

Supplementary File S2

Sequences of the LINE-1 insertions in exon 4 of *RPI* fully covered by targeted adaptive nanopore sequencing from patients III.1 and III.2.

>Patient_III_1_sequence_1

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>Patient_III_2_sequence_1

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>Patient_III_2_sequence_2

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The fully covered LINE-1 insertions were aligned with MUSCLE multiple sequence alignment using Unipro UGENE (v.49.0).

III.1_1 GTGGGGTGTAAAGTCTCCCATTTAA---TGGGAGTCTAAGTCTCTTTGTAGGTCCTGAGGACTTG 70
 III.2_1 GTGGGGTGTAAAGTCTCCCATTTAAATGTGTGGGAGTCTAAGTCTCTTTGTAGGTCCTGAGGACTTG 70
 III.2_2 GT--GGTGTAAAGTCTCCCATTTAAATGTGTGGGAGTCTAAGTCTCTTTGTAGGTCCTGAGGACTTG 70
 ** *****

III.1_1 CTTTATGAATCTGGGTGCTCCTGTATTGGGTGCATAAATATTTAGGATAGTTAGCTCCTCTGTTGAATT 140
 III.2_1 CTTTATGAATCTGGGTGCTCCTGTATTGGGTGCATAAATATTTAGGATAGTTAGCTCCTCTGTTGAATT 140
 III.2_2 CTTTATGAATCTGGGTGCTCCTGTATTGGGTGCATAAATATTTAGGATAGTTAGCTCCTCTGTTGAATT 140

III.1_1 GATCCCTTTACCATTATGTAATGGCCTTCTTTGTCTCTTTTGATCTTTGTTGGTTTAAAGTCTGTTTTAT 210
 III.2_1 GATCCCTTTACCATTATGTAATGGCCTTCTTTGTCTCTTTTGATCTTTGTTGGTTTAAAGTCTGTTTTAT 210
 III.2_2 GATCCCTTTACCATTATGTAATGGCCTTCTTTGTCTCTTTTGATCTTTGTTGGTTTAAAGTCTGTTTTAT 210

III.1_1 CAGAGACTAGGATTGCAACCCCTGCCTTTTTTTGTTTTCCATTGGCTTGGTAGATCTTCCTCCATCCTTT 280
 III.2_1 CAGAGACTAGGATTGCAACCCCTGCCTTTTTTTGTTTTCCATTGGCTTGGTAGATCTTCCTCCATCCTTT 280
 III.2_2 CAGAGACTAGGATTGCAACCCCTGCCTTTTTTTGTTTTCCATTGGCTTGGTAGATCTTCCTCCATCCTTT 280

III.1_1 TATTTGAGCCTATGTGTCTCTGCACGTGAGATAAAT---GGAATACAGCACACTGATGGGTCTTGA 350
 III.2_1 TATTTGAGCCTATGTGTCTCTGCACGTGAGATGGGTTTCCTGAATACAGCACACTGATGGGTCTTGA 350
 III.2_2 TATTTGAGCCTATGTGTCTCTGCACGTGAGATGGGTTTCCTGAATACAGCACACTGATGGGTCTTGA 350
 ***** * *****

III.1_1 CTCTTTATCCAACCTGCCAGTCTGTCTTTTAAATGTCAGAATTTAGTCCATTTATATTTAAAGTTAATA 420
 III.2_1 CTCTTTATCCAACCTGCCAGTCTGTCTTTTAAATGTCAGAATTTAGTCCATTTATATTTAAAGTTAATA 420
 III.2_2 CTCTTTATCCAACCTGCCAGTCTGTCTTTTAAATGTCAGAATTTAGTCCATTTATATTTAAAGTTAATA 420

III.1_1 TTGTTATGTGTGAATTTGATCCTGTCATTATGATGTTAGCTGGTATTTTGTCTCATTAGTTGATGCAGTT 490
 III.2_1 TTGTTATGTGTGAATTTGATCCTGTCATTATGATGTTAGCTGGTATTTTGTCTCATTAGTTGATGCAGTT 490
 III.2_2 TTGTTATGTGTGAATTTGATCCTGTCATTATGATGTTAGCTGGTATTTTGTCTCATTAGTTGATGCAGTT 490

III.1_1 TCTTCCTAGTCTCGATGGTCTTTACATTTTGGCATGATTTTGCAGCGGCTGGTACCGGTTGTTCCTTTCC 560
 III.2_1 TCTTCCTAGTCTCGATGGTCTTTACATTTTGGCATGATTTTGCAGCGGCTGGTACCGGTTGTTCCTTTCC 560
 III.2_2 TCTTCCTAGTCTCGATGGTCTTTACATTTTGGCATGATTTTGCAGCGGCTGGTACCGGTTGTTCCTTTCC 560

