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Molecular characteristics of Human Endogenous Retrovirus type-W in schizophrenia and bipolar disorder.

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SUPPLEMENTARY INFORMATION

Molecular characteristics of Human Endogenous Retrovirus type-W (HERV-W) in schizophrenia and bipolar disorder.

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I. Complementary Statistical analyses:

Table S1: HERV-W RNA relative expression of the MSR/V subtype, all controls

| Variables | BP,N=91 | SZ,N=45 | Controls,N=73 | P for all | P BP vs TEM | P BP vs SZ | P SZ vs TEM |
|-----------|------------|------------|---------------|-------------------------------------|-------------|------------|-------------|
| | Mean(SD) | | | P value Kruskal Wallis/Mann Whitney | | | |
| RNA | 1.62 (4.6) | 0.84 (0.5) | 0.65 (0.6) | <0.0001 | <0.0001 | 0.01 | 0.012 |
| DNA | 0.61(0.3) | 0.55(0.3) | 0.77(0.3) | 0.0005 | 0.0016 | 0.575 | 0.0003 |

Table S2: HERV-W relative expression of the MSR/V subtype, Controls with negative CRP (C-)

| Variables | BP,N=91 | SZ,N=45 | Controls,N=46 | P for all | P BP vs TEM | P BP vs SZ | P SZ vs TEM |
|-----------|------------|------------|---------------|-------------------------------------|-------------|------------|-------------|
| | Mean(SD) | | | P value Kruskal Wallis/Mann Whitney | | | |
| RNA | 1.62 (4.6) | 0.84 (0.5) | 0.62 (0.6) | <0.0001 | <0.0001 | 0.01 | 0.007 |
| DNA | 0.60(0.3) | 0.55(0.3) | 0.77(0.3) | 0.0015 | 0.003 | 0.575 | 0.0006 |

Table S3: HERV_W RNA relative expression and DNA copy numbers of the MSR/V subtype. Statistical analyses excluding Bipolar Disorder Patients treated with Valproate.

| Variables | BP,N=68 | SZ,N=45 | Controls,N=73 | P for all | P BP vs TEM | P BP vs SZ | P SZ vs TEM |
|-----------|------------|------------|---------------|-------------------------------------|-------------|------------|-------------|
| | Mean(SD) | | | P value Kruskal Wallis/Mann Whitney | | | |
| RNA | 1.71 (5.3) | 0.84 (0.5) | 0.65 (0.6) | <0.0001 | <0.0001 | 0.087 | 0.007 |
| DNA | 0.61(0.3) | 0.55(0.3) | 0.77(0.3) | 0.0009 | 0.006 | 0.468 | 0.0003 |

II. Sequence analyses**Figure S1: Sequence alignments with the HERV-W/MSRV-env specific Probe**

Figure S1A: HC RNA

```

MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG
              10      20
              AAGAAGTTTACCTCGGGTCTACGTC

1. RNA-H12_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

2. RNA-H12_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

3. RNA-H12_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

4. RNA-H12_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

5. RNA-H12_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

6. RNA-H12_6  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

7. RNA-H12_8  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

8. RNA-H12_9  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

9. RNA-H16_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

10. RNA-H16_  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

11. RNA-H16_  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

12. RNA-H16_  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

13. RNA-H16_  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

14. RNA-H1_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

15. RNA-H1_1  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

16. RNA-H1_2  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

17. RNA-H1_3  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCAG

18. RNA-H12_  40      50
[ 100 ]      TTCTTCAAATGGAGCCCAGATGCA>
              |||
MSRVqPCR p  TTCTTCAAATGGAGCCCAGATGCA

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19. RNA-H16_ 40 50
 [100] TTCTTCAAATGGANCCCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

20. RNA-H1_8 40 50
 [100] TTCTTCAAATGGAGCCCCAGATGCA>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCA

21. RNA-H12_ 130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

22. RNA-H12_ 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

23. RNA-H12_ 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

24. RNA-H16_ 130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

25. RNA-H16_ 130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

26. RNA-H16_ 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

27. RNA-H16_ 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

28. RNA-H1_1 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

29. RNA-H1_1 130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

30. RNA-H1_1 130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

31. RNA-H1_7 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

32. RNA-H16_ 130 120 110
 [92] <TTCTTCAAACGGAACCCAGATGCAG
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

33. RNA-H12_ 320 330
 [88] TTCTTCAAATGGAGCCCCAGA--CAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

Figure S1B: HC DNA

