

Supplementary Materials

1.1 Supplementary Figures

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LBCbarr2 GAAATTAGCTGTAGCCAATCGATTGCCATGTTCTCAACTCTTAACAATTTACTACCCGAT 60
LBC-ori GAATTTTTC----GGTGAACCGGAATTATGTCGTCTCTGTAAATTCATTACTACCAGAA 56
LBclus4 GAATTTTTC----AGTGAACCGGAATTATGTCGTCTCTGTAAATTCATTATTACCAGAA 56
      *** ** * * * * * * * * * * * * * * * *
      5' conserved Start of Gag and Gag-Pol
LBCbarr2 ACTTTAAACCCCTCGTAAGAATTTCAAACCTACTCACCATAGAATTAAATATGGTATGAAT 120
LBC-ori TATTTTAAACCTAAACCTAATTTGAATATCAACTCTTCTAGGGTCCAATATGGCTTTAAT 116
LBclus4 TATTTTAAACCCAAACAAATTTGAATATCAACTCCTCTAGGATCCAATATGGTTTAAAT 116
      *** ** ** * * * * * * * * * * * * * * * *

LBCbarr2 GCCAACATCAATTTTCGATGTTTCTGATGACTTTGGGAAATATGAAGGTAATAGACCGGGT 180
LBC-ori GCTCGCATTGATATGCAGTATGAAGACGATAGTGGGACTAGAAAAGGCTCAAGACCCAAT 176
LBclus4 GCTCGCATTGATATGCAGTATGAAGACGATAGTGGGACTAGAAAAGGCTCAAGGCCCAAT 176
      ** *** ** * * * * * * * * * * * * * * * *

LBCbarr2 GCTTTTATTGGAAATGAAGTATCTCTTTATGGTAATTACAATTCCTTATATCACGGATGAC 240
LBC-ori GCATTTATGTCTAACACAGTTGCTTTTATAGGAACTATGAAGGTATTATTGTTGATGAC 236
LBclus4 GCCTTTATGTCTAATACGTTGCTTTTATTGGAACTATGAAGGTGTCATCGTTGATGAC 236
      ***** ** ** * ** * * * * * * * * * *

LBCbarr2 GTGCCAATCTATGATGGTATGCGGTCTGATGTGATCACTCCTGAAGGAGAGTTTCAGCCAT 300
LBC-ori ATTCGATATTTGGATGGTCTTAGGGCCGACATTTTGATACTCATGGTGACTTAGACATG 296
LBclus4 ATCCCGATATTTGGATGGCCTTAGAGCTGACATTTTGATACTCATGGTGATTTAGACATG 296
      * * * * * * * * * * * * * * * * * * * *

LBCbarr2 GAATTAGCTGAGCAAGTGTTAAGTAAAGCGACATCGGACCGAGCATCCGCTCAGAAGATC 360
LBC-ori GGCCTCGTTGAGGATGCATTGTCTAAGAGTACCATGATTAGAAGGAATGTACCAACTTAT 356
LBclus4 GGCCTCGTAGAGGATGCATTGTCCAAAAGTACTATGATTAGAAGGAATGTACCAACTTAT 356
      * * * * * * * * * * * * * * * * * * *

LBCbarr2 ACGCAATACTTGGCATACAATGGAGGTATGCGCAATTGTGTATCTATATTGTATAACTTA 420
LBC-ori ACTGCTTACGCGAGTGAATTACTGTATAAGAGAAACCTTACATCTCTATTTTACAATATG 416
LBclus4 ACTGCTTACGCGAGTGAATTATTGTATAAGAGAACTTAACATCTCTGTTTTACAATATG 416
      ** *** * * * * * * * * * * * * * * * *

LBCbarr2 CTGCGTATGTATGTATGAATGAGTTTGGCGAGGTGGTCTATGACCCAAACGAGATATTC 480
LBC-ori CTCCGTTTATACTACATTAATAAATGGGGCAGTATTAAGTATGAAAAAGATGCCATCTTT 476
LBclus4 CTCCGTTTATAATTACATTAATAAATGGGGTAGTATTAAGTATGAAAAAGATGCCATTTT 476
      ** * * * * * * * * * * * * * * * * * * *

