

Supplementary Materials

1.1 Supplementary Figures

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LBbarr2 GAAATTAGCTGTAGCCAATCGATTGCCATGTTCTCAACTCTTAACAATTTACTACCCGAT 60
LBC-ori GAAATTTTC----GGTGAACCGGAATTATGTCGTCTCTGTTAAATTCATTACTACCAGAA 56
LBclus4 GAAATTTTC----AGTGAACCGGAATTATGTCGTCTCTGTTAAATTCATTATTACCAGAA 56
      *** ** * * * * * * * * * *
5' conserved
LBbarr2 ACTTTAAACCCCTCGTAAGAATTTCAAACCTACTCACCATAGAATTAAATATGGTATGAAT 120
LBC-ori TATTTTAAACCTAAACCTAATTTGAATATCAACTCTTCTAGGGTCCAATATGGCTTTAAT 116
LBclus4 TATTTTAAACCCAAACAAATTTGAATATCAACTCCTCTAGGATCCAATATGGTTTAAAT 116
      *** ** * * * * * * * * * *

LBbarr2 GCCAACATCAATTTTCGATGTTTCTGATGACTTTGGGAAATATGAAGGTAATAGACCGGGT 180
LBC-ori GCTCGCATTTGATATGCAGTATGAAGACGATAGTGGGACTAGAAAAGGCTCAAGACCCAAT 176
LBclus4 GCTCGCATTTGATATGCAGTATGAAGACGATAGTGGGACTAGAAAAGGCTCAAGGCCCAAT 176
      ** *** ** * * * * * * * * * *

LBbarr2 GCTTTTATTGGAAATGAAGTATCTCTTTATGGTAATTACAATTTCTTATATCACGGATGAC 240
LBC-ori GCATTTATGTCTAACACAGTTGCTTTTATAGGAACTATGAAGGTATTATTGTTGATGAC 236
LBclus4 GCCTTTATGTCTAATACGTTGCTTTTATTGGAACTATGAAGGTGTCATCGTTGATGAC 236
      ** * * * * * * * * * *

LBbarr2 GTGCCAATCTATGATGGTATGCGGTCTGATGTGATCACTCCTGAAGGAGAGTTTACGCCAT 300
LBC-ori ATTCGATATTTGGATGGTCTTAGGGCCGACATTTTGATACTCATGGTGACTTAGACATG 296
LBclus4 ATCCGATATTTGGATGGCTTAGAGCTGACATTTTGATACTCATGGTGATTTAGACATG 296
      * * * * * * * * * *

LBbarr2 GAATTAGCTGAGCAAGTGTTAAGTAAAGCGACATCGGACCGAGCATCCGCTCAGAAGATC 360
LBC-ori GGCCTCGTTGAGGATGCATTGTCTAAGAGTACCATGATTAGAAGGAATGTACCAACTTAT 356
LBclus4 GGCCCTCGTAGAGGATGCATTGTCCAAAAGTACTATGATTAGAAGGAATGTACCAACTTAT 356
      * * * * * * * * * *

LBbarr2 ACGCAATACTTGGCATACAATGGAGGTATGCGCAATTGTGTATCTATATTGTATAACTTA 420
LBC-ori ACTGCTTACGCGAGTGAATTACTGTATAAGAGAAACCTTACATCTCTATTTTACAATATG 416
LBclus4 ACTGCTTACGCGAGTGAATTATTGTATAAGAGAACTTAACATCTCTGTTTACAATATG 416
      ** *** * * * * * * * * * *

LBbarr2 CTCCGTATGTATGTATGAATGAGTTTGGCGAGGTGGTCTATGACCCAAACGAGATATTC 480
LBC-ori CTCCGTTTATACTACATTAATAAATGGGGCAGTATTAAGTATGAAAAAGATGCCATCTTT 476
LBclus4 CTCCGTTTATACTACATTAATAAATGGGGTAGTATTAAGTATGAAAAAGATGCCATTTT 476
      ** * * * * * * * * * *

LBbarr2 TACGACAATGGACATGTGTGTATTAATAATCATCAGATGTTTCCAAAACATCTAGAGAAG 540
LBC-ori TATGATAATGGCCAGCCTGTCTTTTAAACAGGCAATTGTTTCCAAAGTCTCGTGATGCT 536
LBclus4 TATGATAATGGCCAGCCTGTCTTTTAAACAGGCAATTGTTTCCGAAGTCTCGTGATGCT 536
      ** * * * * * * * * * *

LBbarr2 AAGTCATTAGCTAAGGCTGTT---GAGTACACTCCTGCTATGATCGAAGATGCTAGCACC 597
LBC-ori TCTTTGGAATCAAGCCTCTCTTTGCGCTGAGGCTGAAATTGCAATGCTTGATCCTGGCCTG 596
LBclus4 TCTTTGGAATCAAGCCTCTCTTTACCTGAGGCAGAAATTGCAATGCTTGATCCTGGATTG 596
      * * * * * * * * * *