```

MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG
               10      20
               AAGAAGTTTACCTCGGGTCTACGTC

1. DNA-H12_1   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

2. DNA-H12_5   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

3. DNA-H16_1   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

4. DNA-H16_1   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

5. DNA-H16_1   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

6. DNA-H16_140 50      60
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

7. DNA-H16_5   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

8. DNA-H16_8   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

9. DNA-H1_13   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

10. DNA-H1_1   40      50
[ 104 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

11. DNA-H12_ 130     120     110
[ 98 ]       <TTCTTCAAATGGAGCCCAGATGCAG
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

12. DNA-H12_   40      50
[ 98 ]       TTCCTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

13. DNA-H12_   40      50
[ 98 ]       TTCCTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

14. DNA-H16_40 50      60
[ 98 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

15. DNA-H16_40 50      60
[ 98 ]       TTCCTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

16. DNA-H16_   40      50
[ 98 ]       TTCTTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

17. DNA-H1_1 130     120     110
[ 98 ]       <TTCCTCAAATGGAGCCCAGATGCAG
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

18. DNA-H1_7   40      50
[ 98 ]       TTCCTCAAATGGAGCCCAGATGCAG>
               |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

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19. DNA-H1_1 40 50
 [96] TTCTTCAAATGGAGCCCCAGATG-AG>
 |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

20. DNA-H1_4 40 50
 [96] TTCTTCAAATGGAGCCCCAGATG-AG>
 |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

21. DNA-H12_ 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

22. DNA-H12_ 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
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23. DNA-H12_ 40 50
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24. DNA-H12_ 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

25. DNA-H12_ 40 50
 [92] TTCTTCAAATTGAGCCTCAGATGCAG>
 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

26. DNA-H12_ 40 50
 [92] TTCTTCAAATTGAGCCTCAGATGCAG>
 ||||| ||
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27. DNA-H16_ 130 120 110
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29. DNA-H16_ 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
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30. DNA-H16_ 40 50
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

31. DNA-H16_ 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

32. DNA-H1_1 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
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33. DNA-H1_1 40 50
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 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

34. DNA-H1_3 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

35. DNA-H1_6 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

36. DNA-H1_9 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| ||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