III.1_1 ATGTTTAGCGCTTCCTTCAGGAGCTCTTTTAGGGCAGGCCTGGTGGTGACAAAATCTCTCAACATTTGCT 630
 III.2_1 ATGTTTAGCGCTTCCTTCAGGAGCTCTTTTAGGGCAGGCCTGGTGGTGACAAAATCTCTCAACATTTGCT 630
 III.2_2 ATGTTTAGCGCTTCCTTCAGGAGCTCTTTTAGGGCAGGCCTGGTGGTGACAAAATCTCTCAACATTTGCT 630

III.1_1 TGTCTATAAAGTATTTTATTTCTCCTTCACTTATGAAGCTTAGTTGGCTGGATATGAAATTCTGGGTTG 700
 III.2_1 TGTCTATAAAGTATTTTATTTCTCCTTCACTTATGAAGCTTAGTTGGCTGGATATGAAATTCTGGGTTG 700
 III.2_2 TGTCTATAAAGTATTTTATTTCTCCTTCACTTATGAAGCTTAGTTGGCTGGATATGAAATTCTGGGTTG 700

III.1_1 AAAATTCCTTTCTTTAAGAATGTTGAATATTGGCCCCACTCTCTCTGGCTTGTAGGGTTCTGCCGAG 770
 III.2_1 AAAATTCCTTTCTTTAAGAATGTTGAATATTGGTCCCACTCTCTCTGGCTTGTAGGGTTCTGCCGAG 770
 III.2_2 AAAATTCCTTTCTTTAAGAATGTTGAATATTGGCCCCACTCTCTCTGGCTTGTAGGGTTCTGCCGAG 770

III.1_1 AGATCCGCTGTTAGTCTGATGGGCTTTC---TGAGGGTAACCTTCCCTT--TGCTTGGCTGCCCTTAACA 840
 III.2_1 AGATCCGCTGTTAGTCTGATGGGCTTTCCTTTGAGGGTAACCCGACCTTTCTCTCTGGCTGCCCTTAACA 840
 III.2_2 AGATCCGCTGTTAGTCTGATGGGCTTTCCTTTGAGGGTAACCCGACCTTTCTCTCTGGCTGCCCTTAACA 840

III.1_1 TTTTTCCTTCATTTCAACTTTGGTGAATCTGACAATTATGTGTCTTGGAGTTGCTCTTCTCGAGGAGTA 910
 III.2_1 TTTTTCCTTCATTTCAACTTTGGTGAATCTGACAATTATGTGTCTTGGAGTTGCTCTTCTCGAGGAGTA 910
 III.2_2 TTTTTCCTTCATTTCAACTTTGGTGAATCTGACAATTATGTGTCTTGGAGTTGCTCTTCTCGAGGAGTA 910

III.1_1 TCTTTGTGGCGTTCTCTGTATTTCCCTGAATCTGAACGTTGGCCTGCCTTGCTAGATTGGGGAAGTTCTCC 980
 III.2_1 TCTTTGTGGCGTTCTCTGTATTTCCCTGAATCTGAACGTTGGCCTGCCTTGCTAGATTGGGGAAGTTCTCC 980
 III.2_2 TCTTTGTGGCGTTCTCTGTATTTCCCTGAATCTGAACGTTGGCCTGCCTTGCTAGATTGGGGAAGTTCTCC 980

III.1_1 TGGATAATATCCTGCAGAGTGTTCCTCAACTTGGTTCATTCTCCACATCACTTTCAGGTACACCAATCA 1050
 III.2_1 TGGATAATATCCTGCAGAGTGTTCCTCAACTTGGTTCATTCTCCACATCACTTTCAGGTACACCAATCA 1050
 III.2_2 TGGATAATATCCTGCAGAGTGTTCCTCAACTTGGTTCATTCTCCACATCACTTTCAGGTACACCAATCA 1050

III.1_1 GACGTAGATTTGGTCTTTTACATAGTCCCATATTTCTTGGAGGCTTTGCTCATTCTTTTTATTCTTTT 1120
 III.2_1 GACGTAGATTTGGTCTTTTACATAGTCCCATATTTCTTGGAGGCTTTGCTCATTCTTTTTATTCTTTT 1120
 III.2_2 GACGTAGATTTGGTCTTTTACATAGTCCCATATTTCTTGGAGGCTTTGCTCATTCTTTTTATTCTTTT 1120

III.1_1 TTCTCTAAACTTCCCTTCTCGCTTCATTTTCATTTTCATCTTCCATTGCTGATACCCTTCTTCCAGT 1190
 III.2_1 TTCTCTAAACTTCCCTTCTCGCTTCATTTTCATTTTCATCTTCCATTGCTGATACCCTTCTTCCAGT 1190
 III.2_2 TTCTCTAAACTTCCCTTCTCGCTTCATTTTCATTTTCATCTTCCATTGCTGATACCCTTCTTCCAGT 1190