LBbarr2 TTATGGCGCGAAGGTGACATACCTGAATGTCCTTCATTGATTTGGACAGGATTTATGCGT 657
LBC-ori GAAATTTCCAGAAGAGGATGTGCTGCG-----AATTTTATGGCACGGCAGAGTGTCA 647
LBclus4 GAAATTTCCAGAAGAGGATGTGCTGCG-----AATTTTATGGCATGGCAGAGTGTCA 647
      ** * * * * * * * * * *

LBbarr2 GATAAGCAAGCTACTATCGTTTACGGGCAGCAGGTGGATTTCATTACAGAGCACCTTTC 717
LBC-ori TCCAGAGCAACGTGTATCTTAGGGCAAGCTTGCTCAGAGTTGCGGCTCTGGCCCCCTTT 707
LBclus4 TCCAGAGCTACGTGTATCTTAGGGCAAGCCTGTCTGAATTTGCGCCTCTGGCCCCCTTT 707
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LBbarr2 GGAGTAGCTCATGAGTCAAAAAATCTTACTGAAAGATTAGGTATCATGGCAACTGGAGGA 777
LBC-ori TCGATTGCGCATTATTCACCACAATTGACGAGAAAACTATTGTCAATGCGCCCGCTGGG 767
LBclus4 TCAATTGCGCATTATTCACCACAATTGACAAGAAAACTATACGTCAATGCGCCCGCTGGG 767
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LBCbarr2 CTCTCTAATGTAGAAGATTATAACTATGGTCCTTCTGATATATTGTTTCGTCCTTAACAAG 837
 LBC-ori ATTGAGCCTA--GCTCCGGGCGGTATACTCACGAGGATGTAAAAGATGCGATTACGATC 824
 LBclus4 ATTGAGCCTA--GCTCCGGGCGGTATACTCACGAGGATGTAAAAATGCGATTACGATC 824
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 LBCbarr2 CTGGTGACAGATAACGGGCTTTTACTGACTTCACCTTACGCTTATCTAATGTTGTTACAA 897
 LBC-ori CTTGTGTCTGCAAACAGGCTTATACTGACTTTGAAGCAGCATACCTTGATGCTTGCTCAA 884
 LBclus4 CTTGTGTCTGCTAACCAGGCTTATACTGACTTTGAGGCAGCATACCTTGATGCTTGCTCAA 884
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 LBCbarr2 GTATTAGTGTCCTCTATACCAAGGTCTGCTGAAGCTGCAGCATGGTTCGTCGGTGTCCAG 957
 LBC-ori ACGTTGGTCTCACCTGTACCACGCACTGCCGAAGCAAGTGCATGGTTCATCAATGCTGGC 944
 LBclus4 ACATTGGTCTCACCTGTACCACGCAAGCCGAAGCTAGTGCATGGTTCATTAATGCTGGT 944
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 LBCbarr2 ACAGTGTCTTTACCTAGGTTGGTGACTGACACAGGAAACATACCACAGTTATATCAGGGG 1017
 LBC-ori ATGGTCAATATGCCAATTTGTGTCATGTGCAAATGGTTATTATCCAGCACTGACCAATGTC 1004
 LBclus4 ATTGTTAACATGCCTATCTTGTGTCATGTGCTAATGGCTACTACCCAGCCTTAACAAATGTT 1004
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 LBCbarr2 AAAGTCTATGCTAGGTTTAAATGACTGGAAGAGACTATGGCTAACTTCAGAGCATATCCT 1077
 LBC-ori AATCCTTACCACCGCTAGACACATGGAAAGATACGTTAAATCATTGGGTGGCTTATCCC 1064
 LBclus4 AATCCTTACCACCGGTTAGACACATGGAAAGACACTTTAAATCATTGGGTGTCTTACCCC 1064
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 LBCbarr2 AAGTCATGTTTATTGCATAGTATGTAGTGAATGAAGCTGTTTACGTTGAATGAACAAT 1137
 LBC-ori GACATGCTGTTTACCATTTCAGTGGCAATGATTGAGAGCTGCTATGTTGAACTCGGGAAT 1124
 LBclus4 GACATGTTATTTTACCATTTCGGTGGCAATGGTTGAGAGCTGTTATGTTGAACTGGGGAAT 1124
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 LBCbarr2 CTTAACAGAGTGAGTCCTTTTGTATGCAATTAATCGAGAAAATTTTGTGAGGTAGCTGTA 1197
 LBC-ori GTGGCTCGTGTGTGACACAGTGTATGCAATAAACAAATACACTTTCACTGAGCTATCAGTG 1184
 LBclus4 GTCGCACGTGTGTGACACAGTGTATTAATTAACAAGTATACCTTCACTGAGCTATCTGTG 1184
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 LBCbarr2 CAAGGGCAGCCTGTCACAATGGGCGGGATATTGAATGATCTGACTTTAGTGTGATGCGG 1257
 LBC-ori CAAGGACGGCTGTATGAATCGAGGAATATTGTAGATCTGACACTTGTGGCAATGCGT 1244
 LBclus4 CAAGGCCGGCTGTATGAACCGAGGGATTATTGTTGACTTGACACTTGTAGCAATGCGT 1244
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 LBCbarr2 TATTCTAAGGAATTTGCACTGGCATATCCTGTGTCCACAGGACTTACAAGGACTAACATT 1317
 LBC-ori ACTGGTAGGAGATCTCACTACCTTACCCGGTCAGCTGTGGCCTGACCCGTACAGACGCG 1304
 LBclus4 ACTGGTAGAGATCTCACTACCTTACCCAGTTAGTTGTGGTTTGACCCGTACAGACGCA 1304
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 LBCbarr2 ATGGCACAAGAAATAGCTCTTGAGGTACCAATAACAGTAAAAGACCTAGATGCACCTAAA 1377
 LBC-ori TTATTGCAAGGTACTGAGATTACGTTCCAGTTGTTGTCAAAGATATCGACATGCCCCAG 1364
 LBclus4 TTATTGCAAGGTACGGAGATTCTGTTCCAGTTGTCGTCAAAGACATGGACATGCCTCAG 1364
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 LBCbarr2 TATTACAACATTGCAGAACCTATTATAACCGCAAATCAACATGCAACACTCATTGTTACT 1437
 LBC-ori TATTACAACGCGATTGATAAGGATGTTATTGAGGGGCGAGAACTGTGATTAAAGTGAAA 1424
 LBclus4 TATTATAATGCAATCGATAAGGATGTTATTGAAGGGCAAGAACTGTAATAAAGTGAAG 1424
 ***** ** * * * * * * * * * * * * * * * *