Figure S1C: BD RNA

```

MSRVqPCR p      10      20
                TTCTTCAAATGGAGCCCCAGATGCAG
                AAGAAAGTTTACCTCGGGTCTACGTC

1. RNA70_10.    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

2. RNA70_13.    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

3. RNA70_15.    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

4. RNA70_16.    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

5. RNA71_3.n    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

6. RNA71_6.n    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

7. RNA71_9.n    40      50
[ 104 ]        TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

8. RNA71_16.n   40      50
[ 100 ]        NTCTTCAAATGGAGCCCCAGATGCA>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCA

9. RNA71_7.n0   50      60
[ 100 ]        CTCTTCAAATGGAGCCCCAGATGCA>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCA

10. RNA66_1.    40      50
[ 98 ]         TTCTTCAAATGGATCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

11. RNA66_10   130     120     110
[ 98 ]         <TTCTTCAAATGGAACCCAGATGCAG
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

12. RNA66_12   40      50
[ 98 ]         TTCTTCAAATGGAACCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

13. RNA66_15   130     120     110
[ 98 ]         <TTCTTCAAATGGAACCCAGATGCAG
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

14. RNA66_16   40      50
[ 98 ]         TTCTTCAAATGGAACCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

15. RNA66_2.    40      50
[ 98 ]         TTCTTCAAATGGAACCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

16. RNA66_5.   130     120     110
[ 98 ]         <TTCTTCAAATGGAACCCAGATGCAG
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

17. RNA66_6.    40      50
[ 98 ]         TTCTTCAAATGGAACCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

18. RNA66_7.   130     120     110
[ 98 ]         <TTCTTCAAATGGAACCCAGATGCAG
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

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19. RNA66_8. 40 50
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20. RNA70_1.130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

21. RNA70_12 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

22. RNA70_14 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

23. RNA70_4. 320 330
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

24. RNA70_5. 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

25. RNA70_6. 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

26. RNA70_7. 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

27. RNA70_9. 130 120 110
 [98] <TTCTTCAAATGGAACCCAGATGCAG
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

28. RNA71_12 40 50 60
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

29. RNA71_5. 40 50
 [98] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

30. RNA66_13 40 50
 [92] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

31. RNA66_3. 40 50
 [92] TTCTTCAAATGGAACCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

32. RNA66_9. 40 50
 [92] TTCTTCAAATGGAACCCAGATGCAG>
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33. RNA71_11 40 50
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34. RNA71_15 40 50
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35. RNA71_8. 130 120 110
 [92] <TTCTTCAAATGGAACCCAGATGCAG
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36. RNA70_11 320 330
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

37. RNA70_2. 40 50
 [88] TTCTTCAAATGGAGCCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

38. RNA70_8. 320 330
 [88] TTCTTCAAATGGAGCCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

39. RNA71_4.130 120 110
 [88] <TTCTTCAAATGGAGCCCAGATGCAG
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

Figure S1D: BD DNA

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MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG
              10      20
              AAGAAGTTTACCTCGGGTCTACGTC

1. DNA66_14.  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

2. DNA66_4.n  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

3. DNA66_7.n  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

4. DNA66_9.n  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

5. DNA70_9.n  40      50
[ 104 ]      TTCTTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

6. DNA66_5.n  40      50
[ 98 ]      TTCCTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

7. DNA70_11. 130     120     110
[ 98 ]      <TTCTTCAAATGGAACCCAGATGCAG
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

8. DNA70_12.  40      50
[ 98 ]      TTCTTCAAATGGAACCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

9. DNA70_5.n  40      50
[ 98 ]      TTCCTCAAATGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

10. DNA71_12  40      50
[ 98 ]      TTCTTCAAATGGAACCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

11. DNA66_8.  40      50
[ 96 ]      TTCTTCAAATGGAGCCCAGATG-AG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

12. DNA70_2.  40      50
[ 96 ]      TTCTTCAAATGGAGCCCAGATG-AG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

13. DNA71_15  40      50
[ 96 ]      TTCTTCAAATGGAGCCCAGATG-AG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

14. DNA71_4.  40      50
[ 96 ]      TTCTTCAAATGGAGCCCAGATG-AG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

15. DNA71_6.  40      50
[ 96 ]      TTCTTCAAATGGAGCCCAGATG-AG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

16. DNA66_11  40      50
[ 92 ]      TTCTTAAATTGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

17. DNA66_13  40      50
[ 92 ]      TTCTTAAATTGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

18. DNA66_15  40      50
[ 92 ]      TTCTTAAATTGGAGCCCAGATGCAG>
              |||
MSRVqPCR p   TTCTTCAAATGGAGCCCAGATGCAG

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19. DNA70_1. 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
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20. DNA70_10 40 50
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 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

21. DNA70_13 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

22. DNA70_16 40 50
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 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

23. DNA70_4. 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

24. DNA70_8. 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

25. DNA71_10 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| || |||||
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26. DNA71_11 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

27. DNA71_13 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

28. DNA71_14 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

29. DNA71_2. 130 120 110
 [92] <TTCTTAAATTGGAGCCCCAGATGCAG
 ||||| || |||||
 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

30. DNA71_3. 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

31. DNA71_5. 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
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32. DNA71_7. 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

33. DNA71_8. 40 50
 [92] TTCTTAAATTGGAGCCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCCAGATGCAG

Figure S1E: SZ RNA

```

MSRVqPCR p      10      20
                TTCTTCAAATGGAGCCCCAGATGCAG
                AAGAAGTTTACCTCGGGGTCTACGTC

1. RNA11_10.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

2. RNA11_11.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

3. RNA11_12.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

4. RNA11_14.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

5. RNA11_15.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

6. RNA11_2.n    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

7. RNA11_3.n    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

8. RNA11_6.n    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

9. RNA11_8.n    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

10. RNA11_9.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

11. RNA16_10    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

12. RNA16_2.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

13. RNA16_3.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

14. RNA16_9.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

15. RNA23_12    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

16. RNA23_16    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

17. RNA23_2.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

18. RNA23_4.    40      50
[ 104 ]         TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG
    
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20. RNA23_9. 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
 |||
 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

