

Colorectal cancer somatic L1 Sanger sequences

In blue: nt. changes compared to reference genome or reference L1 (L1RP)

HKSS_A1_5PFS_C4A1FS_018

AATGCTCCATGGGATGAATCTTTGATCGGTAGGAGGTAGAATCAGGTATACTGATTG
TTACCCTGGGCAGGCTATGCAATCATACATTTTATATATATTCTTGAAGAACAGTCCT
ACAGAATCAAGCAACAAGTTGTGCCTTGTGGCAGCCAAATTGATAATGCATCTTTTT
ATTTTATTTCAACCTATGTTCCCTATTTTCGTCTTCCTTTTCCCTCACTTCTACTCTCTGG
GATACATAATAAAGAACTATCATATAGGATCTTACCTGGGGCTCTGTTTTCCAACT
GAGGCTATAACAGCCTATGTTTTTCTGATTCCTAAGTCCATTCTAGGACACTGTGCT
GTATTTGTTCTAGGCACAAATCTTCAGGATGGTCTGACTCCCTGATGAGACACTAAT
GGCCTTTTGGAAATTTGATCATCTACCCCTTCCCTCTTCCCATTCTTACCTCAAATCC
TGATCTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	470	549	98.8%	4	-	14763854	14764318	465

HKSS_POLYP5_A2

AGCATTAAAAACCTTAATACCAAGGTGCGGGGTAGGGGGAGTGGGAACCCCTCAGT
ATAAGGAGAGAGAGAGGAAAAGAATTGGTGCTGCTCTACATTTCCAAAGAAGAATAAC
TTCTGTGCTTTTTCTGGTTTTTCCCTCTTCTCTGTCTGTCTCACACTCTCTTGTCTCAG
CAATCTTCCTTGCTTTCTTGCTTATTTTTGTCTTATCTTACTGGCTTTCCTTTCTACCT
CTGATCTCCTTCTCTGTTACTCTCTGACTTTCTCTTCTTTTTTTTTTTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	270	325	100.0%	11	+	93913532	93913801	270

HKSS_A2GTG5PC4LR_A2ES_033 (long-range PCR 5' junction with GTG primer)

CTTGCTGCAGTTTACTATCTCTCAGGTGCTTCCTATGGGAAGTTCATAAACCATTCTT
CCATAACCTTTTGTTGATCACCATTTCCATTAGGGACTCAATAAGACATGCTCAGTAT
CTCCACCAAGAACCATTATTTGCAAACCAGCTGTGAAACCAACAGGGGTGCTTTAGC
CAAATTAAATCCCATGTGCGCAGAAGTCACAGATTTACAGCTCAAGGAAAAAAATCA
TCAGCAAGAAGAATCCAGAAGTCTCTGTCGGGCATTCTTCTCTCCATTATTTGCTTTA
GTTTCACTGTCTATGTTTCATACCTGTCAAATTTGAAAACAAATATTTATGACAGAAA
CATAGCAGGAATTACCAATACTAATCAATTTTTCTTCTGCCAAAAATTCCTCTCACA
GTCTATACCATGTTTTGCTTCTTGGCCTAACTAAAAGAATCAATAAACTTTTAGTCCC
CTTTGAAAGAGAAAGTCAATTGCTTTTGGTGTGTTTGGGGAATTGAACAATGAGATCAC
ATGGACACAGGAAGGGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGGAGG
GGGGAGGGATAGCATTGGGAGATATACCTAATGCT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	477	607	100.0%	11	-	93913788	93914264	477

In grey: 17/17 bp identity with L1RP (nt. 4990-4974)

In grey: 113/113 bp identity with L1RP (nt. 5806-5918)

TSD: 14 bp

HKSS_A9_1BV_T, HKSS_A9_1BV_M

CTTTTATTCTTTTTTCTTTTCATTTCCCTGTCTGGGTAATTTGAAATATGCTTTCTTT
GAGCTTGCTGATTCTTTCTTTGCTTGATTGAGTCCACTGTTGAAGCTTTGTATAAAAT
TTTCAGTTCAGTCATTGATTTGTAGTGCCACAACCTTTTGTGGTTATTTTTTATAGCA
TATCTTTGTTCTACTTTTTATTCTGTACATGTATTGTTTTCTAATTTTATTTTTTTTTT
ATTTATGTTCTTTTGTAGCTAAGTGGGCTTCTTTAAATTTT TTTTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	282	360	99.7%	3	+	168480298	168480579	282

HKSS_A9_312_LR_A9ES_071

AACAAGCGCACTGCAGTGGATCTCAGCCACAAGCTGAGCCCCAGTGACTCAGGATT
CAAGCCCACCGCAGCAGATTCAAGCTCCAGACTCCAGAGTGGACTCAGGCTCTGGG
CTCAACCCTGTGGACCCAGGCACTAAGCCTACACCTGTGGAACCAGGTGCTAAGCCT
GCCAAGCTTCTGACCCTACACCAGGCCCAAGACTCTAGCAGCAAGTCTACCCATGA
ACCCTGCAAGATGGTCTTCCAAGAATCTTTGGATAAACTGACTAGTGGAACTTTTCT
TTCCAAGCCTGTCTGTAAAGACTGAAATAGGTGCTTACTTTTTCATATGTGCACAT
ACTAATTTATGTCCACATAATCATAAACATCAGGAAAACATAATACCACCAAAGGA
AAAAAAGTAAAGCACCAGTAACTGACCCTTCCTTAAAAAATAGAGGTCTGTGAAC
TCCTGACAAAGAATTCAAAATAATTTTAAAGTGTGATATTCCCCTTCCTGTGTCCAT
GTGATCTCATTGTTCAATTCCCACCTATGAGTGAGAATATGCGGTGTTTGGTTTTTG
TTCTTGCGATAGTTTACTGAGAATGATGGTTTCCAATTCATCCATGTCCCTACAAAG
GATATGAACTCATCATTTTTTATGGCTGCATAGTATTCCATGGTGTATATGTGCCACA
TTTTCTTAATCCAGTCTATCATTGTTGGACATTTGGGTTGGTTCCAAGTCTTTGCTATT
GTGAATAGTGCCGCAATAAACATACGTGTGCATGTGTCTTTATAGCAGCATGATTTA
TACTCATTTGGGTATATACCCAGTAATGGGATGGCTGGGTCAAATGGTATTTCTAGT
TCTAGATCCCTGAGGAATCGCCACACTGACTTCCACAATGGTTGAACTAGTTTACAG
TCCCACCAACAGTGTAAGAGTGTTCCTATTTCTCCGCATCCTCTCCAGCACCTGTTGT
TTCCTGACTTTTTAATGATTGCCATTCTAACTGGTGTGAGATGAT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	481	481	100.0%	3	-	168480567	168481047	481

In grey: 535/535 bp identity with L1RP (nt. 5855-5321)

TSD: 8-13 bp

HKSS_A10_3BV_T

TCTATTTCTGCTGAGATGTATGATTAAATCCATAAATCATATCCATGGTGTCTTTATC
TAATGGTTGTTTACGCGACATCCTTAGGATTCTCTTTTGAAAATACTTTCTCATTTTCT
GCAATATAGATGGGCTAATGATTGTGTAAATCTTCAAGTTCTGGTTCTTCCTTGCATA
AAGATTTCTTCAATTGCTTGCTCTCCTCTTGTAGGTACTATAAGTGATGAGGAGAA
ACCAAACCACTCCTTCAATCCTTTGCTCTGAAATCTCCTCAGCTAAATTTCTATGTTT
GTTATTCACAACTTCTGCCTTCCACAAAACACTAGAAGACAAGGCAGCAGCCATTTT
GTTTGCTACTTTGTAACAAAGATTACCTTTCTTCCAATTTCCAAGACATGTCCCTCA
TTTATATCTGAGACCACAACAAAATAGACTTTAATGCCCTTATTCTTTTTTTTTTT
TTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	451	473	99.8%	6	-	49811509	49811959	451

HKSS_POLYP5_B2

TCCTGATTTCCCTTATTAGTTCCATTTTTTCCTTTTTTCGCTTATACAGATGTTGGCAATT
 TTTGCATGTAGCTACCCAGATTGACCAGCAAATTTCTTCAGTGAATTGCATGCATTG
 CTCAGGCCAGCCATGACTGCTGTACTGGCTCTCTGTGGCCAAGTAGCTCTGAAGATT
 ATGAGCTGTGTGGCTGACTGAGGGAACCATTTCCAATCTGACAGATCTGTTTGCCTTT
 TGCTTTTAGACCTGATCCTTGTCTTAGTATGACTTTTAATGTCAAATTTCCAAAGATCA
 AAAAAAAAAAATTATCATTAGCTTAAACTTTTCANACAGTAACAGCAATTGTCTTACT
 GTATTGAGTCACTTGGCTTACTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	371	429	100.0%	5	-	63294465	63294835	371

HKSS_B2GTG5PC4LR_B2ES_048 (long-range PCR 5' junction with GTG primer)