 LBCbarr2 AATATGACGGCACCTTTGTATCCAGTAATGTCTTACGGGATTAATACTGATGACTATTAT 1497
 LBC-ori CAGCTGCCACCAGCATGTATCCAATTTATACTTACGGGATCAACACTACTGAATTCTAT 1484
 LBclus4 CAAGTGCCACCAGCAATGTATCCGATTTATACTTATGGTATCAACACTACAGAGTTTAC 1484
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 LBCbarr2 TGTAACGATACGAACATCAGTATCAAATTTA--AGGCACCTGTGACTGCAAGTGGGATA 1554
 LBC-ori TCTGACCATTTTGAAGACCAGGTACAAGTTGAAATGGCACCAATCGATAATGGAAAAGCA 1544
 LBclus4 TCCGACCATTTTGAAGACCAGGTACAAGTAGAAATGGCTCCTATCGATAATGGGAAGGCA 1544
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 LBCbarr2 TCTTTTACAGAAGCAGAAAATTTCTCAAAGTTTATGAACGTTATGCGTATGTGTGGGTAT 1614
 LBC-ori GTTTTAAACGATGCAAGAAAGTTTCGAAATTTATGTCCATAATGCGCATGATGGGGAAT 1604
 LBclus4 GTCTTTAATGATGCTCGAAAATTTCTCTAAATTCATGTCTATAATGCGCATGATGGGGAAT 1604
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 LBCbarr2 AACGTTGAGGCCAGAGAGATGTTTTCAGGCAAGACTGTCATTAACCTGGGCAGATAATGCT 1674
 LBC-ori GATGTTACTGCTACTGATTTAGTTACAGGTAGAAAAGTGTGCAATTGGGCCGACAACCTCA 1664
 LBclus4 GATGTTACGCAACTGATTTAGTAACAGGTAGAAAGGTGTGCAATTGGGCCGACAACCTCA 1664

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LBCbarr2 AGTGGAAAGATTTTTATATACAGATGCTCAAGTTGGTGAGGATATACATTATCATGTACCT 1734
 LBC-ori TCAGGGCGTTTCTTGTACACGGATGTGAAGTATGAAGGACAAACTGCCTTTTGGTTGAT 1724
 LBclus4 TCAGGGCGTTTCTTATACCTCAGATGTCAAGTATGAAGGCCAAACTGCTTTTGGTTGAT 1724
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LBCbarr2 TACGCCAACATTTCATAGGCGGAGTAATTCATGGTTAAACGTGATAACCTTTAGAGGTGAA 1794
 LBC-ori ATGGATACTGTCAAGGCGAGAGACCACTGTTGGGTGTCAATTGTTGATCCTAATGGTACA 1784
 LBclus4 ATGGACACTATTAAGGCTAGAGACCATTGCTGGGTGTCAATTGTGGATCCTAATGGCACG 1784
 *

LBCbarr2 ACAGCCTTCAATGCGAACATCACAGCTGTGAATTTTAAATGTTCAACGGCCCATCTGAA 1854
 LBC-ori ATGAACTTGTTCATATAAGATGACCAATTTTAGAGCAGCAATGTTTCTAGAAACAAGCCC 1844
 LBclus4 ATGAGCTTGTTCATATAAGATGACAAATTTAGGGCAGCAATGTTTCAAGAAACAACCT 1844
 *