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 [104] TTCTTCAAATGGAGCCCAGATGCAG>
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23. RNA32_12 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
 |||
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24. RNA32_13 40 50
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25. RNA32_14 40 50
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26. RNA32_16 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

27. RNA32_3. 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
 |||
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28. RNA32_4. 130 120 110
 [104] <TTCTTCAAATGGAGCCCAGATGCAG
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29. RNA32_5. 40 50
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30. RNA32_7. 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
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31. RNA32_8. 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

32. RNA32_9. 40 50
 [104] TTCTTCAAATGGAGCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

33. RNA23_10 40 50
 [100] TTCTTCAAATGGAGCCCAGATGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

34. RNA11_16 40 50
 [98] TTCTTCAAATGGAGCCCAGAGGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

35. RNA11_4. 40 50
 [98] TTCTTCAAATGGAGCCCAGAGGCAG>
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 MSRVqPCR p TTCTTCAAATGGAGCCCAGATGCAG

36. RNA23_3. 40 50
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37. RNA23_5. 40 50
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38. RNA16_11 40 50
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Figure S1F: SZ DNA

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MSRVqPCR p      10      20
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                AAGAAGTTTACCTCGGGGTCTACGTC

1. DNA16_1.n      40      50
[ 104 ]          TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

2. DNA23_11.     40      50
[ 104 ]          TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

3. DNA23_15.     40      50
[ 104 ]          TTCTTCAAATGGAGCCCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

4. DNA16_11.    130     120     110
[ 98 ]          <TTCTTCAAATGGAGCCCCAGATGCAG
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

5. DNA23_9.n     40      50
[ 98 ]          TTCTTCAAATGGAACCCAGATGCAG>
                |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

6. DNA32_1.n     40      50
[ 98 ]          TTCTTCAAATGGAGCCCCAGAGGCAG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

7. DNA11_2.n     40      50
[ 96 ]          TTCTTCAAATGGAGCCCCAGATG-AG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

8. DNA11_3.n     40      50
[ 96 ]          TTCTTCAAATGGAGCCCCAGATG-AG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

9. DNA11_6.n    130     120     110
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                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

10. DNA-VIP3     40      50
[ 92 ]          TTCTTAAATTGGAGCCCCAGATGCAG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

11. DNA11_1.     40      50
[ 92 ]          TTCTTCAAATTGAGCCTCAGATGCAG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

12. DNA11_12    40      50
[ 92 ]          TTCTTCAAATTGAGCCTCAGATGCAG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

13. DNA11_14    130     120     110
[ 92 ]          <TTCTTAAATTGGAGCCCCAGATGCAG
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MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

14. DNA11_15     40      50
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                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

15. DNA11_16    130     120     110
[ 92 ]          <TTCTTCAAATTGAGCCTCAGATGCAG
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MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

16. DNA11_7.     40      50
[ 92 ]          TTCTTAAATTGGAGCCCCAGATGCAG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

17. DNA11_8.     40      50
[ 92 ]          TTCTTAAATTGGAGCCCCAGATGCAG>
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG

18. DNA16_8.    130     120     110
[ 92 ]          <TTCTTAAATTGGAGCCCCAGATGCAG
                ||| |||
MSRVqPCR p      TTCTTCAAATGGAGCCCCAGATGCAG
    