LBCbarr2 TACGACAATGGACATGTGTGTATTAATAATCATCAGATGTTTCCAAAACATCTAGAGAAG 540
LBC-ori TATGATAATGGCCACGCCCTGTCTTTTAAACAGGCAATTGTTTCCAAAGTCTCGTGATGCT 536
LBclus4 TATGATAATGGCCACGCCCTGTCTTTTAAACAGGCAATTGTTTCCGAAGTCTCGTGATGCT 536
      ** ** * * * * * * * * * * * * * * * * *

LBCbarr2 AAGTCATTAGCTAAGGCTGTT--GAGTACACTCCTGCTATGATCGAAGATGCTAGCACC 597
LBC-ori TCTTTGGAATCAAGCCTCTCTTTGCGCTGAGGCTGAAATGCAATGCTTGATCCTGGCCTG 596
LBclus4 TCTTTGGAATCAAGCCTCTCTTTACCTGAGGCAGAAATGCAATGCTTGATCCTGGATTG 596
      * * * * * * * * * * * * * * * *

LBCbarr2 TTATGGCGCGAAGGTGACATACCTGAATGTCCTTCATTGATTTGGACAGGATTTATGCGT 657
LBC-ori GAATTTCCAGAAGAGGATGTGCCTGC-----AATTTTATGGCACGGCAGAGTGTCA 647
LBclus4 GAATTTCCAGAAGAGGATGTGCCTGC-----AATTTTATGGCATGGCAGAGTGTCA 647
      ** * * * * * * * * * * * * * * * *

LBCbarr2 GATAAGCAAGCTACTATCGTTTACGGGCAGCAGGTGGATTCAATACAGAGCACCTTTC 717
LBC-ori TCCAGAGCAACGTGTATCTTAGGGCAAGCTTGCTCAGAGTTCGCGCCTCTGGCCCCCTTT 707
LBclus4 TCCAGAGCTACGTGTATCTTAGGGCAAGCCTGCTCTGAATTTGCGCCTCTGGCCCCCTTT 707
      * * * * * * * * * * * * * * * *

LBCbarr2 GGAGTAGCTCATGAGTCAAAAAATCTTACTGAAAGATTAGGTATCATGGCAACTGGAGGA 777
LBC-ori TCGATTGCGCATTATTACCACAAATTGACGAGAAAACTATTTGTCAATGCGCCCGCTGGG 767
LBclus4 TCAATTGCGCATTATTACCACAAATTGACAAGAAAACTATACGTCAATGCGCCCGCTGGG 767
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LBCbarr2 CTCTCTAATGTAGAAGATTATAACTATGGTCCTTCTGATATATTGTTTCGTCCTTAACAAG 837
 LBC-ori ATTGAGCCTA--GCTCCGGGCGGTATACTCACGAGGATGTAAAAGATGCGATTACGATC 824
 LBclus4 ATTGAGCCTA--GCTCCGGGCGGTATACTCACGAGGATGTAAAAATGCGATTACGATC 824
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LBCbarr2 CTGGTGACAGATAACGGGCTTTACTGACTTCACCTTACGCTTATCTAATGTTGTTACAA 897
 LBC-ori CTTGTGTCTGCAAACAGGCTTATACTGACTTTGAAGCAGCATACTTGATGCTTGCTCAA 884
 LBclus4 CTTGTGTCTGCTAACCAGGCTTATACTGACTTTGAGGCAGCATACTTGATGCTTGCTCAA 884
 ** *** * * *** * *** ***** ** * * * *** * ***