III.1_1 TG----ATCGGCTCCTGAGGCTTGTGCATTCTTACGTAAGTTCTCGAGCCTTGGTTTTTCAGCTCCATCA 1260
 III.2_1 TGATCGCATCGGCTCCTGAGGCTTGTGCATTCTTACGTAAGTTCTCGAGCCTTGGTTTTTCAGCTCCATCA 1260
 III.2_2 TGATCGCATCGGCTCCTGAGGCTTGTGCATTCTTACGTAAGTTCTCGAGCCTTGGTTTTTCAGCTCCATCA 1260
 ** *****

III.1_1 GCTCCTTTAAGCACTTCTCTGTATTGGTTATTCTAGTTATACATTCTTCTAAATTTTTTTCAAAGTTTTT 1330
 III.2_1 GCTCCTTTAAGCACTTCTCTGTATTGGTTATTCTAGTTATACATTCTTCTAAATTTTTTTCAAAGTTTTT 1330
 III.2_2 GCTCCTTTAAGCACTTCTCTGTATTGGTTATTCTAGTTATACATTCTTCTAAATTTTTTTCAAAGTTTTT 1330

III.1_1 AACTTCTTTGCCTTTGGTTTGAATGTCCCTCCCGTAGCTCAGAGTAATTTGATCGTCTGAAGCCTTCTTCT 1400
 III.2_1 AACTTCTTTGCCTTTGGTTTGAATGTCCCTCCCGTAGCTCAGAGTAATTTGATCGTCTGAAGCCTTCTTCT 1400
 III.2_2 AACTTCTTTGCCTTTGGTTTGAATGTCCCTCCCGTAGCTCAGAGTAATTTGATCGTCTGAAGCCTTCTTCT 1400

III.1_1 CTCAGCTCATCAAAATCATTTCTCCATCCAGCTTTGTTCTGTTGCTGGTGAGGAACGCGTTCCTTTGGAG 1470
 III.2_1 CTCAGCTCATCAAAATCATTTCTCCATCCAGCTTTGTTCTGTTGCTGGTGAGGAACGCGTTCCTTTGGAG 1470
 III.2_2 CTCAGCTCATCAAAATCATTTCTCCATCCAGCTTTGTTCTGTTGCTGGTGAGGAACGCGTTCCTTTGGAG 1470

III.1_1 GAGGAGAGGCGCTCTGCGTTTTAGAGTTTCCAGTTTTTCTGTTCTGTTTTTTCCCATCTTTGTGGTTTT 1540
 III.2_1 GAGGAGAGGCGCTCTGCGTTTTAGAGTTTCCAGTTTTTCTGTTCTGTTTTTTCCCATCTTTGTGGTTTT 1540
 III.2_2 GAGGAGAGGCGCTCTGCGTTTTAGAGTTTCCAGTTTTTCTGTTCTGTTTTTTCCCATCTTTGTGGTTTT 1540

III.1_1 ATCTACTTTTGGTCTTTGATGATGGTGATGTACAGATGGGTTTTTGGTGTAGATGTCCTTTCTGGTTGTT 1610
 III.2_1 ATCTACTTTTGGTCTTTGATGATGGTGATGTACAGATGGGTTTTTGGTGTAGATGTCCTTTCTGGTTGTT 1610
 III.2_2 ATCTACTTTTGGTCTTTGATGATGGTGATGTACAGATGGGTTTTTGGTGTAGATGTCCTTTCTGGTTGTT 1610

III.1_1 AGTTTTCCTTCTAACAGACAGGA-CTTTTAACTCCACTGTCAACATTAGACAGATCAACGAGATAGAA 1680
 III.2_1 AGTTTTCCTTCTAACAGACAGGACCCCTTAAACACCCACTGTCAACATTAGACAGATCAACGAGACAGAA 1680
 III.2_2 AGTTTTCCTTCTAACAGACAGGACCCCTTAAACACCCACTGTCAACATTAGACAGATCAACGAGACAGAA 1680

III.1_1 AGTCAACAAGGATACCCAGGAATTGAACCTCAGCTCTGCACCAAGCAGACCTAATAGACATCTACAGAACT 1750
 III.2_1 AGTCAACAAGGATACCCAGGAATTGAACCTCAGCTCTGCACCAAGCAGACCTAATAGACATCTACAGAACT 1750
 III.2_2 AGTCAACAAGGATACCCAGGAATTGAACCTCAGCTCTGCACCAAGCAGACCTAATAGACATCTACAGAACT 1750

III.1_1 CTCCACCCCAAATCAACAGAATATACATTTTTTTTTCAGCACCACACCACCTATTCCAAAATTGACCACA 1820
 III.2_1 CTCCACCCCAAATCAACAGAATATACATTTTTTTTTCAGCACCACACCACCTATTCCAAAATTGACCACA 1820
 III.2_2 CTCCACCCCAAATCAACAGAATATACATTTTTTTTTCAGCACCACACCACCTATTCCAAAATTGACCACA 1820

III.1_1 TAGTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGAAATTATAACAACTATCTCTCAGACCA 1890
 III.2_1 TAGTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGAAATTATAACAACTATCTCTCAGACCA 1890
 III.2_2 TAGTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGAAATTATAACAACTATCTCTCAGACCA 1890