```


Figure S2: Phylogenetic tree representation of aligned clones with related HERV-W and distant HERV-K env gene sequences:

Figure S2A: RNA and DNA clones from BD

Method: Neighbor Joining; Bootstrap (1000 reps); tie breaking = Systematic
Distance: Kimura 2-parameter; Gamma correction = Off
Transition/Transversion Ratio = Estimate (Av. = 2.98); Gaps distributed proportionally

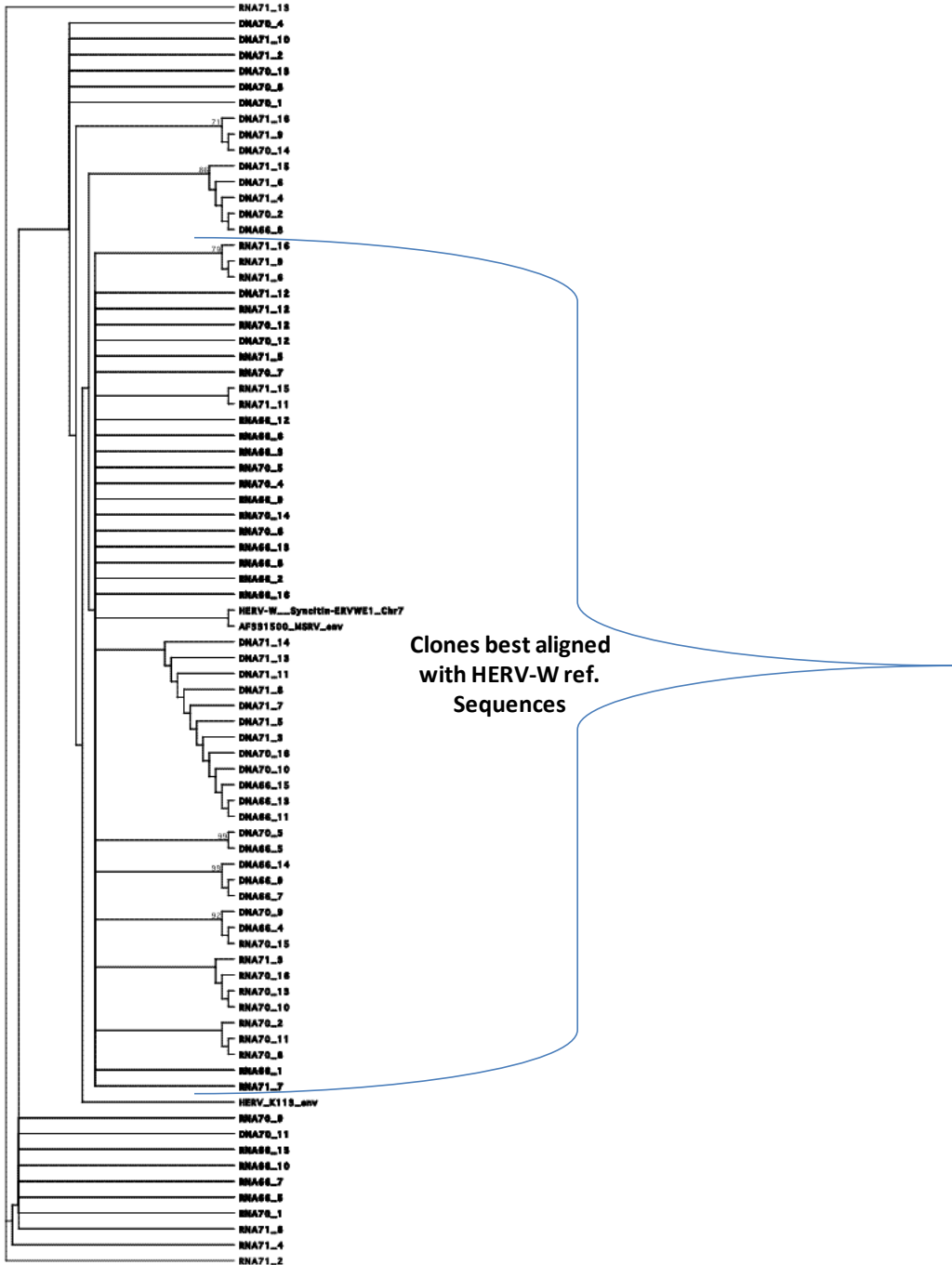


Figure S2B: RNA and DNA clones from SZ