LBCbarr2 GTATTAGTGTCCTCTATACCAAGGTCTGCTGAAGCTCCAGCATGGTTCGTCGGTGTCCTAG 957
 LBC-ori ACGTTGGTCTCACCTGTACCACGCACTGCCGAAGCAAGTGCATGGTTCATCAATGCTGGC 944
 LBclus4 ACATTGGTCTCACCTGTACCACGCACTGCCGAAGCTAGTGCATGGTTCATTAATGCTGGT 944
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Mitochondrial cytochrome oxidase I of *Cherax tenuimanus* (93%)
 LBCbarr2 ACAGTGTCTTTACCTAGGTTGGTGACTGACACAGGAACATACCACAGTTATATCAGGGG 1017
 LBC-ori ATGGTCAATATGCCAACTTTGTCTGTGCAAAATGGTTATTATCCAGCACTGACCAATGTC 1004
 LBclus4 ATTGTTAACATGCCTATCTTGTCTGTGCTAATGGCTACTACCCAGCCTTAACAAATGTT 1004
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LBCbarr2 AAAGTCTATGCTAGGTTTAAATGACTGGAAGAGACTATGGCTAACTTCAGAGCATATCCT 1077
 LBC-ori AATCCTTACCACCGGCTAGACACATGGAAGATACGTTAAATCATTGGGTGGCTTATCCC 1064
 LBclus4 AATCCTTACCACCGGTTAGACACATGGAAGACACTTTAAATCATTGGGTGTCTTACCCC 1064
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LBCbarr2 AAGTCATGTTTATTGCATAGTATTGTAGTGAATGAAGCTGTTTACGTTGAATTGAACAAT 1137
 LBC-ori GACATGCTGTTTACCATTCACTGGCAATGATTGAGAGCTGCTATGTTGAACCTCGGGAAT 1124
 LBclus4 GACATGTTTATTTACCATTCCGTTGGCAATGGTTGAGAGCTGTTATGTTGAACCTCGGGAAT 1124
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LBCbarr2 CTTAACAGAGTGAGTCTTTTGTATGCAATTAATCGAGAAAATTTTGTGAGGTAGCTGTA 1197
 LBC-ori GTGGCTCGTGTGTGACACAGTGTGCAATAAACAAATACACTTTCCTGAGCTATCAGTG 1184
 LBclus4 GTCGCACGTGTGTGACACAGTGTGTAATTAACAAGTATACCTTCCTGAGCTATCTGTG 1184
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LBCbarr2 CAAGGGCAGCCTGTCACAATGGGCGGGATATTGAATGATCTGACTTTAGTGTGATGCGG 1257
 LBC-ori CAAGGACGGCTGTATTGAATCGAGGAATATTGTAGATCTGACACTTGTGGCAATGCGT 1244
 LBclus4 CAAGGCCGGCTGTATTGAACCGAGGGATTATTGTTGACTTGACACTTGTAGCAATGCGT 1244
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LBCbarr2 TATTCTAAGGAATTTGCACTGGCATATCCTGTGTCCACAGGACTTACAAGGACTAACATT 1317
 LBC-ori ACTGGTAGGAGATCTCACTACCTTACCCGGTCAGCTGTGGCCTGACCCGTACAGACGCG 1304
 LBclus4 ACTGGTAGAGAGATCTCACTACCTTACCCAGTTAGTTGTGGTTTGACCCGTACAGACGCA 1304
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LBCbarr2 ATGGCACAGAAGAAATAGCTCTTGAGGTACCAATAACAGTAAAAGACCTAGATGCACCTAAA 1377
 LBC-ori TTATTGCAAGGTACTGAGATTACGTTCCAGTTGTTGTCAAAGATATCGACATGCCCCAG 1364
 LBclus4 TTATTGCAAGGTACGGAGATTCTGTTCCAGTTGTCGTCAAAGACATGGACATGCCTCAG 1364
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LBCbarr2 TATTACAACATTGCAGAACCTATTATAACCGCAAATCAACATGCAACACTCATTGTTACT 1437
 LBC-ori TATTACAACCGGATTGATAAGGATGTTATTGAGGGGCGAGAACTGTGATTAAAGTGAAA 1424
 LBclus4 TATTATAATGCAATCGATAAGGATGTTATTGAAGGGCAAGAACTGTAATAAAGTGAAAG 1424
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LBCbarr2 AATATGACGGCACCTTTGTATCCAGTAATGTCTTACGGGATTAATACTGATGACTATTAT 1497
 LBC-ori CAGCTGCCACAGCATGTATCCAATTTATACTTACGGGATCAACACTACTGAATTCTAT 1484
 LBclus4 CAAGTGCCACAGCAATGTATCCGATTTATACTTATGGTATCAACACTACAGAGTTTAC 1484
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LBCbarr2 TGTAACGATACGAACATCAGTATCAAATTTA--AGGCACCTGTGACTGCAAGTGGGATA 1554
 LBC-ori TCTGACCATTTTGAAGACCAGGTACAAGTTGAAATGGCACCATCGATAATGGAAAAGCA 1544
 LBclus4 TCCGACCATTTTGAGGACCAGGTACAAGTAGAAATGGCTCCTATCGATAATGGGAAGGCA 1544
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AAGTTTATGAATGT⁶TATGCGTATGTGTGGGCAC
 LBCbarr2 TCTTTTACAGAAGCAGAAAATTTCTCAAGTTTATGAACGTTATGCGTATGTGTGGGTA 1614
 LBC-ori GTTTTAAACGATGCAAGAAAGTTTCGAAATTTATGTCCATAATGCGCATGATGGGGAAT 1604
 LBclus4 GTCTTTAATGATGCTCGAAAATTTCTTAAATTCATGTCTATAATGCGCATGATGGGGAAT 1604
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AAT *Protopolystoma xenopodis*, *Xenopus* parasitic worm (95%)
 LBCbarr2 AACGTTGAGGCCAGAGAGATGTTTTCAGGCAAGACTGTCATTAACTGGGCAGATAATGCT 1674
 LBC-ori GATGTTACTGCTACTGATTAGTTACAGGTAGAAAAGTGTGCAATTGGGCCGACAACCTCA 1664
 LBclus4 GATGTTACGGCAACTGATTAGTTACAGGTAGAAAAGTGTGCAATTGGGCCGACAACCTCA 1664