LBCbarr2 GTACTAATGACAGGGCCTCGAGTTATGCCAGTACAGATGAATGACTTCGTAGACAAGGCA 1914
 LBC-ori TTGTATATGACAGGGGGGTGAGTACAGGACCATAGCTACTGGCAATTCGAGATGCTGCT 1904
 LBclus4 CTATACATGACAGGTGGATCAGTACGACTATAGCTACTGTTAACTACCGGTGATGCCGCT 1904
 *

LBCbarr2 ATTGAAATTGCTTCTCGTACTGACACGATTAATACTTACCTCTACGAAAACTATGCTG 1974
 LBC-ori GAAAGATTACGTGCAATGGATGAAACGCTCAGATTAATACTTTAAGATTACTGAGAAG 1964
 LBclus4 GAGAGGTTGCGTGCATGGACGAAACGTTGAGGTTAAAGCCTTTAAGATTACTGAGAAG 1964
 *

LBCbarr2 CCGGATTTTCGATTCTCAGGTATCAGTTCCTCGGGTGTGTCGGGGATGGGGAATACTGTC 2034
 LBC-ori TTGGATTTTCGTGTAGCAGCTTACGCGATACCAAGTTTGTGCGGCAGCAATATGCCATCC 2024
 LBclus4 TTGGATTTTCGTGTAGCAGCTTATGCGATACCAAGTCTGTGCGGCAGCAATATGCCATCC 2024

 -1 Frame-shift site *Stem-loop for frame-shift ($\Delta G = -21.9$ kJ/mol in LBCbarr2, $\Delta G = -35.1$ kJ/mol in LBC-ori)*

LBCbarr2 TTGCCACGGGAGAGCACACAACAGTTTGGCCAGGAAGAACAGAGCTAGTGAATCCAGAG 2094
 LBC-ori TTACACCATCAGGAACAACATACAGATATCAGAAGTGGACGCGGAACCAATCAATCCTATA 2084
 LBclus4 TCACACCATCAGGAACAACATACAGATATCAGAAGCGGACGCGGAGCCGATCAATCCTGTG 2084
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LBCbarr2 GCGAGAGATATGTCAATCCAGGATGTAGAG **TAG**-----TACCGACATATCTA 2141
 LBC-ori GGAGAGGACGAACCTCCACCGGATATAGAA **TAG**GTGTCGAAGACGATGAGGACTTAGATA 2144
 LBclus4 GGAGAGGACGAACCTCCACCGGATGTAGAG **TAG**GTGTTGAAGATGATGAAGACTTAGATA 2144
 *

Stop of Gap LBC and LBCbarr

LBCbarr2 A-----CAATAGAC-----GGG---GAGATGACGACAACGC 2169
 LBC-ori TTGGTACGGTCAAATACATTGTGCCATTGTATTGAACGGTGATAATGTGGCACAACCT 2204
 LBclus4 TTGGTACGGTCAAATACATTGTGCCATTGTATTGAACGGTGATAATGTGGCACAACCT 2204
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LBCbarr2 CAGAGGAAGCTGACAAAGTGCT---TCTGGCCATGTATTATCAAACCAGAAAGTGATTA 2226
 LBC-ori GTTTAGAAGCAACACAGTGCTTATCAAAGCTTGTAGTATTGCGAACCGGATTGTAGATG 2264
 LBclus4 GTTTAGAAGCAACACATGTACTTATTAAGCTTGTAGTGTGCAAACCGGATTGTAGATG 2264
 ***** * * * * * * * * * * * * * * * *

LBCbarr2 AGACTAAGGCAGGATCTTTCACTCAGACTGGATTATCTAAGCAGATGATAGTTTATAATG 2286
 LBC-ori ACGGAGAGGGTCACTGTTTACACAGCAAGGGCTGGCGCAGCAGTGGATCTTCCATAGGG 2324
 LBclus4 ATGGAGAGGGTCACTGCTTACACAGCAAGGGCTAGCACAGCAGTGGATCTTCCATAGGG 2324
 *

LBCbarr2 GGATGACAGTTAATACCGAGCTCATCAGAATTGGGGATGTCAATTGTTATTATGTACGGT 2346
 LBC-ori GGGAGATGATATTTGTGAAGGCGGTACGCATTGGTCAACTCAATGCATATTATGTAGACT 2384
 LBclus4 GGGAGATGATATTTGTGAAGGCGGTACGCATTGGCCAGCTCAATGCATACTATGTAGACT 2384
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LBCbarr2 TGAAGTTTTGTGATGCAGCATCAAAGAAATTACACGTCAAGCAGGAGCAACGATGTGTG 2406
 LBC-ori ATAAGAACGTCACAAATATAGTCTTAAACCGCTGCTCAAGTAGGAGCGACGATATCAA 2444
 LBclus4 ATAAGAACGTCAACAATTACAGTCTTAAACCTGCTGCTCAAGTGGGAGCGACGATATCAA 2444
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LBCbarr2 GTAACCTCAGACACTTGTTTGCGAACTCAACTGGTACAGTATACGATTGGCTGGACCGGG 2466
 LBC-ori ATAACCTACGCCACGGATTGTTGACAAATCAACAAGACGCATACACGCGCTTGGTTGCCA 2504
 LBclus4 ACAACTTACGTATGGATTGCTTGAACACAGCAAGACGCATACACGCGCTTGGTTGCCA 2504
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LBCbarr2 ACAAACCGTATTAAGAATGTACGACAGGCTTGCTAGTTACAAGTATGACTACAATATAG 2526