III.1_1 CAGTGCAATCAAACCTAGAACTCAGGATTAAGAATCTCACTCAAAGCCGCTCAACTACATGGAACCTGAAC 1960
 III.2_1 CAGTGCAATCAAACCTAGAACTCAGGATTAAGAATCTCACTCAAAGCCGCTCAACTACATGGAACCTGAAC 1960
 III.2_2 CAGTGCAATCAAACCTAGAACTCAGGATTAAGAATCTCACTCAAAGCCGCTCAACTACATGGAACCTGAAC 1960

III.1_1 AACCTGCTCCTGAATGACTACTGGGTACATAACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCA 2030
 III.2_1 AACCTGCTCCTGAATGACTACTGGGTACATAACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCA 2030
 III.2_2 AACCTGCTCCTGAATGACTACTGGGTACATAACGAAATGAAGGCAGAAATAAAGATGTTCTTTGAAACCA 2030

III.1_1 ACGAGAACAAGACACCACATACCAGAATCTCTGGGACGCATTCAAAGCAGTGTGTAGAGGGAAATTTAT 2100
 III.2_1 ACGAGAACAAGACACCACATACCAGAATCTCTGGGACGCATTCAAAGCAGTGTGTAGAGGGAAATTTAT 2100
 III.2_2 ACGAGAACAAGACACCACATACCAGAATCTCTGGGACGCATTCAAAGCAGTGTGTAGAGGGAAATTTAT 2100

III.1_1 AGCACTAAATGCCTAAGCAAGAAAGCAGGAAAGATCCAAAATTGACACCCCTAACATCACAATTTAAAAG 2170
 III.2_1 AGCACTAAATGCCTA--AAAGAGAAAGCAGGAAAGATCCAAAATTGACACCCCTAACATCACAATTTAAAAG 2170
 III.2_2 AGCACTAAATGCCTA--CAAGAGAAAGCAGGAAAGATCCAAAATTGACACCCCTAACATCACAATTTAAAAG 2170

III.1_1 AACTAGAAAAGCAAGAGCAAACACATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAAATCAGAGCAGA 2240
 III.2_1 AACTAGAAAAGCAAGAGCAAACACATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAAATCAGAGCAGA 2240
 III.2_2 AACTAGAAAAGCAAGAGCAAACACATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAAATCAGAGCAGA 2240

III.1_1 ACTGAAGGAAATAGAGACACAAAAACCCTTC--AAAAATCAATGAATCCAGGAGCTGGTTTTTTGAAAG 2310
 III.2_1 ACTGAAGGAAATAGAGACACAAAAACCCTTC--AAAAATCAATGAATCCAGGAGCTGGTTTTTTGAAAG 2310
 III.2_2 ACTGAAGGAAATAGAGACACAAAAACCCTTC--AAAAATCAATGAATCCAGGAGCTGGTTTTTTGAAAG 2310

III.1_1 GATCAA--AAAATTGATAGACCGCTAGCAAGACTAATAAAGAAAAAAGAGAGAAGAAATCAAATAGACACA 2380
 III.2_1 GATCAACAAAATTGATAGACCGCTAGCAAGACTAATAAAGAAAAAAGAGAGAAGAAATCAAATAGACACA 2380
 III.2_2 GATCAACAAAATTGATAGACCGCTAGCAAGACTAATAAAGAAAAAAGAGAGAAGAAATCAAATAGACACA 2380

III.1_1 ATAAAAAATGATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACA 2450
 III.2_1 ATAAAAAATGATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACA 2450
 III.2_2 ATAAAAAATGATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACA 2450

III.1_1 AACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATACATTCCTCGACACATACACTCTCCC 2520
 III.2_1 AACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATACATTCCTCGACACATACACTCTCCC 2520
 III.2_2 AACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATACATTCCTCGACACATACACTCTCCC 2520

III.1_1 AAGACTAAACCAGGAAGAAGTTGAATCTCTGAATCGATCAATAACAGGCTCTGAAATTGTGGCAATAATC 2590
 III.2_1 AAGACTAAACCAGGAAGAAGTTGAATCTCTGAATCGATCAATAACAGGCTCTGAAATTGTGGCAATAATC 2590
 III.2_2 AAGACTAAACCAGGAAGAAGTTGAATCTCTGAATCGATCAATAACAGGCTCTGAAATTGTGGCAATAATC 2590

III.1_1 AATAGTTTACCAACCAAAAAGAGTCCAGGACCAGATGGATTTCACAGCCGAATTCTACCAGAGGTACAAGG 2660
 III.2_1 AATAGTTTACCAACCAAAAAGAGTCCAGGACCAGATGGATTTCACAGCCGAATTCTACCAGAGGTACAAGG 2660
 III.2_2 AATAGTTTACCAACCAAAAAGAGTCCAGGACCAGATGGATTTCACAGCCGAATTCTACCAGAGGTACAAGG 2660