LBC-ori ACTACTCTG--ATACGCGGAAGTGGATACGTGACAATTTTACATATAATTATAAT--A 2558
 LBclus4 ATTACTATG--ATACACGGAAGTGGATACGTGACAATTTTACATATAATTATAAT--A 2558
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LBCbarr2 CTGATAAAATAACAGAAAAATAAGTCAGTTTCATCATGTACACGTGAGGCTGAAGGACT 2586
 LBC-ori TGGAGAAAGAAAAGTATAGGATAACCCAAATACCACCATACACATGTGAGGTTGAAAGATT 2618
 LBclus4 TGGAGAAAGAAAATATAAGATAACTCAATATACCACACACACGTAGATTGAAAGATT 2618
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LBCbarr2 TATATGCTAATAAGGATATTGTGACAGTAAACGGTCATGAAGCATATCTCGTGAACCTTAC 2646
 LBC-ori TGTTTCCATCCAGGAAAATAGTTAACTAGAGGGATATGAAGCCTTGTGGCAATGATGC 2678
 LBclus4 TGTTTCCATCTAGGAAAAGTAGTCAAATAACAGGATACGAGGCCCTACTGGCAATGATGT 2678
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AGGTTTAACTATAGAGTCAACGCATGTTACTTCTTCACATATTTAAGAGCAC
 LBCbarr2 TTGATAAGTACACAGACAAAGCTATTACACATGCTACTTTCTAACCTATCTAAGAGCAC 2706
 LBC-ori TAGACAGGTTTAAACAATAGAGTCAACACATGTAACCTTCTTCACATATTTAAGAGCAC 2738
 LBclus4 TAGATAGGTTCAACAATATAGAGTCAACACATGTACCTTTTACATACCTGAGGCGAT 2738
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5' extra ScV-M1-EX231 (94%) ATTAAGTATGGTAAAAATACACC
 TACCTGATCGTGAATAATAA ATGGAAC
 LBCbarr2 TGCCTGTTAGGGAAGCAAGGCTCTTCATAAAATTAGTCATTAAGTATGGTAGCATAGACC 2766
 LBC-ori TACCTGACCGTGAAAAAGAACTCTTTATAGCTTAGTCTTAACTATAATGGCCTTGGCA 2798
 LBclus4 TGCCTGATCAAGAGAGGGAATCTTCATTAGCTTAATTTGAACTACAACGGGCTTGGTA 2798
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AAGCATGG Homo sapiens chromosome 18 (93%) / Vitis vinifera contig VV78X249912.5 (80%)
 AAGAAAGGTTAAAGAATAAGCAA - GAAGGAAAGAAATAAAGGGC
 LBCbarr2 AAGAATGGTTAAAGAAGAAGGAGGCTGTAGCAAAGCAAAATACAGGGCAGCACTGACTTTG 2826
 LBC-ori GAGAGTGGTTGAAGTCTGAAGGTGTTAGGGCTAAACAAGCACAAGGTACTGTGAAATACG 2858
 LBclus4 GAGAGTGGTTAAAGTCAGAAGGTGTTAGGGCAAAGCAAGCGCAAGGTACTGTAAAGTATG 2858
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LBCbarr2 ATCTAAGCAAAATTTTGGAGCTTAATGTACTGCATAATCGGGTTGAACTACAGTTGATT 2886
 LBC-ori ATATGAGTAACTATTTGAACTGAATGTACTAGAGAACGGAGTTGACGAAGAAGTTGACT 2918
 LBclus4 ATATGAGTAAATTTTGGAGCTCAATGTGTTGAAAAATAGGGTTGACGAAGAGTTGACT 2918