LBC-ori ACTACTCTG--ATACGCGGAAGTGGATACGTGACAATTTTACATATAATTATAAT--A 2558
 LBclus4 ATTACTATG--ATACACGGAAGTGGATACGTGACAATTTTACATATAATTATAAT--A 2558
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LBCbarr2 CTGATAAAATAACAGAAAAATAAGTCAGTTTCATCATGTACACGTGAGGCTGAAGGACT 2586
 LBC-ori TGGAGAAAGAAAAGTATAGGATAACCCAAATACCACCATACACATGTGAGGTTGAAAGATT 2618
 LBclus4 TGGAGAAAGAAAATATAAGATAACTCAATATCACCACACACACGTTAGATTGAAAGATT 2618
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LBCbarr2 TATATGCTAATAAGGATATTGTGACAGTAAACGGTCATGAAGCATATCTCGTGAACCTTAC 2646
 LBC-ori TGTTTCCATCCAGGAAAATAGTTAAACTAGAGGGATATGAAGCCTTGTTGGCAATGATGC 2678
 LBclus4 TGTTTCCATCTAGGAAAGTAGTCAAACCTAACAGGATACGAGGCCCTTACTGGCAATGATGT 2678
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LBCbarr2 TTGATAAGTACACAGACAAAGCTATTACACATGCTACTTTCATAACCTATCTAAGAGCAC 2706
 LBC-ori TAGACAGGTTTAAACAACATAGAGTCAACACATGTAACCTTCTTCACATATTAAAGAGCAC 2738
 LBclus4 TAGATAGGTTCAACAATATAGAGTCAACACATGTACCTTTTTCACATACTTGAGGGCAT 2738
 *

LBCbarr2 TGCCTGTTAGGGAAGCAAGGCTCTTCATAAAATTAGTCATTAAGTATGGTAGCATAGACC 2766
 LBC-ori TACCTGACCGTGAAAAAGAAGTCTTTATTAGCTTAGTCTTAACTATAATGGCCTTGGCA 2798
 LBclus4 TGCCTGATCAAGAGAGGGAATCTTCATTAGCTTAATTTTGAACATAACCGGCTTGGTA 2798
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LBCbarr2 AAGAATGGTTAAAAGAAGAAGGGACTGTAGCAAAGCAAATACAGGGCAGCACTGACTTTG 2826
 LBC-ori GAGAGTGGTTGAAGTCTGAAGGTGTTAGGGCTAAACAGCACAAGGTAAGTGTGAAATACG 2858
 LBclus4 GAGAGTGGTTAAAGTCAGAAGGTGTTAGGGCAAAGCAAGCGCAAGGTAAGTGTGAAAGTATG 2858
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LBCbarr2 ATCTAAGCAAAATTTTGGAGCTTAATGTACTGCATAATCGGGTTGAAACTACAGTTGATT 2886
 LBC-ori ATATGAGTAAACTATTTGAACTGAATGTACTAGAGAACGGAGTTGACGAAGAAGTTGACT 2918
 LBclus4 ATATGAGTAAATTTTGGAGCTCAATGTGTTGAAAAATAGGGTTGACGAAGAGGTTGACT 2918
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LBCbarr2 GGAATGAAGAAAGAGAACATAGGACGCATCCTGATACAGTGAATATATCTTATCCAGATG 2946
 LBC-ori GGGAGAAAGAGAAACGCAACAGGTCAGATATCAAGACTGTTAACATAAGTTATGCAAAAG 2978
 LBclus4 GGGAAAAAGAAAAAGCAAGACGACGAACATCAAGACTGTAGACATAAGTTATGCAAAAG 2978
 ** *

LBCbarr2 TCTATACTAAGTGCAGAGAATTGTTTGAATAGCAAAGCAGGAAGGAAAGTCACCTATTA 3006
 LBC-ori TTCTCGAACATTGTAGAGAGCTATTATCATGCGCAGGGCCGAAGGGAAACGGCCAATGA 3038
 LBclus4 TTCTTGAGCAGCTGTAGAGAATTTATCATGGCAAGGGCTGAAGGAAAGCGGCCAATGA 3038
 *

