTCCCCCGGTAAACAATACTCATCTCTCATCTG 804
AC241669.2_12558-20556  -----CACTCTGGGAGCTCTGGGAGCAAGGACTCCCCCGGTAAACAATACTCATCTCTCATCTG 7999
AC203657.2_c41170-33172  -----CACTCTGGGAGCTCTGGGAGCAAGGACTCCCCCGGTAAACAATACTCATCTCTCATCTG 7999
AC241258.1_c31008-23012  -----CACTCTGGGAGCTCTGGGAGCAAGGACTCCCCCGGTAAACAATACTCATCTCTCATCTG 7997
AC013759.6_36174-44171  -----CACTCTGGGAGCTCTGGGAGCAAGGACTCCCCCGGTAAACAATACTCATCTCTCATCTG 7998

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Additional file 5. Alignment of HERV-W consensus with 18q21.1\_W2 solo LTR and provirus. The target site duplications (TSD) are marked in red. The 5' and 3'LTRs are highlighted in pink, and open reading frames for gag, pol and env genes are highlighted in green, light red and orange respectively. The HERV-W consensus sequence is from Repbase (LTR17 and HERV17).