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LBCbarr2 GGAATGAAGAAAGAGAACATAGGACGCATCCTGATACAGTGAATATATCTTATCCAGATG 2946
 LBC-ori GGGAGAAAGAGAAACGCAACAGGTCAGATATCAAGACTGTTAAACATAAGTTATGCAAAAG 2978
 LBclus4 GGGAAAAAGAAAAACGGAACAGGACGAACATCAAGACTGTAGACATAAGTTATGCAAAAG 2978
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AGAATTTTAAATTAGCAAACAAGAAGG
 LBCbarr2 TCTATACTAAGTGCAGAGAATTTGTTGAATTAGCAAAGCAGGAAGCAAGTCACTTATTA 3006
 LBC-ori TTCTCGAACATTGTAGAGAGCTATTTCATCATGGCGAGGGCCGAAGGAAACGGCCAATGA 3038
 LBclus4 TTCTTGAGCACTGTAGAGAACTATTTATCATGGCAAGGGCTGAAGGAAAGCGCCAATGA 3038
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Marinilactibacillus sp. (93%)
 LBCbarr2 AGATGGACTGGAATAAGTACTGGATGCAGCGAGCCTCAATAATGCCATCTGGTGCAGTCC 3066
 LBC-ori GGATGAAATGGCAAGAGTACTGGAGGCAGAGAGCAGTTATCATGCCAGGTGGATCGGTCC 3098
 LBclus4 GGATGAAATGGCAGGAGTATTGGAGGCAGAGAGCAGTTGTGATGCCAGGCGGTTCACTCC 3098
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LBCbarr2 ACTCACAACATAGTGAGCTTGACAAGTATGTGAGGAAATTACCTCGTGAAGTCAAAAACA 3126
 LBC-ori ACAGTCAACATCCAGTCAACAGGACGTGATTAGAGTATTACCCAGAGAAATCAGAAGTA 3158
 LBclus4 ACAGTCAGCATCCAGCCGAACAAGATGTGATTAGATATTACCCAGGAAATTAAGAGTA 3158
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LBCbarr2 AGAAGGGGTTGGCTGCCTCGCTACCTAATATAGACCAGAGGTACTTTCTGAGTAAATAC 3186
 LBC-ori AGAAGGGGTTGGCAAGTGTCTATGCCATACAAAGAACAGAAGTATTTACAGTCCAGAGGC 3218
 LBclus4 AGAAGGGGTTGGCAAGTGTATGTCATATAAAGAACAAAAATATTTACATCAAGGCGAC 3218
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CTTCTATTGAAGCGTATGTCTAGTACAAAGTATGAATGGGGAAAAGTCAGGGCTTTATATG
 LBCbarr2 3246
 LBC-ori CGGAAATACACGCTTACACTTCAACGAAATACGAGTGGGGAAAAGTGAGGGCACTATATG 3278
 LBclus4 CAGAAATACATGCTTACACTTCCACAAAATATGAGTGGGGAAAAGTGAGAGCGTTGTACG 3278
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Highly conserved RdRp domain TTATTAATTTTGAAGATACT
 LBCbarr2 GATGTGATTTTACGAGTCATGTTAATGCAGACTTTGGAATTAATTTTGAAGATACT 3306
 LBC-ori GGTGTGATTTTTCATCACAATACATGGCTGATTTTGGATTGTTACATGCGAGGATACAT 3338
 LBclus4 GGTGTGACTTTTTCATCACAATACATGGCTGATTTTGGGCTGTTACAGTGTGAGGATACAT 3338
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Saccharomycopsis fibuligera chromosome B6 (89%)
 TTTCTTCACTATATA CTGAAGGGGCTCTCAAAACACTTTTGA