III.1_1 AGGAACTGGTACCATTCTCTGAAACTATTCCAATCAATAGAAAAAGAGGGAATCCTCCCTAACTCATT 2730
 III.2_1 AGGAACTGGTACCATTCTCTGAAACTATTCCAATCAATAGAAAAAGAGGGAATCCTCCCTAACTCATT 2730
 III.2_2 AGGAACTGGTACCATTCTCTGAAACTATTCCAATCAATAGAAAAAGAGGGAATCCTCCCTAACTCATT 2730

III.1_1 TTATGAGGCCAGCATCATTCTGATACCAAAGCCGGGCAGAGACACAACCAAAAAAGAGAATTTAGACCA 2800
 III.2_1 TTATGAGGCCAGCATCATTCTGATACCAAAGCCGGGCAGAGACACAACCAAAAAAGAGAATTTAGACCA 2800
 III.2_2 TTATGAGGCCAGCATCATTCTGATACCAAAGCCGGGCAGAGACACAACCAAAAAAGAGAATTTAGACCA 2800

III.1_1 ATATCCTTGATGAACATTGATGCAAAAAATCCTCAATAAAAATACTGGCAAACCGAATC---CAGCACATCA 2870
 III.2_1 ATATCCTTGATGAACATTGATGCAAAAAATCCTCAATAAAAATACTGGCAAACCGAATC---CAGCACATCA 2870
 III.2_2 ATATCCTTGATGAACATTGATGCAAAAAATCCTCAATAAAAATACTGGCAAACCGAATC---CAGCACATCA 2870

III.1_1 AAAAGCTTATCCACCATGATCAAGTGGGCTTCAT-CCCTGGGATGCAAGGCTGGTTCATATACGCAAAAT 2940
 III.2_1 AAAAGCTTATCCACCATGATCAAGTGGGCTTCAT-CCCTGGGATGCAAGGCTGGTTCATATACGCAAAAT 2940
 III.2_2 AAAAGCTTATCCACCATGATCAAGTGGGCTTCAT-CCCTGGGATGCAAGGCTGGTTCATATACGCAAAAT 2940

III.1_1 CAATAAATGTAATCCAGCATATAAACAGAGCCAAAGACAAAAACCACATGATTATCTCAATAGATGCAGA 3010
 III.2_1 C---AATGTAATCCAGCATATAAACAGAGCCAAAGACAAAAACCACATGATTATCTCAATAGATGCAGA 3010
 III.2_2 CAATAAATGTAATCCAGCATATAAACAGAGCCAAAGACAAAAACCACATGATTATCTCAATAGATGCAG- 3010
 * *****

III.1_1 AAAAGCCTTTGACAAAATCAACAACCCCTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACG 3080
 III.2_1 AAAAGCCTTTGACAAAATCAACAACCCCTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACG 3080
 III.2_2 AAAAGCCTTTGACAAAATCAACAACCCCTCATGCTAAAAACTCTCAATAAATTAGGTATTGATGGGACG 3080

III.1_1 TATTTCAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAAGTGG 3150
 III.2_1 TATTTCAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAAGTGG 3150
 III.2_2 TACTTCAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATATCATACTGAATGGGCAAAAAGTGG 3150
 ** *****

III.1_1 AAGCATTCCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCGCTCCTATTCAACATAGTGTT 3220
 III.2_1 AAGCATTCCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCGCTCCTATTCAACATAGTGTT 3220
 III.2_2 AAGCATTCCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCGCTCCTATTCAACATAGTGTT 3220

III.1_1 GGAAGTTCTGGCCAGGGCAATCAGGCAGGAGAAGGAAATAAAGGGTATTCAATTAGGAAAAGAGGAAAGTC 3290
 III.2_1 GGAAGTTCTGGCCAGGGCAATCAGGCAGGAGAAGGAAATAAAGGGTATTCAATTAGGAAAAGAGGAAAGTC 3290
 III.2_2 GGAAGTTCTGGCCAGGGCAATCAGGCAGGAGAAGGAAATAAAGGGTATTCAATTAGGAAAAGAGGAAAGTC 3290

III.1_1 AAATTGTCCTGTGTTGCAGACGACATGATTGTTTATCTAGAAAACCCCATCGTCTCAGCCCAAAATCTCC 3360
 III.2_1 AAATTGTCCTGTGTTGCAGACGACATGATTGTTTATCTAGAAAACCCCATCGTCTCAGCCCAAAATCTCC 3360
 III.2_2 AAATTGTCCTGTGTTGCAGACGACATGATTGTTTATCTAGAAAACCCCATCGTCTCAGCCCAAAATCTCC 3360