GACTTTAGGGAGGAGTTTGGGAATATAGAACAAGGAGAACAAGGGCAAGAATATA
 GCATGTGTAAAGAATAAGTTTGAGCCTGCATACACAAAAGGGAAAGATAGAGAT
 CTTCTAATGCTTCTTCTGTTTTAGAAAGAAAACAGACTAGTTTTAAGCAATAAACAAC
 ATCTTTACCATCAACACTTGGTCTACTCATCTATTTGCTTCTTGGAAAAAAAAAACCCG
 AAAACTCGGAACCTCTGAATAAGAAAAGGTAAATATGTCATTCTCAGTATGAAAAGG
 CTCAGAGCGATGTAGGCCTGTTGGTTGGTTTACTTTCTGCACCCTTGACTTCATCTTA
 GAAAGTAAGCCAATTGCTTTTGGTGTTTTGGACATGAAGTCCTTGCCACGCCTATGT
 CCTGAATGGTAATGCCTAGGTTTTCTTCTAGGGTTTTTATGGTTTTAGGTTTAACGTT
 TAAATCTTTAATCCATCTTGAATTGATTTTTGTATAAGGTGTAAGGAAGGGATCCAG
 TTTCAGCTTTCTACATATGGCTAGCCAGTTTTCCAGCACCATTATTAAATAAAGAC
 ACATGCACACGTATGTTTATTGCGGCACTATTCACAATAGCAAAGACTTGGAACCAA
 CCCAAATGTCCAACAATGATAGACTGGATTAAGAAAATGTGGCACATATACACCAT
 GGAATACTATGCAGCCATAAAAAATGATGAGTTCATATCCTTTGTAGGGACATGGAT
 GAAATTGAAACCATCATTCTCAGTAAACTATCGCAAGAACAACAAAACCAACACC
 GCATATTCTCACTCATAGGTGGGAATTGAACAATGAGATCACATGGACACAGGAAG
 GGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGGAAGGGGGGAGGGATAG
 CATTGGGAGATATACC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	352	492	100.0%	5	+	63294126	63294477	352

In grey: 217/217 bp identity with L1RP (nt. 4994-4778)

In bold/grey: 360/361 bp identity with L1RP (nt. 5552-5911)

TSD: 9-13 bp

HKSS_B9ESL17_B9FS_068 (ES PCR, truncated L1, sequenced with FS primer)

TTATGGGAATTCAATGAGATCAGGTAAGTCTCCTGCCACAGATCCAGGCCAGTANN
 NNNNNNTTGGTTATGGTTGCACAGGCACTGGCGATACAAAAACATGCCAGACAAGA
 CCACTGCCCTTGAGGAGCTCACCTTTGAGAGTAGAAGAGGACCTGCAGNATTCCTTC
 CACAACCTGCCAATTCTTCATTGAAAACACATTAAATTGTCTCTGCATTTCTTCCACAA
 CTGTGTGCATATTGGATCCATGACTCCAAGTGACCATCGCTTTGTGTTGTGACTAGCC

TGTGAGGTGAAATGAATGAAGAGTGGAAGCTTGGAAGTCTGGATTGTTGATTTC
 AACTTGTCTCCCTCCTGCAACTGCACAGGCAGTGGTGCTTTAG **AAGGCCAAATGTT**
ACGACTTCCTAATCTGGTAAAAAATATTATTCTAATTATGCA **TTTTNNTTNNAGTTG**
TTCNCNGGTTNTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	440	473	100.0%	14	-	38408459	38408898	440

In blue: additional seq. from chr. 14 resembling translocation

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
9	50	83	100.0%	14	-	38408481	38408522	42

HKSS_B9ESL1_B9ES_026

GGGCACTGAGCTCAATAAGTGGAAGGGGCTAGCACTCGGAAAACAGAATCTGCAGG
 ATATCAAATATAGATTACTACTTTTTGCAGTAATAATTGATGTATATGAAAAATTG
 ATTTGCTTCAATATGTTCCACAAAGTACTGGCTTTTATTTTCATGATGCTGGGCTCTT
 CTGTATCCTGACCAATTCTGTATTTGTGTTCTTTTATGGGGGACACCGTCTCTCTTTCA
 GTCACATTTAATATTCAGTTTTTCTAGTGGTAGGAGGAGCATTTTAAATGATTTCTA
 TGAGTCCTTATTAGAAATGAACTCCCTACTGTGGCATCATAAGGTTTCATGTGTA
 ACCATTAACTTGAGAGCTGGAGCTGATGAGGCCTACCATCTAAGCACTTTATGTTC
 AA **TAACATTTGGCCTT** TCTCTGATGGCCAGTGATGATGAGCATT **GACTGGATTAAG**
 AAAATGTGGCNCATATACACCATGGAATACTATGCAGCCATAAAAAATGATGAGTT
 CATATCCTTTGTAGGGACATGGATGAAATTGGAAACCATCATTCTCAGTAAACTATC
 TCAAGAAC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	417	579	100.0%	14	+	38408055	38408471	417

In bold/grey: 29/29 or 27/27 bp identity with L1RP (nt. 5295/5293-5266)

In grey: 131/133 bp identity with L1RP (nt. 5638-5770), afterwards sequence continues, but becomes low quality

TSD: 12-14 bp

HKSS_B10

TCAATACAAATCACCAACCTTTAGATGACACCCTGTCTTCAAAGTGCTTTCAAAGTC
 TGGCAGAGGAG **GAAGTACGCAGTGGCTATAAGACCACCT** **IAGGAGTTCAATCATGCAT**
 TCTAAGTAGCAGATCACTCGAATGTAATTGGCTAGTGAGTTCATTTACTCTTCTCTT
 CTTGGTCACATGTTACCGCCCTTGTACCGTGCACGTTCTCTTTCCAGACTTACAAAG
 CATGTTCTCTTGAATTCGTTCTCTTTTTAAATTCACACAGTCT **TTTTTTTTTTTTTTTT**
TTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	273	310	99.0%	11	-	49247088	49247360	273

HZSS_B10104LR_B10ES_081

TTCCTGCTTCTTCGCAATGAGAATATTCAAAAATCTCGCTTCAAGGTGGTGATAAA
 TTACCTCAATTTGGTCATTACACAATGCACCCATTTAAACACACATCGAAACATCAG
 GTTGTACCCTATAAGTATGCACAATTATTATGTGTCAATTATTTTTGTTTAAATTC
 TACTTCCAGTCACCACTCCAGAGGACTGCTGACGTGAGGAGGTTTTAGACAATATTC
 TGTTCTGGCCTAGCCAAGGGATTAGGGAGGCAATGTAAGCCAACTTCCTTTTTTCCAC
 AGCAAGCTCTTGGACTGCAGGGATCAAATTTTCATTCATCTTTTTATTCCCTTTTCCCC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	433	722	100.0%	11	+	49246656	49247088	433

TSD: 1 bp

CCCCATGTGGAAAGCTCAGTTTTCCCTGCTTCCTTTAAAGAGCTAGTAAGTGATGGG
CAGGAAGCTGCCTCCCCCTGGAAAGACCATCTCCTCTCCTATGTGTCTACAGGCTTC
TCTGTCCTCACTTCTGCATCCCCACTTTTCAGGAGGAGAAAGTTGTGCAGGAGACCTT
GTAAAGCGTTATTAGCCTTGCTAAGCATCTGAAGTGCTGCTGGGTTCAAAGGTTCAA
ATCGAAGACTCTATTTTTAGCAAAATGAGGCTGGAGCAGACTGTTCTGAGCAGCCTC
CATTCACAATGACAAGTACTTTAACAAGTCATGGTGTAAGTTGGATTTATTAAAGT
AGGATCCCAATTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	358	467	100.0%	4	-	5237330	5237687	358

GCTCTGCCAGCAAACAGCCTGCAGACTCGAGCTGCAATGCCAGTGCTTCCTCGGGTG
TCCAGCCTGCCCACCAGCACTGCAGGTTTCAGACCTGCCCGTCCCCACAATCGTGTG
AGACAACCCCTTAAAATTATTTCTCTCTCTCTCTCTCTCTCTCTCCATACATACACA
TCCTATTGGTTCAGCTTCTCTGGACAGCCTTAGCTAACACAGTTATACTTTAAGGTT
CTTCTAAAACAGTCATGCTTCTAGCATTGTAACCAAATAAACCAAATCAAAAGTAC
AAAACAATAAATTTGAGATCAAATGTAAAAACATTATACCTGTTACATTGTCTCAG
CATTCCTTCTTTTACATTTTTTAAAGAAGAAAGTAAAATATAGACACAATATTTTTTT
TT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	397	483	98.8%	18	+	76594091	76594487	397

ACCTTATTAAAGGAGCCTATCCCTGGTGATTCTCAGAGGTGCTTTATCATCCTTCTAA
GGGTAACATCCCAGATGGTTCCAAGATACTAAGGTGATTATCTGTTGCTTTTTTCGCA
GAAAAGAAGAGAAAAGGGACTCACTTATATATGTGTATTTACAAC TACCGAAATAA
CTGGCATTATGCCTTATGGGCAAATTTGAGTCCCACTCACTTGTGAAGATTTTCTAAT
TTTTTCATATTCACACAGTCCTCCAATCTTTGCACTTCTGTTTTTGTGAGAGTGTCTTC

CATTTTAGTTTATAACTGATCTCTCTTTATGTAAATTAAAAATAAACAAATCCAGAAT
TCCAACCTTAATATTTAGTGAAGAATACAGGCTGTG**GCGATTGAAATACTTGTTTTT**
TT
TTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	400	478	100.0%	4	-	68933134	68933533	400

HKSS_C2GTG5PC4LR_C2ES_046 (long-range PCR, 5' junction with GTG primer)