Method: Neighbor Joining; Bootstrap (1000 reps); tie breaking = Systematic
Distance: Kimura 2-parameter; Gamma correction = Off
Transition:Transversion Ratio = Estimate (Av. = 2.75); Gaps distributed proportionally

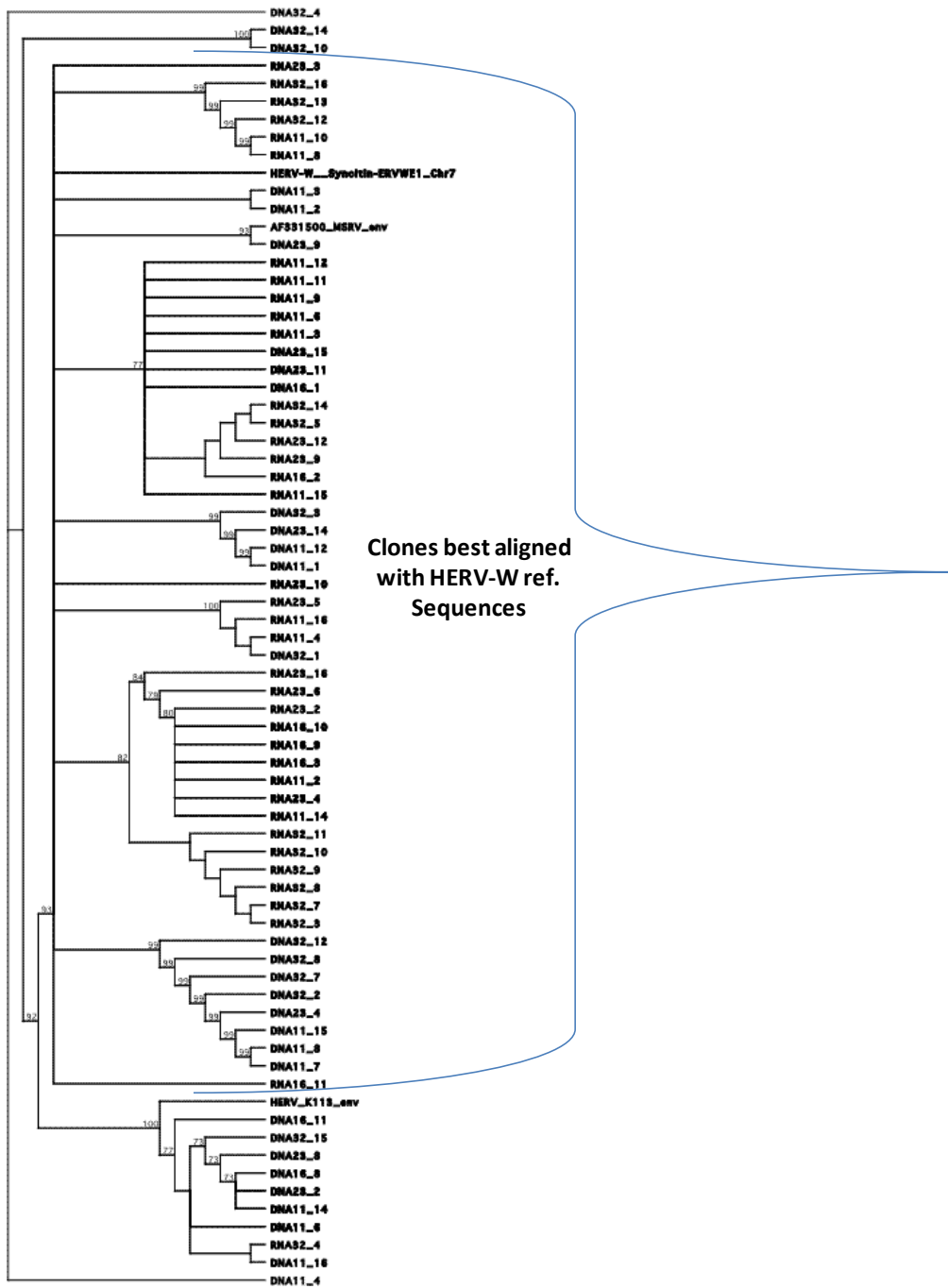


Figure S2C: RNA and DNA clones from HC

Method: Neighbor Joining; Bootstrap (1000 reps); tie breaking = Systematic
Distance: Kimura 2-parameter; Gamma correction = Off
Transition:Transversion Ratio = Estimate (Av. = 3.02); Gaps distributed proportionally