III.1_1 TTAAGCTGATAAGCAACTTCAGCAAAGTCTCAGGATACAAAATCAATGTACAAAATCACAAGCATCTCT 3430
 III.2_1 TTAAGCTGATAAGCAACTTCAGCAAAGTCTCAGGATACAAAATCAATGTACAAAATCACAAGCATCTCT 3430
 III.2_2 TTAAGCTGATAAGCAACTTCAGCAAAGTCTCAGGATACAAAATCAATGTACAAAATCACAAGCATCTCT 3430

III.1_1 ATACACCAACAACAGACAAAACAGAGAGCCAAATCATGGGTGAACTCCCATTCACAATTGCTTCAAAGAGA 3500
 III.2_1 ATACACCAACAACAGACAAAACAGAGAGCCAAATCATGGGTGAACTCCCATTCACAATTGCTTCAAAGAGA 3500
 III.2_2 ATACACCAACAACAGACAAAACAGAGAGCCAAATCATGGGTGAACTCCCATTCACAATTGCTTCAAAGAGA 3500

III.1_1 ATAAAATACCTAGGAATCCAACCTTACAAGGGATGTGAAGGACCTCTTCAAGGAGAACTACAACCCTGTC 3570
 III.2_1 ATAAAATACCTAGGAATCCAACCTTACAAGGGATGTGAAGGACCTCTTCAAGGAGAACTACAACCCTGTC 3570
 III.2_2 ATAAAATACCTAGGAATCCAACCTTACAAGGGATGTGAAGGACCTCTTCAAGGAGAACTACAACCCTGTC 3570

III.1_1 TCAAGGAAATAAAAGAGGAGACAAAACAAATGGAAGAACATTCATGCTCATGGGTAGGAAGAATCAATAT 3640
 III.2_1 TCAAGGAAATAAAAGAGGAGACAAAACAAATGGAAGAACATTCATGCTCATGGGTAGGAAGAATCAATAT 3640
 III.2_2 TCAAGGAAATAAAAGAGGAGACAAAACAAATGGAAGAACATTCATGCTCATGGGTAGGAAGAATCAATAT 3640

III.1_1 CGTGAAAATGGCCATACTGCCCAAGGTAATTTACAGATTCAATGCCATCCCCATCAAGCTACCAATGACT 3710
 III.2_1 CGTGAAAATGGCCATACTGCCCAAGGTAATTTACAGATTCAATGCCATCCCCATCAAGCTACCAATGACT 3710
 III.2_2 CGTGAAAATGGCCATACTGCCCAAGGTAATTTACAGATTCAATGCCATCCCCATCAAGCTACCAATGACT 3710

III.1_1 TTCTTACAGAAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAAAAAAGAGCCCGCATTGCCAAGT 3780
 III.2_1 TTCTTACAGAAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAAAAAAGAGCCCGCATTGCCAAGT 3780
 III.2_2 TTCTTACAGAAATTGGAAAAAACTACTTTAAAGTTCATATGGAACCAAAAAAGAGCCCGCATTGCCAAGT 3780

III.1_1 CAATCCTAAGCCAAAAGAACAAGCTGGAGGCATCACACTACCTGACTTCAAACATATACTACAAGGCTAC 3850
 III.2_1 CAATCCTAAGCCAAAAGAACAAGCTGGAGGCATCACACTACCTGACTTCAAACATATACTACAAGGCTAC 3850
 III.2_2 CAATCCTAAGCCAAAAGAACAAGCTGGAGGCATCACACTACCTGACTTCAAACATATACTACAAGGCTAC 3850

III.1_1 AGTAACCAAAACAGCATGGTACTGGTACCAAAACAGAGATATAGATCAATGGAACAGAACAGAGCCCTCA 3920
 III.2_1 AGTAACCAAAACAGCATGGTACTGGTACCAAAACAGAGATATAGATCAATGGAACAGAACAGAGCCCTCA 3920
 III.2_2 AGTAACCAAAACAGCATGGTACTGGTACCAAAACAGAGATATAGATCAATGGAACAGAACAGAGCCCTCA 3920

III.1_1 GAAATAATGCCGCATATCTACAACATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGG 3990
 III.2_1 GAAATAATGCCGCATATCTACAACATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGG 3990
 III.2_2 GAAATAATGCCGCATATCTACAACATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGG 3990

III.1_1 ATTCCCTATTTAATAAATGGTGTGGGAAAACCTGGCTAGCCATATGTAGAAAAGCTGAAACTGGATCCCTT 4060
 III.2_1 ATTCCCTATTTAATAAATGGTGTGGGAAAACCTGGCTAGCCATATGTAGAAAAGCTGAAACTGGATCCCTT 4060
 III.2_2 ATTCCCTATTTAATAAATGGTGTGGGAAAACCTGGCTAGCCATATGTAGAAAAGCTGAAACTGGATCCCTT 4060

III.1_1 CCTTACACCTTATACAAAATCAATTCAAGATGGATTAAGATTTAAACGTTAAACTCAAACCATAAAA 4130
 III.2_1 CCTTACACCTTATACAAAATCAATTCAAGATGGATTAAGATTTAAACGTTAAACTCAAACCATAAAA 4130
 III.2_2 CCTTACACCTTATACAAAATCAATTCAAGATGGATTAAGATTTAAACGTTAAACTCAAACCATAAAA 4130