TAATATATCACTTCTAAATTGCACTTTTTTTTCTCTAGGATCATCACTTTACCCAACTC
TTTTGGATTATTATTATCAGCATAAAATATGCTATAATGTGTCTCCCATATTTTTAAA
AATCTTTCCTTTAACTTCACAACCTCCCTCAACTGTCAAATTTGGTCTGATCCCTTTC
ATTTAAAAACTTCTTAAAAGCAGTTTAAAAATTTACTGCATCTAATCCTCCTTCCATT
TTCTATTGAATCATTCCCATCCCTATCACATTAGAAAACTTCTTTTATCA**G**AGTCAC
TAGTAATCTCTACTTCATCAAGCTCAATGGGCAATTCCCATGTAGGTCTGTGAGTAC
CCAGAGCCTGCACTGGACCTGCTG**AAACAAGTATTCAATCGC**TTTCAAAAAACCA
GCTCCTGGATTCAATTGATTTTTTTGAAGGGTTTTTTGTGTCTCTATTTCCCTCAGTTCTG
CTCTGATTTTAGTTATTTCTTGCCTTCTGCTAGCTTTTGAATGTGTTTGCTCTTGCTTT
TCTAGTTCTTTTAATTGTGATGTTAGGGTGTCAATTTTGGATCTTTCCTGCTTCTCTT
GTAGGCATTTAGTGCTATAAATTTCCCTCTACACACTGCTTTGAATGCGTCCCAGAG
ATTCTGGTATGTGGTGTCTTTGTTCTCGTTGGTTTCAAAGAACATCTTTATTTCTGCCT
TCATTTTCGTTATGTACCCAGTAGTCATTACAGGAGCAGGTTGTTTCAGTTTCCATGTAGT
TGAGCGGCTTTGAGTGAGATTCTTAATCCTGAGTTCTAGTTTGATTGCACTGTGGTCT
GAGAGATAGTTTGTATATAATTTCTGTTCTTTTACATTTGCTGAGGAGAGCTTTACTTC
CAACTATGTGGTCAATTTTGAATAGGTGTGGTGTGGTGTGCTGAAAAAAAGGTATATT
CTGTTGATTTGGGGTGGAGAGTTCTGTANNTGTCTATTAGGTCTGCTTGGTGCAGAG
CTGAATTCAATTCCTGGGTATCCTTGTTGACTTTCTG

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	391	574	99.8%	4	+	68932762	68933152	391

In bold/grey: 631/636 or 626/631 bp identity with L1RP (nt. 3095-2461 or 3090-2456)

TSD: 14-19 bp

HKSS_POLYP5_C3

TTGGTTTGTCTCCTCCGAACAATTCTAAAAAGACTTTTTGACTTGTAGGACACATTTATT
CACTTGTCTGAAACCCCTACCAATTCTTATGATCAAATTTTTATTCTCTTCCCTCTTT
CTTTTTTCCCATTAATTTCTAATTTGCTATTTTTCTCAAATTCTCTATTGTGTATTAA
CTCACTTTCTTCAATCCTCCTTTCCTTCTGCTCTATCAAAGTATCACTTCCTAAATTAG
CCTTCTTGAGCTAGACAATATAGAATCTCACCACTACCTAACACTCCTTGTCTCTA
CTTTGATTTTATTCTAATACTATATACTATGTACTATCTAGTATAGTGCATAGTGT
AATCATATATGTGATATA**TATATTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT**
TTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	378	430	99.8%	12	+	73901751	73902128	378

HKSS_C3GTG5PC4LR_C3ES_044 (long-range PCR 5' junction with GTG primer)

TATATTTTGTATCTTAGCATTTGTAATATTTTACAGTTACACTTTTGTTTGATAATTT
GCATAAATGTCACCATTCACCAAACTGTAAGGTCCATGAAATATGGGACCACAC

ACTTAGAGTATAAT AATAAAAAAAAAA TATGCTATAAAAAAAAAAANNAAAAAA
AAAAAAAAAANNAAAAAAAAAAAAAAAAAAATTTTCAAAAAA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	344	660	99.2%	1	+	158497345	158497688	344

In grey: 228/229 bp identity with L1RP (nt. 5791-6019)

HKSS_C8_4BV_T

CTTCTTGACTTTTATATCTGTTGTTGCTGTCAAGAAATCTGCTGCCTAATTATATTTCC
TACAAAAAAATCTTGATTGCTTTAAGAACTTTTTGGCATCAGTATTTTGAATTTCA
TTATAGTGGACTTGAAGTTTGAATTCACACTTACTTATTCAGCTCATGACTTACTGTA
CTTCTGAATCTTATGATATTTATCTTTTAGACATTGTAAAAAAATTCTCAGTCTTTT
TCTCTCTGAATATTTCTTCTCCTTCATTTTCTATTTCTACTTCTAAACGCTTATTCTCAT
TCTTTCCTCCATATCTTTAGTTACTCCCTCACATGTTTACGTTTTTGTGATGCATTCTG
AATTGGAATTAAATCTCTTCCAGTTTAC TACTTTTTCTT TTTTTTTTTTTTTTTT
TTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	394	425	99.8%	9	-	16037730	16038124	395

HKSS_C8_13_LR_C8ES_065, HKSS_C8_14_LR_C8ES_080

GGCACAAAACCTCTCCTGGTTGTGAGGTCACGTCCTCAACCCAGACCACACAAGATCC
CCTGAATAGAGAAAGCTCCACTGAAGATGATCTCAGCTTCCAAAATTATGAAGAAT
ATTAGGAAATGGTTTCCCATGAGAGAGAACCAGTGGATAGAATACAGAGCGAGATC
AGATCCCCAGGCACTTCAGATAATAAATGTATTACATAAAGACTATAAGTAGGTTTA
AAAATGATTCAAAGCATAAAATTAGGAATTGAAAACATAATAAATTATGACAATAT
ATAAGGTACCATGAAAAAATAAAATAGAGATTTTAAAAAGAAACAAATGAACTTC
TAAAGTAATAAATATTGTTCATCAATTTTAAACAGATTAGACATGGTT AAAGAAAAA
AGTA TAAATGTCTTCTTTTGAGAAGTGTCTGTTTCATGTCCTTCGCCCACTTTTTGATG
GGGTTGTTTGTTTTTTCTTGTAATTTGTTTGAGTTTATTGTAGATTCTGGATATTAG
CCCTTTGTCAGATGAGTAGGTTGCAAAAATTTTCTCCCATGTTGTAGGTTGCCTGTTG
ACTCTGATGGTAGTTTCTTTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCAT
TGTCAATTTTGTCTTTTGTGTCATTGCTTTTGGTGTTTGGACATGAAGTCCTTGCCC
ACGCCTATGTCCTGAATGGTAATGCCTAGGTTTTCTTCTAGGGTTTTATGGTTTTAG
GTTTAACGTTTAAATCTTTAATCCATCTTGAATTGATTTTGTATAAGGTGTAAGGAA
GGGATCCAGTTTCAGCTTTCTACATATGGCTAGCCAGTTTCCCAGCACCATTTATTA
AACAGGGAATCCTTTCCCCATTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT
TGTAGATATGCGGCATTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCT
GTTTTGGGACCAGTACCATGCTGTTTTGGTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	402	569	99.8%	9	+	16037345	16037747	403

In grey: 608/610 (or 607/609) bp identity with L1RP (nt. 5244-4635)

TSD: 12-13 bp

HKSS_C9

TATTGTGAGTTCTAGTCCCAATTTGACTCTCTTTCCTTTGCATTTGGCTTCCCCAACAC
ATTTGGAAGCTTTTTAGAAATCTTCTCTTTATCTCTGTGGTTCTAAAATTGTATAACAG

TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	455	507	100.0%	7	+	18573143	18573597	455

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	384	483	100.0%	7	-	18573583	18573967	385

TSD: 13-15 bp

ACACTTCGATAGATCITTTCTCTGGCCAGTAAGAGGTCTTCAGAGGCTCCAGAAGCT
CATTAAATATATTGAGCTTTGAAGTTTTTGATTTGGCAGAATTTCTATGTTGACTCAGT
ATCAAGTGACCTAATGCTCAGATTTCTTGTCTAGCTAGTTATCTCCATGGGTTAGAAA
ATGCTGCTAGCAAAGCCATTTATTCTCTGTGGGTTAGAGAAAGTTGCTCTTCCAAAC
TATTGGTTAGACCCTTAACCCAGCTTATAAATGTTTGTGGTGTTCACAAGGTGGG
AACCAGGAACAATCAAACCATTCGATTTATAGTGTCTTCTGGGCTTTGCTAAGCTTG
ATGTAATCACCAAAGGGAAATAAACAGTGCCACTTTCCTCCTACCCCTAAGAATCTT
GTCTTGCTCCGTCAAATCCACACCATCTTTT

TTTTCTTTTCTATTAI ICTGTATTTACTTCCTGACTGTTTCGTGAAATATTGTCATTTT
ATTCAAAGAATGAAAAGAGAAAATGAAAGGAGGTAAAATTAAATGAGCAAACCTCT
ACATGCTTTAGCATGTTTGGCCTCAAATTTTGGTAGGGGAAGAGATTAATATAAGGT
TTCTGGACCATCTAAGACCTTG GTTGCTACATAATCATTGTTTCCTATTCTTTTTAAT
ATTGCATCAAAAGTTGATTGAGGCTGCCTATCATTTAAAATGAGATAGAGAGCTACA

ACTATCAGGAATGAATGGCCTGCAATGGAAATTCTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	323	357	100.0%	4	-	94641338	94641660	323