LBCbarr2 TCCCTCAGCTTTATATCTTACTGGGCCACAAGCTACTGAGGGGTACGTAAAAACACTTTTAA 3366
 LBC-ori TCCCGGGCTTTGTACCAACAGGGTCTTACGCCAATGAGGATTATGTCAGGACCAGAATTG 3398
 LBclus4 TCCCGGATTTGTACCAACAGGGGTCATATGCTAACGAGGACTATGTCAGGACTAGGATAG 3398

Sus scrofa chromosome 7 (85%)
 AAAGAGCTAAATA
 LBCbarr2 AAACAGCTAAATATAATGTGCCTTTCTGTTATGACTATGATGACTTCAACAGTCAGCATT 3426
 LBC-ori CTGGGACTCACTCATTTGATCCCTTTCTGTTACGATTTTCGATGATTTCAACAGCCAACATT 3458
 LBclus4 CAGGGACACACTCGTTGATTCCTTTCTGTTATGACTTTGATGATTTTAATAGTCAACACT 3458
 *
 LBCbarr2 CAAAGTCAAGTATGCAAGCAGTGATAGACGCTTGGATAAATACATATTTTCGATGACCTGA 3486
 LBC-ori CAAAGGAAGCCATGCAAGCAGTGATGATGCAATGGATATCTGTCTATCAGGATAAGTTAA 3518
 LBclus4 CAAAGGAAGCTATGCAAGCAGTTATCGATGCAATGGATATCTGTTTACCACGATAAGTTAA 3518