III.1_1 ACCCTAGAAGAAAACCTAGGCATTACCATTTCAGGACATAGGCGTGGGCAAGGACTTCATGTCCAAAACAC 4200
 III.2_1 ACCCTAGAAGAAAACCTAGGCATTACCATTTCAGGACATAGGCGTGGGCAAGGACTTCATGTCCAAAACAC 4200
 III.2_2 ACCCTAGAAGAAAACCTAGGCATTACCATTTCAGGACATAGGCGTGGGCAAGGACTTCATGTCCAAAACAC 4200

III.1_1 CAAAAGCAATGGCAACAAAAGACAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTCTGCACAGC 4270
 III.2_1 CAAAAGCAATGGCAACAAAAGACAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTCTGCACAGC 4270
 III.2_2 CAAAAGCAATGGCAACAAAAGACAAAATTGACAAATGGGATCTAATTAAACTAAAGAGCTTCTGCACAGC 4270

III.1_1 AAAAGAACTACCATCAGAGTGAACAGGCAACCTACAACATGGGAGAAAATTTTTGCAACCTACTCATCT 4340
 III.2_1 AAAAGAACTACCATCAGAGTGAACAGGCAACCTACAACATGGGAGAAAATTTTTGCAACCTACTCATCT 4340
 III.2_2 AAAAGAACTACCATCAGAGTGAACAGGCAACCTACAACATGGGAGAAAATTTTTGCAACCTACTCATCT 4340

III.1_1 GACAAAGGGCTAATATCCAGAATCTACAATGAACCTCAAACAAATTTACAAGAAAAAACAACAACCCCA 4410
 III.2_1 GACAAAGGGCTAATATCCAGAATCTACAATGAACCTCAAACAAATTTACAAGAAAAAACAACAACCCCA 4410
 III.2_2 GACAAAGGGCTAATATCCAGAATCTACAATGAACCTCAAACAAATTTACAAGAAAAAACAACAACCCCA 4410

III.1_1 TCAAAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAAGAAGACATTTATGCAGCCAAAAACACAT 4480
 III.2_1 TCAAAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAAGAAGACATTTATGCAGCCAAAAACACAT 4480
 III.2_2 TCAAAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAAGAAGACATTTATGCAGCCAAAAACACAT 4480

III.1_1 GAAGAAATGCTCATCATCACTGGCCATCAGAGAAATGCAAAATCAAACCCTATGAGATATCATCTCACA 4550
 III.2_1 GAAGAAATGCTCATCATCACTGGCCATCAGAGAAATGCAAAATCAAACCCTATGAGATATCATCTCACA 4550
 III.2_2 GAAGAAATGCTCATCATCACTGGCCATCAGAGAAATGCAAAATCAAACCCTATGAGATATCATCTCACA 4550

III.1_1 CCAGTTAGAAATGGCAATCATTTAAAAGTCAGGAAACAACAGGTGCTGGAGAGGATGCGGAGAAAATAGGAA 4620
 III.2_1 CCAGTTAGAAATGGCAATCATTTAAAAGTCAGGAAACAACAGGTGCTGGAGAGGATGCGGAGAAAATAGGAA 4620
 III.2_2 CCAGTTAGAAATGGCAATCATTTAAAAGTCAGGAAACAACAGGTGCTGGAGAGGATGCGGAGAAAATAGGAA 4620

III.1_1 CACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCCCTCAG 4690
 III.2_1 CACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCCCTCAG 4690
 III.2_2 CACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCCCTCAG 4690

III.1_1 GGATCTAGAACTAGAAAATACCATTGACCCAGCCATCCCATTACTGGGTATATACCCAAATGAGTATAAA 4760
 III.2_1 GGATCTAGAACTAGAAAATACCATTGACCCAGCCATCCCATTACTGGGTATATACCCAAATGAGTATAAA 4760
 III.2_2 GGATCTAGAACTAGAAAATACCATTGACCCAGCCATCCCATTACTGGGTATATACCCAAATGAGTATAAA 4760

III.1_1 TCATGCTGCTATAAAGACACATGCACACGATGTTTATTGCGGCCTATTCAACAATAGCAAAGACTTGGGA 4830
 III.2_1 TCATGCTGCTATAAAGACACATGCACACGATGTTTATTGCGGCCTATTCAACAATAGCAAAGACTTGGGA 4830
 III.2_2 TCATGCTGCTATAAAGACACATGCACACGATGTTTATTGCGGCCTATTCAACAATAGCAAAGACTTGGGA 4830