HKFM_C12101mwLR_C12ES_058

CAGTGCAGTATGGCATGGGCAGTTAGTTCCAGCAGATAGAACAAGCATCTTTTCCTG
GACATTTCCCTGTGCAGTCTGATTGACTCCCTGATGTTTCCCATTCACTCCAAGCTGCT
TTTTCCCTCCTCCATTCAA AATTGCAGAATTCTCTCCCTGGTCTCAAGCTGCTGTCTC
TATTCTTAAACTATATGCTCAACTTCCTACCACCCCACCTTATTTTTTGATGAAGTCT
GTTTCATCATAGAATCCTTAAATAACAAATCTCATAGAAAAGAGTCTACTCTGCTCC
TGTGTATAACATTAGATTTTAAATGATATGAAAGAACAAAGTCCAATAGTTGGTTTG
AGAGTGAGAGCCCCCAAAAAAAAAATGACTACAAGAAGAGAACA AATGAGTACATAT
TAAAGAAATTCTTTGAAGAGGTCCTTCA CATAGGTGGGAATTGAACAATGAGATC
ACATGGACACAGGAAGGGGAATATCACACTCTGGGGACTGTGGTGGGGTCTGGGGGA
GGGGGGAGGGATAGCATTGGGAGATATACCTAATGCTAGATGACACATTAGTGGGT
GCAGCGCACAGCATGGCACATGTATACATATGTA ACTAACCTGCACAATGTGCAC
ATGTACCCTAAA ACTTAGAGTATAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	412	677	100.0%	4	+	94640937	94641348	412

In grey: 22/22 bp identity with L1RP (nt. 4334-4313)

In grey: 220/221 bp identity with L1RP (nt. 5799-6019)

TSD: 8-11 bp

HKSS_POLYP5_D2

[illegible]

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	331	409	100.0%	4	+	10642314	10642644	331

HKSS_D2GTG5PC4LR_D2ES_042 (long-range PCR 5' junction with GTG primer)

GGGCAATGGGGTCTCCACTGGAGTGAGAGTATTTTCTGCAGTTTACCCTTCACTCCA
CATAAGCTCCTCTTCCTGCTGAAGTCATTCTGCATCCTTAGTGCAGACCCAGATTATT
AGAAACCCCAATGATGGGAACCACTGCTGTCTCTCTACCTCCACTGAGGCTACTGC
TTCAACCAGCAAAACCCCAAGTAACAACATTCCCACTCCCCATCCCTTTCATAACAGT
CCTCCAGCCCCAGGAGGCCTGTGAAACCCCACTGAGTAAGCCTCCCCACACCCCAA
GCAAAACTCCCAGCCTCCCTCCAAGTGTCCCTCAGGAGGCCTGTTCTTCTCTACTTAA
GGGTCGAAATCATGCTAGAAACTTTAAACATGACTCCCTGTATTCTCCCACAGCTAA
AACACACCCAAGGCAAAAATCCTACATTCTGATCCAATGCTTTAATTTTTTTTACATG
AAAAATAGCCCTGACATTGGGGTTGGTTCCAAGTCTTTGCTATTGTGAATAGTGCCG

Probably 9 bp has to be deducted from this due to extension into similar, but not identical sequence:

In bold/grey: 259/260 bp identity with L1RP (nt. 5626-5367)

TSD: 10 bp deletion

HKSS_D8 (KIAA1217)

TATCCTGGATTATCTGTGTGGGCCCAGTCTAATCCTATGAATTTTTTGAAAGTAGAGA
ACTTTCTCCAGTTTGGATTAGAGAGATGTGGCAGAAAAGGAAGTCAGAGAAATTCA
AAGCTTCAGACATACTCGACTCAATGTTTCTGGCTCCATGATGGAGAGGCCAATAGG
ACGAGGATGCAGGTGGCTTTAAGAGTCTGAGAGAAGCTCCCAACTGGCCATCAGCA
AGGAATTTGGACCTCAGTCCTGCAACTACATGAAGCAAATTTTTTTCAGCAGATATG
AACCTGGAAATGGATTCTTCCCCCAGAGCCTCCAGGCCAGCTGACACATGGATTTC
TCCTTGTGAGCCTCAGAGCAGAGAAATCAATTGAGCCACCAGGACTTCTTTTTTTTTT

TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	389	455	100.0%	10	+	24150440	24150828	389

HKSS_D12

TTTTCTTCTGTATTACTCCCTTCCTTTTCAGGTGTTCCATTACTATATTCACACTGAAG
TCCACGAGAATCTCAGAGACAGGTAGGTAGCAACCTCCTTAGGTCTATACTTGAAGT
CCCTTTGTAAGTCAATATTCAGCTGAGTTAGGCATCAGTCACTTAGGAAACTGCTTC
AGGTTTTTCATCATATTATGTGCTGTTATTTTAGTATACTTATACTATGGGGCTTAGAA
TTATCAGATAGACATAATACATAGTTTATCTGGTAATTCACCTATTCACTCAAAATTC
ATTAACAGTACACTACGTGTAACGTATTACTATACAATTTTTCAAATGTAGTAAGTT

GTTT TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	350	406	100.0%	7	+	77937927	77938276	350

HKSS_D12ESL1_D12ES_006

ATTATGTGAATTCTTTTTTATGGCTGCATAGTATTCCGTGGTGTATATGTATCATATTTT
CTTTATCCAAACCACTGTTGATGGGCATCTAGGTTGATTCTTGTCTTCGCTATTGTG
AATAGTGCCACAGTGAACATCAAATGCATGTGTCTTTTTGGTAGAGCGATTATTT
TCCTTTGGGCATGTACCCAGTAATGGGATTGCGGGGTCAAATAGTAGCTCTGTTTTA
AGTTATTTGAGACATCTCCAAAATGCCTTCCATGGTAGCTGAACATAATTACATTCCC
ACCAACAGTGTGTAAGTATTCCCTTTTCTCCACAGCCTCACCAGCATCTGTTATTTTT
TTTCTTTTTTAATAATAGTCATTCTGATTAGTGTGAGATGATATCTCATTGTGATTTT
GAATAATCATTTTAAACAAATATCATTGGGAGATATACTAATGCTAGATGACACATT
AGTGGGTGCAGCGCACCAACATGGCACATGTATACATATGTAACCTGCACAA
TGTGAACATGATCCCAAAAACCTTAAAGTATAATAAAAAAAAAAAAAAAAAAAAA
AGCACAAAATATGATAAAATCCTGTAGCAGTTTCCTAAGTGACTGATGCCTAACTCA
GCTGAATATTGACTTACAAAGGGACTTCAAGTATAGACCTAAAAGAGGTTGCTACCT
ACCTGTCTCTGAGATTCTCGTGGACTTCANTGTGAATATAGTAATGGAACACCTGAA
AAGGAAGGGAGTAATACAGAAGAAAAATGGTAGGCCAAGAAATGGG

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	424	424	98.9%	7	-	77938271	77939015	745

Sequence becomes low quality at the L1 junction.

In bold+grey: 121/128 bp identity with L1RP (nt. 5892-6019), or 121/127 bp identity with L1RP (nt. 5893-6019), afterwards sequence continues, but becomes low quality

[poly(A) continues in the background; after poly(A) there's no polymerase slippage and the 3' junction is readable]

TSD: 5-6 bp

HZSS_D1213LWCR_D12ES_084

TTATGTAATTCTTTTTTATGGCTGCATAGTATTCCCTGGTGTATATGTATCATATTTTC
TTTATCCAAACCACTGTTGATGGGCATCTAGGTTGATTCTTGTCTTCGCTATTGTGA
ATAGTGCCACAGTGAACATCAAATGCATGTGTCTTTTTGGTAGAGCGATTATTTTC
CTTTGGGCATGTACCCAGTAATGGGATTGCGGGGTCAAATAGTAGCTCTGTTTTAAG
TTATTTGAGACATCTCCAAAATGCCTTCCATGGTAGCTGAACTAATTTACATTCCAC
CAACAGTGTGTAAGTATTCCCTTTTCTCCACAGCCTCACCAGCATCTGTATTTTTTT
TCCTTTTTTAATAATAGTCATTCTGATTAGTGTGAGATGATATCTCATTGTGATTTTGA
ATAATCATTTTAACAATAGCATTGGGAGATATACCTAATGCTAGATGACACATTAG
TGGGTGCAGCGCACCAGCATGGCACATGTATACATATGTAACCTGCACAATGT
GCACATGTACCCTAAAACTTAGAGTATAATAAAAAAAAAAAAAAAAAAANTAACN
NTAAAATGNNNTAAAATNNNCTAAAAAAAAAAAAAAAAANTNNAAAAAAAAAAAAANNA
NNAAAAAAAAATAAACNNANAAAA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	423	441	98.2%	7	-	77938271	77938692	422

In bold+grey: 128/128 bp identity with L1RP (nt. 5892-6019), or 127/127 bp identity with L1RP (nt. 5893-6019)

TSD: 4-5 bp

HKSS_E3_E3FS_063

CCAAGTCCCTTTGCCTTTGATTTCATTTTAGACTGTGGTCTTTTATTCTGATTTAAAAA
GCCCACAGAATTGGATATATGTATCAGCAGCATGAAAAATTAACATAAATCTGACA
AAAATAACCTTTAAGATAGTAAGAAATTTTCACTAAAGTTATTTTTTTTTTTTTTN
TTNTNT
TNTTTTTTTTTTCTTTTTNTTNTNTNTNTNTTTTTTTTTTTTTTTTTNTNTTTTTTTT