 LBCbarr2 CTGAAGACCAGATTGCCTCAGCCCTATGGACTAGAGAAAAGTGTGGTGAAAATGTTTGTGA 3546
 LBC-ori CAGATGACCAGATAGAGGGCGGCAAGTGGACACGAACTCGGTAGATAGAATGGTCGCTC 3578
 LBclus4 CAGATGATCAAGTAGAAGCAGCAAGTGGACAAGAACTCAGTAGATAGAATGATCGCAC 3578
 *
 LBCbarr2 ATGATGTAAAGAACAGTGTGATATGAAGCCATGGGAACCTCTGTTTAGCGGATGGAGGC 3606
 LBC-ori ACCAACCTAACACTGGTGAGACTTATGATGTTAAAGGGACACTGTTTAGTGGCTGGCGAT 3638
 LBclus4 ACCAAAACGAACACCGGCGAGACTTATGATGTCAAAGGGACACTATTTAGTGGCTGGCGAT 3638
 *
 LBCbarr2 TGACAACCTTTTATAAACACCGCTCTTAATTATGCATATCTTGCTAAGGCAGGGATAAATA 3666
 LBC-ori TAACACACTTTTCAATACGGCGTTGAACCTATTGCTACCTGGCTAATGCAGGTATAAACT 3698
 LBclus4 TAACACACTTTTATCAACACAGCATTAACCTATTGCTACTTGCCCAATGCAGGTATAAACT 3698
 *
 LBCbarr2 AATTAACCAATATAAGTATCCATAATGGTGATGATGCTATGCAGGGACGAGAAAATTGA 3726
 LBC-ori CACTAGTGCCAACGAGTCTCCATAATGGTGATGATGTTTTGCAGGGATAAGGACAATAG 3758
 LBclus4 CACTAGTACCAACGAGCCTCCACAAACGGTGATGATGCTTTGCAGGTATAAGGACGATAG 3758
 *
 LBCbarr2 AAGATATTGCTAGGCTTTTGAAGAATAGCAAGCAGATGGGAATACGTGCCAATACCAGA 3786
 LBC-ori CTGACGGTATTTCTTTGATCAAAAACGCCGACGCCAGGGAGTTCGCGCTAATACAACTA 3818
 LBclus4 CTGACGGTATTTCTTAATCAGAAATGCGGCAGCTACTGGAGTACGTGCAATACGATTA 3818
 *
 LBCbarr2 AAATGAGCATTTGGTACTATCGCTGAGTTTTTACGTGTCGACATGAGGGCTGAAAAACCTA 3846
 LBC-ori AAATGAACATTTGGTACGATAGCAGAGTTTTTGAGAGTTGATATGCGTGCAAAAAATAGTA 3878
 LBclus4 AGATGAACATAGGAACAATAGCGGAATTTTGAGAGTTGATATGCGTGCAAAAGACAGTA 3878
 *
 LBCbarr2 CTAGTGCTCAGTACTTAACCTAGAGGGATATCTACTTTTCGTACATGGTAGGATAGAAAAGTG 3906
 LBC-ori CTGGCAGTCAGTATTTAACAAGAGGGATGCTACCTTCACGCACAGTAGGGTTGAGTCTG 3938
 LBclus4 CTGGTAGCCAATATTTGACAAGAGGGGTGCTACTTTTACACACAGTAGGGTCGAGTCAG 3938
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 LBCbarr2 AGGCTCCAGTCGGGTATAGGGCTATGGTTAGTGCTTATAAGACGCGATACGATGAAGTGG 3966
 LBC-ori ATGCACCACTGACATTTGCGCAATCTAGTATCTGCTTACAAAACAGATATGACGAGATT 3998
 LBclus4 ATGCCCCACTAACATTACGTAATCTAGTATCTGCATACAAGACCAGGTATGATGAGATCA 3998
 *
 LBCbarr2 TAGAAAGAGGAGGAAATGCGCAACGACTAAGGCATTTGTATCGTAAACAACTATTTTTCG 4026
 LBC-ori TAGCTCGTGGCGCAAGCATCGATAACATGAAGCCACTCTATCGTAAGCAATATTTTTCG 4058
 LBclus4 TAGCTCGTGGTGCTAACGTTGATGATATGAACCACTTTATCGGAAACAATTATTTTTCG 4058

 LBCbarr2 CTCGTAGAAAGTTTGATGTGTCTGAAGAAATGCAAGAAAAATGTTTAAAGACGCACGTGC 4086
 LBC-ori CTAGAAAGTTGTTCAATGTCGAGAAGGACATTGTTGACAATCTGATAACGATGGACATAT 4118
 LBclus4 CTCGCAAGTTATTCATGTCGAGAAGGGTATAATTGATAATTGATAACGATGGACATAT 4118
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 LBCbarr2 AAGCTGGCGGTCTATCAGTCAATGGTAAGATAGGAACTACACATTGGAAGATGACAGCC 4146
 LBC-ori CATGTGGCGGTTTGCAAGAAAAGGGTAGGGTATCAGAGATGGTGTACAGGAGGTTGACA 4178
 LBclus4 CATGTGGTGGTTTGCAAGATAAAGGTAAGGTGTCAGAAGTGGTGTACAGGAAGTTGATA 4178
 *
 LBCbarr2 TTGCATACGCAGATATTGACGTGAATGAAATAAGC-----AGCTTATTACAGCCTGGAG 4200
 LBC-ori TTGAGAATATAGATAGTTATAGGAAGACAAGGATGATCGCCAACTGATTGACAAGGGGG 4238