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III.1_1 ACCAACCCAAATGTCCAACAATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATGGAATACTA 4900
III.2_1 ACCAACCCAAATGTCCAACAATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATGGAATACTA 4900
III.2_2 ACCAACCCAAATGTCCAACAATGATAGACTGGATTAAGAAAATGTGGCACATATACACCATGGAATACTA 4900
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III.1_1 TGCAGCCATAAAAAATGATGAGTTCATATCCTTTGTAGGGACATGGATG-AAATTGGAAACCATCATTTCT 4970
III.2_1 TGCAGCCATAAAAAATGATGAGTTCATATCCTTTGTAGGGACATGGATGAAAATTGGAAATCATCATTTCT 4970
III.2_2 TGCAGCCATAAAAAATGATGAGTTCATATCCTTTGTAGGGACATGGATG-AAATTGGAAACCATCATTTCT 4970
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III.1_1 CAGCAAATATCGCAAGAACAACAAAAACCAAACACCGCATATTCTACTCATAGGTGGGAATTGAACAATG 5040
III.2_1 CAGTAAATATCGCAAGAACAACAAAAACCAAACACCGCATATTCTACTCATAGGTGGGAATTGAACAATG 5040
III.2_2 CAGTAAATATCGCAAGAACAACAAAAACCAAACACCGCATATTCTACTCATAGGTGGGAATTGAACAATG 5040
*** *****

III.1_1 AGATCACATGGACCAGGAAGGGGAACATCACACTCTGGGGACT-GTGGT-GGGCCGGGGGAGGGGGGAG 5110
III.2_1 AGATCACATGGACCAGGAAGGGGAATATCACACTCTGGGGACT-GTGGTGGGGTC-GGGAGGGGGGAG 5110
III.2_2 AGAT--CATGGACCAGGAAGGGGAATATCACACTCTGGGGACTGGGGTGGGGTGGGGGAGGGGGGAG 5110
**** *****

III.1_1 GGATAGCATTTGGGAGATATACCTAATGCTAGATGACACATTAGTGGGTGCAGCGCACCAGCATGGGCAT 5180
III.2_1 GGATAGCATTTGGGAGATATACCTAATGCTAGATGACACATTAGTGGGTGCAGCGCACCAGCATGGGCAT 5180
III.2_2 GGATAGCATTTGGGAGATATACCTAATGCTAGATGACACATTAGTGGGTGCAGCGCACCAGCATGGGCAT 5180
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III.1_1 GTATACATATGTAACCTAACCTGCACAATGTGCACATGTACCCTAAAACCTTAGAGTATAAT--AAAAAAA 5250
III.2_1 GTATACATATGTAACCTAACCTGCACAATGTGCACATGTACCCTAAAACCTTAGAGTATAAT--AAAAAAA 5250
III.2_2 GTATACATATGTAACCTAACCTGCACAATGTGCACATGTACCCTAAAACCTTAGAGTATAATAAAAAAA 5250
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III.1_1 AAAAAAAAAAATAGAAAGAAAGAAATAAAT--AAAAAAA-GAAAAGAAAGAAAGAAAGAAAGAAAGAAA 5320
III.2_1 AAAAAAAAAAATAGAAAGAAAGAAATAAAT--AAAAAGAAAGAAA-GAAAGAAAGAAAGAAAGAAAGAAA 5320
III.2_2 AAAAAAAAAAATAGAAAGAAAGAAATAAATAAAAAAGAAAGAAA-GAAAGAAAGAAAGAAAGAAAGAAA 5320
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III.1_1 GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAAAAGCAAAT 5390
III.2_1 GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAAAAGCAAAT 5390
III.2_2 GAAAGAAAGAAAG--AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAAAAG--AAAT 5390
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III.1_1 GTCTATTCCGGCTCATTGCCTATTTTTT-GAATTTGGATTTT-GTTTTCTTGCTATTGAGTTGTTTGAGT 5460
III.2_1 GTCTATTCCGGCTCATTGCCTATTTTTT-GAATTTGGATTTTGGTTTTCTTGCTATTGAGTTGTTTGAGT 5460
III.2_2 GTCTATT-CAGTCTATTGCCTATTTTTTGGAAATTTGGATTTTGGTTTTCTTGCTATTGAGTTGTTTGAGT 5460
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III.1_1 TCTTTATATATTTTGGAGTAATACTCCTTATCAGATGTATGCTTTGCAAATAAAA-TTTCCATTCCATGC 5530
III.2_1 TCCTTATATATTTTGGAGTAATACTCCTTATCAGATGTATGCTTTGCAAATAAAA-TTTCCATTCCATGC 5530
III.2_2 TCCTTATATATTTTGGAGTAATACTCCTTATCAGATGTATGCTTTGCAAATAAAA-TTTCCATTCCATGC 5530
** *****

III.1_1 -----AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAATGAGAGAATA 5590
III.2_1 -----AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAATGAGAGAATA 5590
III.2_2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAATGAGAGAATA 5590
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The multiple sequence alignment was used construct a consensus sequence of the LINE-1 insertion in RP1 exon 4 of patients III.1 and III.2.

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>RP1_exon4_LINE1_consensus_sequence
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