Note: low quality sequence

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	160	295	100.0%	4	-	115891758	115891917	160

HKSS_E7-10/1

ATTTGGTCATATGAAAAGCTTGAGAAATTAATTACATTATTAAGAGAGATGTGACTT
TATTTGTTCTGCAACTAGTTACAAGAAATAATAGAGGGGCATTTAATGAGCATTAC
CATGCTCCAGGCACCCAATATTAAGTAATTTACATAACTCTTCTCCTTTATTCTTTGC
AAGATGGAGAGGGTAGGTTGTCTTATCCACATATTATACACAAGGTGACTGAGCCTC
AAGGACAGAACTCTTGTCCAAAGTCACAAAGGTCTGGTGTGGCAGACCCAGAATTC
AGAATCAAGAGTTTTGATAGCAAAGGCCAGATCCTTCCATGGTGAAATACTGCAGT
GCTTGAAATAGGGAGGGAGAACTATTATAATAAATGTGTTATATTATAGGATGTGTA
TGTGTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	413	442	100.0%	22	-	35043271	35043688	418

HKSS_2BVE8TB_Clo4E8FS_029 (CYLD gene, about 1.9 kb away from two exons)

CTGAATATTTTTATTCTTAGAATTCAGTCTATCAAAAATTCTAAAATTTATTCAGCT
ATTATCTGTTGAAACATTGCCTTTTCCCTATTCTCTCTAGTATCTCCTTCTGGAACCTCC

TTAATTATTTTAGATTTTTTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTATTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	432	523	100.0%	16	-	50823644	50824075	432

HKSS_E8ESL1M_E8ES_032

TGCAACAAATAGGAGGATA**AG**GTGGGAATTGAACAATGAGATCACATGGACACAG
GAAGGGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGG**G**AGGGGGGAGGG
ATA...

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	306	398	100.0%	16	+	50823332	50823637	306

In bold+grey: 91/92 bp or 93/94 identity with L1RP (nt. 5804-5894 or nt. 5802-5894), afterwards sequence continues, but becomes low quality

TSD: 7 bp deletion

HKSS_E9

AGGTGACTTTAACATTCTTTCTTTCATTTCAACCTTGGAAAATCTGAGGATTCTGTGT
CTCAGGGATGATCTTCTTGTGTAGCATCTTGCAGAAGTTATCTGTATTTTCTGAATT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	405	454	99.8%	4	+	98861078	98861482	405

HKSS_E11

CTTGACTACNCTGAAAAAAATTCATGTTAGATCTGGGTAGGAAACAACCTTGAATAA
TTTCTACTGAACTTTACAAAACACAAATGCAGCATAGAGAAAGGTTTAGTCTCCAAA
ATCTCTGTTCAATTTCTAGGTAAGTACTTTTTCTTTTGCTTATTTTCGGGTCTTCTCCC
CCACCACCGCCCCCACCACACACACACACAAAATTTGTTGCTGCTGTT
AAAAAGAACCTTGCCACAAATTCAGTTACTTAGAAGCTCCAAGGTGAATTGACTGA
AACTCGAATACAATTTTACTGACAGCCACATAACTCAGTACAAAATGGGGCCTTCTG
GTATTTTCTTTTCTGTAAGAAAATAAACAAAAAAATGTGCAGAACTAGTCAAAACAG

[illegible]

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	464	464	100.0%	1	+	81376404	81376867	464

HKSS_F3_5_F3FS_072

GGCCTTCCTCATTGTTCCTCTAAGGCTTTGCACAGCAGGCAGCTCNNCNNAGAACA
GGCGCCCCGTTCATGGTACAAATCTTCCAGAGCCTTCTAAAGCTTTTGCCTTGGGGAA
GCCATTGTTAAGCACTCCAGCTTCCATCAAAAAATCACTTCTCTGATCATCAACTTCA
TTAGAGGCAGGGCCACACAAATTAGCCCTTGATTGTTTTTAAATTGCTTTCTGTATGA
CTTTTCTCTCCAACCTGATGAACCTCATATTTTCTGTGTCTTTACAG
CATGCGGCTCTGTACTCTGTACATAGTANAAGCTCCGTAGAAATTGGCTGATTGATT
AATTATGAAAGGGCCCATAGATCAGGAGATACNCCACAAGAAAGAAGAAAAAATT
CCACGACAGAATACTTGACACACACTTTACAATTTATCATGCACCTTCACAAACATG
ATTTTATCTTNNCNNTTT

TTTTTTTT

Seq. continues but becomes low quality

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	468	528	99.6%	8	+	40618899	40619366	468

HKSS F5 F5FS 036 (metastasis)

CTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGANCACGAGGTCA
GGAGATCAAGACCACCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATACA
AAAAATTAGCCCTGCGTAGTGGCGGGCACTTGTAGTCCCAGCTACTCCGGAGGCTGA
GGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGC
CACTGCACTCCAGCCTGGGCGACAGAGCCAGACTCCGTCTCAAAAAAAAAAAAAAAAA
AAAAAAAAA...

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	289	492	100.0%	4	-	128239655	128239943	289

Polymerase slippage on poly(A) stretch, so sequence afterwards is not readable, but poly(T) tail is later visible.

HKSS_F5_7_LR_F5ES_093

CTGTACAATCCCTATAAAAAGGAAATTTGGCAATATCTTGCAAAATTATATATACATT
TATCTTTTGACCTAACCATTCTACTGCTAGGACTCTATCCCAAAAATACACTGATAAC
AGCCATATGCACAAGTCTATTTGCTGTACTGCTACTTGAATTAACAAAAGACCGGAC
ACAACTCAAATGTTTCATCACCAAGTGGTTAATTGAAAACTAGGGTACATCTATGGT
ATGGACTCCTGTGTCAATTTTAAGAAGCAGGAGAAATATTTCTATATAGTACTGTGAA
GTTATATCCATAGATAAATTAAGTGAAAATAACAAGATAAGAGAAAAATAGTATATA
GTAGCCTATCACTGATCCAAGAAAGAGAGGCAATACAAATATATAGTATTGGTTCC
AAGTCTTTGCTATTGTGAATAGTGCCGCAATAAACATACGTGTGCATGTGTCTTTAT
AGCAGCATGATTTATACTCATTTGGGTATATACCCAGTAATGGGATGGCTGGGTCAA
ATGGTATTTCTAGTTCTAGATCCCTGAGGAATCGCCACACTGACTTCCACAATGGTT
GAACTAGTTTACAGTCCCACCAACAGTGTAAGTGTTCCTATTTCTCCGCATCCTCT

CCAGCACCTGTTGTTTCCTGACTTTTTTAATGATTGCCATTCTAACTGGTGTGAGATGA
TATCTCATAGTGGTTTTGATTTGCATTTCTCTGATGGCCAGTGATGATGAGCATTCT
TCATGTGTTTTTTGGCTGCATAAATGTCTTCTTTTGAGAAGTGTCTGTTTCATGTCCTTC
GCCCCACTTTTTGATGGGGTTGTTTGTTTTTTCTTGTAATTTGTTTGAGTTCATTGTA
GATTCTGGATATTAGCCCTTTGTCAGATGANTAGGTTGCGAAAAATTTTCTCCCATGT
TGNAGGTTGCCTGTTCACTCTGANGGAGTTTCTTTTGCTGNGCAGAAGCTNNTTTAG
TTTAATTAGATCCCATTGTCA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	392	398	100.0%	4	+	128239153	128239544	392

In bold+grey: 601/609 bp identity with L1RP (nt. 5616-5010), or 599/607 bp identity with L1RP (nt. 5614-5010)

HKSS_F8

GTCCCTTCCAGTGCCCTGATGTCTTAGAAGTGCTGGGTCCAGGTTGGCCCAGGTATC
CATATTTTGTGAAACTCACAACCTATTGCCTCTTTTCCAGTCCTAGGGAGTTCAACAGC
ACCAGAGGGCTCATCCTATATTCCCTAAACACAATACAGAGGTCATACCCTTTCTGA
AGACATTTAGATTGTCTTCTCCACTAACTACTGCCCCAATCCATCAGGCAGTTTCTCT
CCTTTGACCCTTCAAACACAAGAGACTCTGTTTTCTGGATCCCAGGACTCAGTTTCTCT
CCAATGGACTCAGCTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	307	362	100.0%	X	+	24283494	24283800	307

HZSS_F8104LR_F8ES_091

TAAGGAGTTAGATGAAAGAGGACAGCAAAAGGCAGAGCTATTGATCCAGAATTGTG
AGATATTCCTCACAGCAGAGGGAGAGCAAGAACATTGCCATACAATGATGTCTCT
GCACCAGGAAGCAGACCATAAAAGACTTCTCATATAGTCTGTGAATGCAGGGTTGG
GCAGAGTGCGTTTTAGAAAGTTCATCATTTAAAGGATTAAAATGTATGCCATGAGAC
TATATATCTCTATAGATATCTATGTCTAATTATATAGAGATAGATACCTATCTCTCTA
TATAGAGATAGATATCTATATCTCTATATATCTTTATCTCAATGTGTTCTCTCATCGG
ATAAACTTGGGTTTTGGACGCTAGTATCTATCACCTTAGCCACCTTAAGATAATTCTC
GAAACAGAAAAGGGGAGGAAGTGTAACATAAATAAGCTTGCGGTGTGTTTGAAAAG
CTGAGTCCATGTGTTTTTTGGCTGCATAAATGTCTTCTTTTGAGAAGTGTCTGTTTCAT
GTCCTTCACCCACTTTTTGATGGGGTTGTTTGTTTTTTCTTGTAATTTGTTTGAGTT
CATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGAGTAGGTTGCGAAAAATTTTCTC
CCATGTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTCTTTTGCTGTGCAGAAGCTC
TTTAGTTTAATTAGATCCCATTGTGCAATTTTGTCTTTTGTTGCCATTGCTTTTGGTGT
TTTGACATGAAGTCCTTGCCACGCCTATGTCCTGAATGGTAATGCCTAGACTGTA
AACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCAGGGATCTAGAAGTAG
AAATACCATTTGACCCAGCCATCCCATTACTGGGTATATACCCAAATGAGTATAAAT
CATGCTGCTATAAAGACACATGNNCACGTATGTTTATTGCGGCACTATTCNCAATAG
CAAANNACTTGAACCAACCCAAATGTCCAAC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	465	738	100.0%	X	-	24283785	24284249	465