LBCbarr2 AGATGGACTGGAATAAGTACTGGATGCAGCGAGCCTCAATAATGCCATCTGGTGCAGTCC 3066
 LBC-ori GGATGAAATGGCAAGAGTACTGGAGGCAGAGAGCAGTTATCATGCCAGGTGGATCGGTCC 3098
 LBclus4 GGATGAAATGGCAGGAGTATGGAGGCAGAGAGCAGTTGTGATGCCAGGCGGTTTCAGTCC 3098
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LBCbarr2 ACTCACAACATAGTGAGCTTGACAAGTATGTGAGGAAATTACCTCGTGAAGTCAAAAACA 3126
 LBC-ori ACAGTCAACATCCAGTCGAACAGGACGTGATTAGAGTATTACCCAGAGAAATCAGAAGTA 3158
 LBclus4 ACAGTCAGATCCAGCCGAACAAGATGTGATTAGATATTACCCAGGGAAATTAAGAGTA 3158
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LBCbarr2 AGAAGGGGTTGGCTGCCTCGCTACCTAATATAGACCAGAGGTACTTTCTGAGTAAATAC 3186
 LBC-ori AGAAGGGGTTGGCAAGTGTGCATGCCATACAAAGAACAGAAGTATTTACGTCAGAGGCG 3218
 LBclus4 AGAAGGGGTTGGCAAGTGTATGTCATATAAAGAACAAAAATATTTACATCAAGCGCAG 3218
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LBCbarr2 CTTCTATTGAAGCGTATGTCTAGTACAAAGTATGAATGGGGAAAAGTCAGGGCTTTATATG 3246
 LBC-ori CGGAAATACACGCTTACACTTCAACGAAATACGAGTGGGGAAAAGTGAGGGCACTATATG 3278
 LBclus4 CAGAAATACATGCTTACACTTCCACAAAATATGAGTGGGGAAAAGTGAGAGCGTTGTACG 3278
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Highly conserved RdRp domain

LBCbarr2 GATGTGATTTCAGCAGTCATGTTAATGCAGACTTTGGATTATTAAATTGTGAAGATACCT 3306
 LBC-ori GGTGTGATTTTTCATCACATACAATGGCTGATTTTGGATTGTTACAATGCGAGGATACAT 3338
 LBclus4 GGTGTGACTTTTTCATCACACACGATGGCTGATTTTGGGCTGTACAGTGTGAGGATACAT 3338
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LBCbarr2 TCCCTCACTTTATACCTACTGGGCCACAAGCTACTGAGGGGTACGTAAAAACACTTTTAA 3366
 LBC-ori TCCCGGGCTTTGTACCAACAGGGTCTTACGCCAATGAGGATTATGTGAGGACAGAAATTG 3398
 LBclus4 TCCCGGATTTGTACCAACGGGGTCATATGCTAACGAGGACTATGTGAGGACTAGGATAG 3398
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LBclus4  TTGGTGATTACACAGCATTTCTTAAAACTAACTTCTCCGAAATAGCTGATGCTATCACAA 4298
**      **      *      *      *      *      *      *      *      *      *      *

LBCbarr2 AAAAGACAGTGAGAAGGACACTTATGAAAGCCTTCAACATAAATAAAAAACGATATGTA 4320
LBC-ori  GAGAGACACGTGTAGAGTCAGTGACCAAGGCTTATAATGTTAAGAAGAAAAACGTCGTAC 4358
LBclus4  AGAAACATGTTGTAGAGTCATTGACCAAGGCCTACAATGTCAAGAAGAAAACGGTCAGAA 4358
*      *      *      *      *      *      *      *      *      *      *      *

LBCbarr2 TCAAACCAGCCAGTAGCAAGGCGATATATAATCAGATAGCACTAAGAGGTGCATGGAATG 4380
LBC-ori  GCGCGTTTATGGGACCTAAGCGCAGCATATCATGAAAGAGCGGTGAGACATGCTTGGAAAG 4418
LBclus4  GCGCGTTTATGGGACCTAAGCGCAGCATATCATGAGAGAGCAGTTAGACATGCTTGGAAAG 4418
*      *      *      *      *      *      *      *      *      *      *      *
Stem-loop for packaging ( $\Delta G = -52.3$  kJ/mol)
LBCbarr2 ATGACTCTAATTTTCAAGATATTTAACAGAGTTAGACAGGGTGTGAGTAACGTGATAGGCG 4440
LBC-ori  GGATGAGTGGACTACACATAGTCAACAGGATTGCTATGGGAGTGAGCAACTTAGTAATGG 4478
LBclus4  GGATGAGCGGACTACATATAGTTAACAGGGTTCGTATGGGCGTAAGCAACTTAGTAATGG 4478
*      *      *      *      *      *      *      *      *      *      *      *

LBCbarr2 TATTAGGTAACTGTCCAATGCGCATGCAAAAGTATTAAGCGAAACAAATGA 4500
LBC-ori  TTGTTAGCAAAATCAATCCTGCAAAAGCTAATGTGCTAGCCAAATCAGGAGATCCTACAA 4538
LBclus4  TTGTTAGCAAAATCAATCCTGCGAAAGCTAATGTGTTAGCCAAATCAGGGGATCCCACCA 4538
*      *      *      *      *      *      *      *      *      *      *      *
Stop of LBCbarr2 Gag-Pol
LBCbarr2 AATGGTTGTCTATATATATAACATAGATGTAATACCAAGAAAGTTGTGACCTATATGACA 4560
LBC-ori  AATGGCTTGCAGTCCTTACATGATATACAGGCAACCACATAAGACCTGAGAACAAAGAGT 4598
LBclus4  AATGGCTTGTGCTCCTTACATGATATACAGGCAACAACATAAGACCTGAGAACAAAGAGT 4598
***** *      *      *      *      *      *      *      *      *      *      *
Stop of LBC-ori and LBclus4 Gag-Pol
LBCbarr2 ACGGC----- 4565
LBC-ori  ACATACGATACTACGCA 4615
LBclus4  ACATACGATACTACGCC 4615
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Stem-loop for replication ( $\Delta G = -13.8$  kJ/mol)

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Stem-loops for replication in LBV-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.