LBClus4 TTGAAATATAGACAGTTATAAGAAGACTAGGATGATCGCAAACTGATCGACAAGGGGG 4238
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 Stem-loop for packaging $\Delta G = -7.1$ kJ/mol
 LBCbarr2 TTAAGGACTACGTGACTAGTTTGAAGTCTTTGTATCCGGAATACGGGAATTTATAACCG 4260
 LBC-ori TTGGCGATTACTGCATTCTGAAACTAACTTTCCGAGATAGCTGATGCTATCACAA 4298
 LBClus4 TTGGTGATTACACAGCATTCTTAAAACTAACTTCTCCGAAATAGCTGATGCTATCACAA 4298
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 LBCbarr2 AAAAGACAGTGAGAAGGACACTTATGAAAGCCTTCAACATAAAATAAAACACGATATGTA 4320
 LBC-ori GAGAGACACGTGTAGAGTCAGTGACCAAGGCTTATAATGTTAAGAAGAAAACGGTCGTAC 4358
 LBClus4 AGAAACATGTTGTAGAGTCATTGACCAAGGCTACAATGTCAAGAAGAAAACGGTCAGAA 4358
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 LBCbarr2 TCAACCAGCCAGTAGCAAGGCGATATATAATCAGATAGCACTAAGAGGTGCATGGAATG 4380
 LBC-ori GCGCGTTTAGGGACCTAAGCGCAGCATATCATGAAAGAGCGGTGAGACATGCTTGGAAGG 4418
 LBClus4 GCGCGTTTAGGGACCTAAGCGCAGCATATCATGAGAGAGCAGTTAGACATGCTTGGAAGA 4418
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 Stem-loop for packaging ($\Delta G = -52.3$ kJ/mol)
 LBCbarr2 ATGACTCTAATTTTCAAGATATTTAACAGAGTTAGACAGGGTGTGAGTAACGTGATAGGCG 4440
 LBC-ori GGATGAGTGGACTACACATAGTCAACAGGATTGATGGGAGTGAGCAACTTAGTAATGG 4478
 LBClus4 GGATGAGCGGACTACATATAGTTAACAGGGTTCGTATGGGCGTAAGCAACTTAGTAATGG 4478
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 LBCbarr2 TATTAGGTAACTGTCCAATGCGCATGCAAAAGTATTAAGCGAAACAAA TGA CCCTATCA 4500
 LBC-ori TTGTTAGCAAAATCAATCTGCAAAAGCTAATGTGCTAGCCAAATCAGGAGATCCTACAA 4538
 LBClus4 TTGTTAGCAAAATCAATCTGCGAAAGCTAATGTGTTAGCCAAATCAGGGGATCCACCA 4538
 * * * * * * * * * * * * * * * * * * *
 Stop of LBCbarr2 Gag-Pol
 LBCbarr2 AATGGTTGTCTATATATATAACATAGATGTAATACCAAGAAAGTTGTGACCTATATGACA 4560
 LBC-ori AATGGCTTGCAAGTCTTACAT TGA TATACAGGCAACCACATAAGACCTGAGAACAAAGAGT 4598
 LBClus4 AATGGCTTGCTGCTCTTACATGA TATACAGGCAACAACATAAGACCTGAGAACAAAGAGT 4598

 Stop of LBC-ori and LBClus4 Gag-Pol
 LBCbarr2 ACGGC----- 4565
 LBC-ori ACATACGATACTACGCA 4615
 LBClus4 ACATACGATACTACGCC 4615
 **
 Stem-loop for replication ($\Delta G = -13.8$ kJ/mol)

Stem-loops for replication in LBC-ori ($\Delta G = -7.5$ kJ/mol and $\Delta G = -2.9$ kJ/mol, respectively)

Figure S1. Multiple sequence alignment between ScV-LBC1-original, ScV-LBClus4, and TdV-LBCbarr2 (+) strand nucleotide sequences (cDNA). 5'GAA(A/T)TT conserved motif (5' conserved), translation initiation (start of Gag and Gag-Pol, or internal possible start ATG in Pol ORF of LBC1-original, LBClus4 and LBCbarr2), termination codons (stop of Gag and stop of Gag-Pol), ribosome frameshifting site (-1 frameshift site), frameshifting associated sequence (stem loop for frameshift), packaging signal (stem loop for packaging), and replication signal (stem loop for replication) are indicated, shaded and/or underlined in the nucleotide sequence. The highly conserved RdRp domain located in the central third of Pol is also underlined. Ω , ribosomal frameshift. Asterisks (*) indicates identical nucleotide positions. Sequence stretches of V-LBC genomes sharing high local identity with some mitochondrial or genomic sequences of several organisms are brown shaded, the sequences of other organisms are shown above each homologous stretch of LBC genome, and each percentage of identity is in parenthesis.