In bold/grey: 334/336 bp identity with L1RP (nt. 5262-4927) or 331/333 bp identity with L1RP
In bold/grey: 205/210 bp identity with L1RP (nt. 5422-5630), or 204/209 bp identity with L1RP (nt. 5422-5630)
TSD: 13-16 bp

HKSS_F10

CTATGGATATTATTTTTATAGAAGTTACGTGCTTTTCTATTTCTTTTGTAACAAATAA
CAATTAAGTAGCTTAAACAACAAAGATTTATTCTATCAAAGCTCTGAAGTTATTAGT
TTGAAGTGAATTTTATGGGGCTAAGGTCAAGGTGTCAGTGGAAGTCTTTCCTACTG
GTGCTCCAAGGAAGAGTCTATTCCTTGCTTTTTCCAGCTTCTAGAGGCTGGCAATGTT
ACTTGGCTTCCTGACTGCAGCACTGCAACCTCTGCTTCCATCAGCGCATCACCTTCTG
TGACCTTGACTCTCTTGTTCTCTCTTATAAGGGCTATCACAGGAATGAAACAAACA
TTTCTAAATAACTCATGAGCCAAAGGAAAAAAATGGAAAATTTTTTAAAAATTATA
GCTACATTGTAGTTGAAATTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	428	491	100.0%	14	-	83827175	83827602	428

HKSS_F11_101_F11FS_070

TTCATGTGATGATGGACTGAGATTGTTTTATGATTGATAAACTCAGGGGATATAATG
TATCATTTTTGAAGTAGGTGTTATGGTGATTGGTTTAATAATGATAGGAGGTGTCAA
AGATTAAAAATATCAAGGGGAAATGTCTATATAATATGCAAATGACTGTAAAGTGCA
AGCATTTTAACTAGATGGAGACAGAAAGCACATGCGCCAAAAAGACTAGAACATC
ATTCTGTCTGGAACCTCTGCTTCATCCAGACACCTGGAATACTTTAAAGTTCATTTC
TGGAGTGAGTTTATCAATCTCTCAGAGAACGTTCTCTCTCATAATTCAGAGATATAA
ATACAACATTGCAAAGTTGACAATCTTGTAAGGAAAGTAGTAAGTAGACAGAACATT
TTTTAGCAATATTCTTTTTTTAATAAATGCTTCTATTGGAAGAATAATGAATTCTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	453	517	100.0%	16	-	63305233	63305685	453

HKSS_G2_4BV_P

ATCAGCAGTAAAACCTTGGGGGCAGAGCAGGGTTTTCTCCCAGGGCACAATGATACA
AGGTCTATTTTTATGTAATGAAAAATACAGCACATTTGTTACATAAAACCATCTGAG
TGCCAGGGATGACAAAGCATATCGCAGGGCAAGCAAAACACATTCTGCTGAGGCAA
TGTCTGTCTCTATCTCTAGCTCACTACAGTGATCCACTGGGGAAATCAAGGCGGAAG
ATGGAAACACATCCAGCACACTTTAAGCTACAAAGTTAGCAGTAAGGATTCTTAGA
AAAGACCTTGAGGACATTTGGTTCAACGTATCTGTTGAAGAAAAGAGAAGTGACCT
GCTCAGTCTCAAATAAGTATTTGGCAAACTATGTCTAGAAATAAACTGGTCTCT
TGACTACGTGTGATGTTATGAGATGCTGTTCCCTCGTGTCCCTTTTGATACTATGTAGC
CTACTGTATCAAAGATAAGCATAAGCTTTTATTTTTTTTTTTTTTTTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	484	569	100.0%	15	-	94058563	94059046	484

HKSS_G2_12_LWLR_G2ES_078

ATACGATTCAAGTCAATAAGAAATGCCCAGAGTATGCAAATCTATAGAGACAGAAAA
TAGACGAGTAGATGCCTAGCACCAGGTGTTTGGGAGGGGGTGGTCTGGAGTGAAGT
CTAATGGATATGGGATTTCTTCTGGGGTGTGAGAATATTCTAAAATTGATTGTGG
TGGTGGTTGCATAACTCTGAATATACTATAACCCATTGAATTGTACACTTTCAATAG
GTGAACCTTTATGGTATGTGAGTTTTATCTCAAGTTGAACAATGAGATCACATGGACA
CAGGAAGGGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGGAGGGGGGAG
GGATAGCATTGGGAGATATACCTAATGCTAGATGACACATTAGTGGGTGCAGCGCA
CCAGCATGGCACATGTATACATATGTAACCTGCACAATGTGCACATGTACCCT
AAAACTTAGAGTATAATAAAAAAAAATAAATAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	261	282	100.0%	15	+	94058297	94058557	261

In bold+grey: 209/209 bp identity with L1RP (nt. 5811-6019) or 207/207 bp identity with L1RP (nt. 5813-6019) – poly(A) tail sequence is not nice due to polymerase slippage
TSD: 7 bp deletion

HKSS_Metastasis7_G5

TGGACTCTGAGGAGGCGACATTAATTCTGTACTACTTCTGATAAATCTTGGTCTGGG
CTACCACTAATGATATCATAAAAAGGATTAAGTTACTTTTCTTATGCTGTCCTAATT
TTGCATAAGTGTTTCACATTAAATAATCAAAATTAGAGCTCTCATGGAAAGCAATAT
ATATATAAGCCTGAGTGCTAGCCTGCAGTGATGACTCATCACTGTAATTCACGCTCC
CATAATATCTACAATCGACTACTTAGCTTTCAATCTTACTCTTTCTCATCTCCAAATC
TATCCTCCAAACAATGAAATCATATCCTCGATACCTTTATTGAATTATTTTCAAGGACC
TGTCTTTAAACCCTTTCTGTGACTTCCCTTTATATTTAGCATATATTCTTTTTTTTTTT
TT
TTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	394	476	99.8%	12	+	17541609	17542002	394

HKSS_67_101_67FS_074 -: ins. G7

TGCTGCCAAAAATAGGCTTTCCTCTTTTAGTCTCTTTCTCAAAGCATTTGCTCAGTTC
CCCCAGATGAATTACTATGACACATTTTTTTTCTGTTTGATTTTCTAAATGGTATGCT
GATTGTTTGCTCTCTCACCAGAATATAAACTTCATGCAGACAAGAACCATGCCCAAC
CTCCCCACTATTTTATTGTCTCTGATCAGCATAGACCCTCTCATGTAGGAGAGGCTCA
ATGTACTATGTGATGACTGACTGAGCATATGAATGAATAGATAGATGAATGAAACA
CACCCTGAAAACAGAGCATTGGTTGTGATGTTTAAAATAACACTTCTTGGACTGTG
GCATGGCTATTTTAAAAAATTCATTGTGTTATCTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTNAAAANNTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	381	435	100.0%	8	+	73332863	73333243	381

HZSS_G7104LR_G7ES_086

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	342	492	99.8%	8	-	73333231	73333572	342

TSD: 9-13 bp

AAGAGAGTTATCCAATCTGTATAGCACTCAATCTCCCAGGGCTCAGAGCAGGAGAG
AAAGAATGAAACATATGCATTGGGAGGTCGATGGAGAATAAACAGCACATGGGTAC
TGTGTTTTTAAGGCTGATTCGAAGTTATTTATTTCAAACAGGACTACTCAATCATCAA
ATTTCTGGAAGTAGAACCGAAGAGTCTGCATTTTACAAACAGTGCTAAGGTGAATT
AACGCAAAGTTTGAAAACCTTCAAGAGAATCACCTAAAATACTTCTCACACAAGAAA
TACACTTGTACGTATCTTTGTTTAATCAAAAGATTTTAAACAAAGTTTTCCCAAACAGA
TGAGCTCCTCACTCCCTAAGAGTAATTGCACAATCTTAGAAAATTTTCTTAAAATAC
TGGCTTT

ATGTTATTTTATGTTTACATTTATTGAACACCTGCTATGTGCCAAGCATGTGACATTT
TGAATTATCTCAAGTTTGTCTGGTAAAAGATGGAATATAGAAACAGTAATTCCTA
TTCTAGTCCTTAGAACAAAGTCTGGTAGAGTTATATATTCTTATCTTTCCTAGCACAT
TATCAAAGGTGGGATTCCTACCTTAATAATATCCTAAAACCGTGTTCTTTCTACTGT
GCATACTTACATTCTTTGCTATAAAGAGCTTCACATTTTAAGATTGTTTAAATAATTA
ACTCACATAAACAATGGCTAAATAGTGGCTTCTTATTTGGTCCTTTCTATCCCAAATC
ATGATTTTAAATTTCTAGAGATGAAGTCAACATTAAAATCCTCAGACTCCAATTAAA
AAAAATCTATTTCAGGACTTCTTTTTTTTTTGTTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	425	457	100.0%	8	-	117335139	117335563	425