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LBCbarr2 AITHATFITYLRLALPVREARLFIKLVIKYGSIDQEWLKEEGTVAKQIQGSTDFDLSKIFE 940
LBC-ori  ESTHVTFFTYLRLALPDREKEVFISLVLYNGLGREWLKSEGVRKQAQGTVKYDMSKLF 952
LBClus4  ESTHVTFFTYLRLALPDQEREIFISLVLYNGLGREWLKSEGVRKQAQGTVKYDMSKLF 952
      **.*:***** :*  .:.*:**.******: .:.*:**.* ** *:.*:**.*
LBCbarr2 LNVLHNRVETTVDWNEEREHRTHPDTVNISYPDVYTKCRELFELAKQEGKSPIKMDWNKY 1000
LBC-ori  LNVLENGVDEEVDWEKEKRNRSDIKTVNISYAKVLEHCRELFIMARAEGKRPMMRWQ 1012
LBClus4  LNVLENRVDEEVDWEKEKRNRTNIKTVDISYAKVLEHCRELFIMARAEGKRPMMRWQ 1012
      ****.* : * : **.*:..:..:.. :*.*** .* :***** :* : ** *:.*:**.*
LBCbarr2 WMQRASIMPSGAVHSQHSSELDKYVRKLPREVKNKKGLAASLPNIDQRYFLSKIPSI EAYV 1060
LBC-ori  WRQRAVIMPGGSVHSQHPVEQDVIRVLPREIRSKKGVASVMPYKEQKYFTSRRPEI HAYT 1072
LBClus4  WRQRAVIMPGGSVHSQHPAEQDVIKILPREIKSKKGLASVMSYKEQKYFTSRRPEI HAYT 1072
      * ** :*.*** :***** :. : : *****:..***:* : : *:* ** : *.***.
      ▶—3—◀
LBCbarr2 STKYEWGKVRALYGCDFSSHVNADFGLLNCEDTFPHFIPTGPOATEGYVKTLLKTAKYNV 1120
LBC-ori  STKYEWGKVRALYGCDFSSHTMADFGLLOCEDTFPGFVPTGSYANEDYVRTRIAGTHSLI 1132
LBClus4  STKYEWGKVRALYGCDFSSHTMADFGLLOCEDTFPGFVPTGSYANEDYVRTRIAGTHSLI 1132
      *****:*****.* *****.*.***:* : : :
      ▶—A—◀
LBCbarr2 PFCYVDDFNSQHSKSSMOAVIDAWINTYFDDLTEDQIASALWTRESVGMFVNDVKNSV 1180
LBC-ori  PFCYVDDFNSOHSKEAMOQVIDAWISVYHDKLTDDQIEAAKWTRNSVDRMVAHOPNTGE 1192
LBClus4  PFCYVDDFNSQHSKSSMOAVIDAWISVYHDKLTDDQVEAAKWTRNSVDRMVAHQTNTGE 1192
      *****:*****.* *****.*.***:* : * **.*.***: : :
      ▶—B—◀ ▶C◀
LBCbarr2 RYEAMGTLFSGWRLTTFINTALNYAYLAKAGINKLTNISIHNDDVYAGTRNLKDIARLL 1240
LBC-ori  TYDVKGTLFSGWRLTTFINTALNYCYLANAGINSLVPTSLHNGDDVFAGIRTIADGISLI 1252
LBClus4  TYDVKGTLFSGWRLTTFINTALNYCYLANAGINSLVPTSLHNGDDVFAGIRTIADGISLI 1252
      *:. *****:*****.* *****.*. *****.*.***:* : * **.*.
      ▶D◀
LBCbarr2 KNSKQMGIRANTTKMSIGTIAEFLRVDMRAEKPTSAQYLTRGISTFVHGRIESEAPVGYR 1300
LBC-ori  KNAATGVRANTTKMNIGTIAEFLRVDMRAKNSTGSQYLTRGIATFTHSRVESDAPLTLR 1312
LBClus4  RNAATGVRANTTKMNIGTIAEFLRVDMRAKDTGSQYLTRGVATFTHSRVESDAPLTLR 1312
      :* : *:* **.* *****:.. :. *****:*.***:* **.*.***:* :
LBCbarr2 AMVSAYKTRYDEVVERGGNAQRLRHLYRKQLFFARRKFDVSEEMQEKLKTHVQAGGLSV 1360
LBC-ori  NLVSAYKTRYDEILARGASIDNMKPLYRKQLFFARKLFNVEKDIVDNLITMDISCGGLQE 1372
LBClus4  NLVSAYKTRYDEIIARGANVDDMKPLYRKQLFFARKLFNVEKGIIDNLITMDISCGGLQD 1372
      :*****: **.* : : : *****: *:. : :*:.. :..***.
LBCbarr2 NGKIGNYTLLEDDSLAYAD--IDVNEISSLLQPGVKDYVTSLSKSLYPEIREFITEKTVRRT 1418
LBC-ori  KGRVSEMLVQEVDIENIDSYRKTRMIAKLIDKGVGDYTAFLKTNFSEIADAITRETRVES 1432
LBClus4  KGVSEVVLVQEVDIENIDSYKTRMIAKLIDKGVGDYTAFLKTNFSEIADAITKKHVVES 1432
      :*:. :*.***: : * .. **.*: **.*: **.*: **.*: **.*: **.*:
LBCbarr2 LMKAFNINKNTICIKPASSKAIYNQIALRGAWNDDSNFRIFNRVRQGVSNVIGVLGKLSN 1478
LBC-ori  VTKAYNVKKKTVVRFAFRDLAAYHERAVRHAWKMSGLHIVNRIRMGVSNLVMVSKINP 1492
LBClus4  LTKAYNVKKKTVRSAFRDLAAYHERAVRHAWKMSGLHIVNRVRMGVSNLVMVSKINP 1492
      : **.*:*.***: . .* *:. *:* **.* :. :*.***:* *****: *:.***.
LBCbarr2 AHAKVLSETNDPIKWLSIYIT 1499
LBC-ori  AKANVLAKSGDPTKWLAVLT- 1512
LBClus4  AKANVLAKSGDPTKWLAVLT- 1512
      *:.***:..** *****:

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Figure S2. Comparison of the amino acid sequences of Gag-Pol encoded by ScV-LBC1-original, ScV-LBClus4, and TdV-LBCbarr2. The separation between Gag and Pol domains is indicated (Gag ◀▶ Pol). The H156 residue required for 5' cap-snatching is black shaded. The four crucial residues for cap recognition (Tyr-152, Asn-154, Tyr-452 and Trp-545) are grey shaded. The highly conserved RdRp domain located in the central third of Pol is underlined, the five consensus motifs (3, A, B, C, and D) conserved in RNA-dependent RNA polymerases from Totiviruses are indicated above the sequence, and the conserved amino acids for each motif are grey shaded. Asterisks (*) indicate identical amino acids; colons (:) and single dots (.) indicate conserved and semi-conserved amino acids, respectively.

TdV-LBCbarr1-EX1180	100	94	52	52	52	52	52	52
TdV-LBCbarr2-EX1257	94	100	51	52	52	52	52	52
ScV-LBclus4-EX229	52	51	100	89	88	87	89	89
ScV-LBC2-S3920	52	52	89	100	93	94	94	94
ScV-LBC-original	52	52	88	93	100	95	95	95
ScV-LBC2-EX1125	52	52	89	94	95	100	100	100
ScV-LBclusA-EX1160	52	52	89	94	95	100	100	100
ScV-LBC1-EX231	52	52	89	94	95	100	100	100

Colors: *T. delbrueckii* cluster *S. cerevisiae* cluster

Figure S3. Percentage identity matrix for canonical V-LBC nucleotide sequences. Each value was rounded to the nearest whole number.

TdV-LBCbarr1-EX1180	100	99	64	66	66	66	66	66
TdV-LBCbarr2-EX1257	99	100	64	66	66	66	66	66
ScV-LBclus4-EX229	64	64	100	97	97	97	97	97
ScV-LBC2-S3920	66	65	97	100	98	98	98	98
ScV-LBC-original	65	65	97	98	100	99	99	99
ScV-LBclusA-EX1160	66	66	97	98	99	100	100	100
ScV-LBC1-EX231	66	66	97	98	99	100	100	100
ScV-LBC2-EX1125	66	66	97	98	99	100	100	100

Colors: *T. delbrueckii* cluster *S. cerevisiae* cluster

Figure S4. Percentage identity matrix for highly-conserved RdRp-domain amino-acid sequences. Each value was rounded to the nearest whole number.

TdV-LBCbarr1-EX1180	100	99	37	37	37	37	37	37
TdV-LBCbarr2-EX1257	99	100	37	37	37	37	37	37
ScV-LBclus4-EX229	37	37	100	98	97	97	97	97
ScV-LBC1-original	37	37	98	100	99	99	99	98
ScV-LBclusA-EX1160	37	37	97	99	100	100	100	98
ScV-LBC1-EX231	37	37	97	99	100	100	100	98
ScV-LBC2-EX1125	37	37	97	99	100	100	100	98
ScV-LBC2-S3920	37	37	97	98	98	98	98	100

Colors: *T. delbrueckii* cluster *S. cerevisiae* cluster

Figure S5. Percentage identity matrix for Gag amino-acid sequences of LBC viruses. Each value was rounded to the nearest whole number.