HKSS_H7_1BV_T

TGGCAGATCTCACAGGGTAAAGCTGCCCCGCTAACACCAGTTGTGCTGCAGACCAG
TGCAATGCAGTCTCTGGAGGGAGTCACAGACAAGGACTCAAGCCCACCTGCACTGG
CAATGTTCTGTATATAGCTGCATTCCAAGCTCAGGTGCTTCCATCCAGAGGCCCTCT
ATATGTGAAGTCCTTACCCAAGTCCTTTCTTGGTTACCTCTACAGAGACTTCCTCATC
AAGGGACTTTGAAGGCACTATTCTCTACTCTCAGCACTTTCTCATTCCATTTATCTC
CCTTCTTCCTTCCTCCTGGCCTTTTCCCTCTGGCCTCTCGGTCTATA**AAACATCATAA**

ATCTTTT
TTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	350	420	100.0%	4	+	135008659	135009008	350

HKSS_H7_312_MWLR_H7ES_076

ACCTGGAGTTTGAGGAAAAATTGAAACTGGAGATATAAATTTCTATAAATTTAGTTG
GAGGCCACATGATTTTAAACTATGAATCTTGAGTATAACTGGAGAGGAGGGCTCT
AAGGAGTAAACCCCAAGAATATTCTAATTTTATAGGATACAGGGAGATGAGGAGGATA
TAACAATGGGAGACAGAAGGGGAGATCGGTGAGGTAAGAGGAGCAACAGAAATCT
GTCAGAGAAAAAGAGGCCTGAGCTCTTAGGTGGTCAGGTGGTCAGTTAAGACAAGA
AGCCAAACTGAAAAGAACAGTCAGGCTTTATACACTTCCTCAGGTAGTATAATCAAC
ACCCAAAGCAGGAAAAGCTGCCAGTTTCCCAGCATTTTCTATTTTCCCTGTGGAA
TGGTACTAGATGTATTAACGTAGAATGTATGTCCCATGCCATAGAAGCCTTGCTCT
AAAGATTTATGATGTTTGAGAAGTGTCTGTTTCATGTCCTTCGCCCACTTTTTGATGGG
GTTGTTTGTTTTTTCTTGTAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCC
CTTTGTCAGATGAGTAGGTTGCGAAAATTTTCTCCCATGTTGTAGGTTGCCTGTTTAC
TCTGATGGTAGTTTCTTTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCATTG
TCAATTTTGTCTTTTGTTGCCATTGCTTTTGGTGTTTTGGACATGAAGTCCTTGCCAC
GCCTATGTCTGAATGGTAATGCCTAGGTTTCTTCTAGGGTTTTTATGGTTTTAGGT
TTAACGTTTAAATCTTTAATCCATCTTGAATTGATTTTTGTATAAGGTGTAAGGAAGG
GATCCAGTTTCAGCTTTCTACATATGGCTAGCCAGTTTCCCAGCACCATTATTTAAA
TAGGGAATCCTTTCCCATTTGCTTGTTTTCTCAGGTTTGTCAAAGATCAGATAGTTG
TAGATATGCGGCATTATTTCTGANGGCTCTGT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	468	486	100.0%	4	-	135008992	135009459	468

In bold+grey: 540/542 bp identity with L1RP (nt. 5231-4690) or 537/539 bp identity with L1RP (nt. 5228-4690)

TSD: 14-17 bp

HKSS_H9

GTAGATTTTACGATAATCCAATTAAATCCCTCCTTATTGCCTCTTGGCTTTATCCNGC
CGCTGATTTTGTTCCTCACTCTTTGTGGTGTCACTCTCCCTAGACTTCTGCACATGTTT
GGGGTTGCTTTTCTTCTCTTTAGAATCTGATCCAATTTGTTTAAAGTAATTTAGAGAT
TCATCACGATTTTGAACGTTTCATCTTTTAAAGGGAGAGAGTGTGACTATGTATTT
GTTTTTATATCTATACATATACATATATATACACAGACACACAAATATGTATG
CAT**ACATACTTTCATTTC**TTT

TTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
-------	-----	-------	----------	------	--------	-------	-----	------

1 309 371 100.0% 6 + 130869250 130869558 309

HKFM_H9101lwLR_H9ES_062

GTGTTTAGCTGATTATAAACTACCTTCACGTACATTTTTTTTTTTACCTGACCTTCGCA
ATAACACAACCTGAGGGTCAGAGATACTGAATACCTTATTCAAGGTCACAGATCTAAT
AAAGGGAGTTAATGAGACCAAATGCAACCATTTGCAGATTGCTTTCATATTGGTCA
ACACCTACCCCCCTGTATTTAGATTGAAGGAGGCCCTTCTGAGATGAAATCAGAGTT
GATAAAATCATATTTGATGCTGCTTTTCCAATGTATGTAATCAATGCCTTGTGTTATT
CAAGACATCAGATTCAAGTTTAGGAAAATTTCCCAGTGTACAAATACTTCTGATTTA
AAGACAGAATGATCTGATTTCCAAATAGTAGGCTGAGCACACATTGAACCCTAATA
CGCTACAATAAACTCT**AGAAATGAAAGTATGT**TGCCTGTTCACTCTGATGGTAGTTT
CTTTTGCTGTGCAGAAGCTCTTGCAACCTACAACATGGGAGAAAATTTTGTCAACCT
ACTCATCTGACAAAGGGCTAATATCCAGAATCTACAATGAACTCAAACAAATTTACA
AGAAAAAAACAAACAACCCCATCAAAAAGTGGGCGAAGGACATGAACAGACACTT
CTCAAAGAAGACATTTATGCAGCCAAAAACACATGAAGAAATGCTCATCATCAC
TGGCCATCANAGAAATGCAAATCAAACCACTATGAGATATCATCTCACACCAGTT
AGAATGGCAATCATTAATAAAGTCAGGAAACAACAGGTGCTGGAGAGGATGCGGAG
AAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGA
AGTCAGTGTGGCGATTCTC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	432	870	100.0%	6	-	130869543	130869974	432

In bold+grey: 52/53 or 46/47 bp identity with L1RP (nt. 5087/5081-5035) with L1RP

In grey: 390/391 bp identity with L1RP (nt. 5079-5469) with L1RP - internal duplication in L1?

TSD: 10-16 bp

HKSS_H10

ATCTTACTCTATCCACTTAAAACCACTGTCAACTTAGATCGTCTTCCTTGGGTTCTTG
TACTAGGAGTTGTTGATGAACATACAGCGAACATACTTTCCTCATTTTTGTGAATA
ATTTAGCACGTTTCTAATAGATTTATACTTCACTATCACTATTTTCAAAGTGGAAT
TCACTTTGAGCCTTTTACCACCTTATCCTTATGCTTCTTTTACTTCTCACTGTCAATCA
TTTGCCCGGCCCTGTTGACTTTGCCTCTCTTCTATCTGTAACATGAACACTGTCAAC
TACTGCAGTTCAAATTAAGATTTCTTATTCAGGACTACTTGAAAAGTCTATTAACA
GTTTACTTGCTTGAATGGTTTTCTCTCTCTAGTCCAACCTTCTACAGTGCGGCCTCAT
GCAT**TTGCTAAACTTC**TTTTTTTTTTTTTTNCTTTTTTTTTTTTTTTTTTTTTTTTTTT
TT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	421	560	100.0%	13	+	92378236	92378656	421

HKSS_H10ESL17_H10ES_089, HZSS_H1032LR_H10ES_087

GCACTTGGATATGGATTTGATAGAGAGTTTTCTCAGAACAAAGAACAGTGATGATG
GNNNNAGGAAAAGTCCTCAGAGGGTAGGTGCCAGAAAACATGAGGCTGACATGGA
CAATTGACAAAATTTTGCTTTGCTTGGAAGATGGGTTTCTGACTGGTAAGCATAAA
AGGAAATTATATTTAAAGGGTAAGTCAGAGAAAAGATTTTGGAGGGCTTTAAATGC
CAGGCTAAGGAGCTTTATTTT**C**TAGATAAAAGCTCCTGATGGTTGCTCAAAATGTAA
AATGCCACAGCT**GAAGTTTAGCAA**TGATAGACTGGATTAAGAAAATGTGGCACATA

TACACCATGGAATACTATGCAGCCATAAAAAATGATGAGTTCATATCCTTTGTAGGG
ACATGGATGAAATTGGAAACCATCAGTCTCAGTAACTATCGCAAGAACAAAAAAC
CAAACACCGCATATTCTCACTCCTACGTGGGAATTGAACAATGAGATCACATGGACA
CAGGAAGGGGAATATCNCCTCTGGGGACTGTGGTGGGGTGGGGGAGGGGGAAG
GGATA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	305	567	99.7%	13	-	92378645	92378949	305

In bold+grey: 259/265 bp identity with L1RP (nt. 5630-5894) or 256/262 bp identity with L1RP (nt. 5633-5894), afterwards sequence continues, but becomes low quality

TSD: 9-12 bp

HKSS_H11-3/1

CCACACCATCAAGGTCAGCGACAAGAACTGACATGCGTCTCCCTCTGTCCTTTTGAG
GTTCCNGCTCATGCCTGTTGGTTCCAGCCTGCTAGTGATCTCCCCACAGTTGTATCCA
TCTTTCCTTCCCAACTACCTGCAGGCGTCAGGCTCCAACATCAGAGGTAAAAACAGC
AGCCTTAAAAAAAACCTGAACCAACTCTCATGATTGTGTGTCGTCAGATCTCTGCAATA
AATCCCTTAAATATATACACGGCTGTGTGTGTGAGAGAGAGAGAGAGAGAGAAAGA
GAGAGAAATTTATAAATGTATAAGTACATTTTGTATGTATCTATACATATATACATA

TTTTACATGTAAATTTTATTT

TTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	361	408	100.0%	X	-	16277646	16278006	361

HZSS_H1132HWLR_H11ES_094

ACTGGCTCCTGGGCAGAGCATAAGCTATGCTCACATGTGAGCCAACTCGGAACGTA
AATAGTAAGAGATTCTCAGTGAGTCTTCTGCAACTTAACCCCTAGAGTCACCCAAT
ACAGGCCAGTCATTTTTTCTCTCCCCCTTCTACAGACTCTGGGATTCCTGTTTTTTTG
TTTGTGTTGTTTTCTTGCAGCCACAGCATATTCTGCATTGAGAGGAGTTCTGCAGAGTG
GGATGCTGTCTCCAGATCTTTTCAAGGAAAACACAAGAATAAACTCCCACCTAAG
GGATATACAGCAAATTCCTTCAGGAAAAGAGACCAGAGATAGGAAAAATAGCAAAT
ATTGGGAAGTTACAAAAATGGATGATTTATCAGTCAGTTTTTATTTAGAGAAATAGA
ACCACTAGCAGATTATACACATATTATATATAAAATTTACATGTAAATATGTATAT
ATGTATAGATACATAACAAATCATGCTGCTATAAAGACACATGCACACGTATGTTTAT
TGCGGCACTATTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCAACAATGA
TAGACTGGATTAAGAAAATGTGGCACATATACACCATGGAATACTATGCAGCCATA
AAAAATGATGAGTTCATATCC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	476	647	100.0%	X	+	16277217	16277692	476

In bold+grey: 174/174 bp identity with L1RP (nt. 5539-5712) or 171/171 bp identity with L1RP (nt. 5542-5712)

TSD: 44-47 bp

“Mix” plate (“m”):

HKSS_A5m101FS_A5mFS_012

GTGATCTCTCTCTCCAAATATTGTACAGAATACCAGCCCTTTGGGAGGCCAGGGTGG
GAGGATTGTTTGAGCCCAGGAGTTCAAGACTGCCCTGGGCAACATAGTGAGACCCC
CCATCTCTATAAAAACTGAAAGAAAAAATTAGCCAGGCATGGTGCATGCCTGTATTCC
CAGCTACTCAGGGGGCTGAGGTGGGAGGATCGCTTGAGCCCAGGAGATCCAGGCTG
CAGTGAGCCCTGATTGCACCACTGCACTCCAGCTTGGGTGGCAGAACGAGACCCCA
TCTCAAAACAACAACAACAAAAAAATGTACTGGACCACAGGTAAGTAAACCATGG
AAAGCAAAACCATGGATAAGGGGGACTACTGTCTGCTGTGCTTTTCTTTTCATAGCAC
TCAGCACATTTGTAACCTTTTGGCCACAATCTGTCTTCCTTTGCTGGACTGATTGCTTT
TT
TTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	456	536	100.0%	5	-	158507837	158508292	456

SSFM_A5m10-1LR_A5mES_087

TNTGATTCANANNTCTTTTATCCTCGTTCACACATANTNACAGCGCACCAAGTACTT
AGCCCCACACTGCAAATATTNCNNNNACTGCTTCTATTAATACAAATACTCTTACTA
TTAATAATAACAGTAGATATTCATTACTTACTGTGTGTAAAGNNNNNTGNGATAAGCA
TTTGTGGGGATTATTGCATTTAAGCNTAATCACCAACTTCTGAGATAAGTAATATTA
TCCTCTATTTTCAGAAATACGAAAACCTGAAGACAGAGGAACACCCATTAACCTTCCTTG
CCTTCAAAAAGCATTTCAGTCCTC...

Low quality sequence

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	306	309	96.6%	5	+	158507547	158507852	306

Potential TSD highlighted.

HKFM_C1m-101-FS_C1mFS_068 – about 300 bp away from RIMS1 exon

GATGGAGCTCACACTTTCTTGTTTTTAATCTTTAGTATAACATACATAAAGATCAGTA
CAGAAGCTGTGATAACGTCTCTGCCAAATCATCAGATAGTGATGTCAGTGATGTTTC
CGCCATTTCCCGAACCAGCAGTGCCTCACGCCTCAGCAGCACAAGCTTTATGTCAGA
GCAATCTGAGCGCCCCAGGGGTAGAATCAGGTGAGTTGGCAATACTGTTTATATAA
ACTGGATCTTTATCTGTGATATAAAAATACAACTAGCTTCCTGAATATTTTTTCTATA
ATACAGTTTAGGTCACAGTGGGTAAAGTATTTATCGACTACTATGTAGTATTGCCAA
CAGAAATGTTTAGTATTGACTACTATCAGATACAGCTTATAACCCTAGTCACAATTTT
AGAGATCACTCTGAGTCACATTTGTAGTAGTTTCCTCTAATATGATTAAATCCCTTC
CTTTAGTCCAACATCAGAAAGTGATTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	489	566	100.0%	6	+	73023174	73023662	489

HKFM_C4m-101-FS_C4mFS_093

AATCTAGTTAGTTCCCAAGATCATTTTTGCATAGATTATTTGCTATGTTTTTTGTAGT
GAACAAGATACAAAAGCCCTGATCTCCTATAGTTTATAGTGATGTCATTATGTCTCT
CAGTTCATAAACTCTACCATCATTCTAATCTAGACACTTTTTGTGTCCTGCATGCAGA
GCACAAATAAATGAATTCAAAATGAACAAAACAATACAAAAAGATCAACCCAAAGTT
GGCTTTTTAAAAGATAAACTATATTGACAAACCTTTAGCTACACTAAGAAAAAAG

AGTGAAAGCCTAAATAAAATAAAATCAGAGATTTAAAAGGAGACATTACGACTGCCA
CTGCAAAATTCATAGCATAATTGGTGGCCACTATGTGCCAATAAATTGGAAAACCTAG
AAGAAGTGGATTAATTCCTAGACACATGAAACCTACCAAGTTTAAATCATGAAGAA
ATCCAAAACCTGAACAGACCAGTAACATGTAATGAAATTGAAGCCGTAAGAAAAAT
TCTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	514	550	100.0%	X	-	121123577	121124090	514

HKFM_D1m-101-FS_D1mFS_066 – exonic insertion into STX11 (3'UTR)

GCTAATTTTGTATTTTCTGTAGAGACAGGGTTTGCCATGTGGCCCAGGCTGGTCTCA
AACTTGTGAGCTTGAGCAATCCGCCCACCTTGGCCTCCCAA

CGTGCTGAGATTACAG
GCCTGAGCCACTGACCCTGGCCAAATTTTTTTTCTACTAGCTACTGAGGCTGCCACAT
CTGGATGGAACCTGAGTGGAGGGGGAAAAGAATGAAAACTCAAAAGAATTCCCAT
GAGGGTGTCTTGCTTTCTCTCCTGAGTTACAATACTTTAGCAAAATCATGAGGCTTA
GAGATATGGTGTAGTCTGCAAACCTCTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	314	410	99.7%	6	+	144510322	144510635	314

HKFM_D4m-13-FS_D4mFS_070

GTCTTTATAACAAAGTGCCTACAAAAGCATTGCAGGACCTGTTCTCATGGCATTTC
GCTCTTTTTGGGAACCTGAGATTCAGTGTAAGGTGGACTCTTTAATTTTAAAGATC
TAGATACTCTAGATACTTTGCCTTTCAACTGTACCTGCTTTTCATATATTTAAATTATT
AGGCCCTAAAACTACAAATGTTTTGTTGGCCCTTTTCCTTATTGGGCTCTGCCCTGA
ACTCAATGGTCCAGTTAAAAAACAGAGACTAAATTAATTAATAAGGGGTCTATGTC
TGCTTATCCATCTTCATGTATAGGTTGTATGGATTGTAATAT

TGGGCAGGGCCTCTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	347	391	100.0%	11	+	87163424	87163770	347

HKFM_D4m13mw_D4mES_053

TCCTTCTACTCCTATCAGGAGTTCGGCTCACACACGAGGGGCATGATTGAAGCCTA
CCATGGTGGAGGAAATGGGAGGCCACTTGTGCCCCATTTCCCACTTCCCAATAAGCC
CAAATGACCTGAGTGACCTTGAAGACATGATATAGGAGGTTATAGCTCATTGCTTCT
TTCAACAAGTATCTGTAAACCCAAATGTGCAAAACCCTGTTTCAGGGGATGCATAG
AGTTTGCAATCTAGCCAGAAAGACAACATTGAACAAAAAATTGTAAGTGCATTATA
TATCAGAAAGTAGAGATGTTGGTGCCAAAAATCTGAAAACCTCCTGAAGCATATGAG
ACCAAGATGGAATAGGTGTTAGTTCAGAGAAGGGAGTGAGGAGCCTTAAAGCATA
ATAGTTGAAAT

AAAGAGGCCCTGCCA

GTGATGATGAGCATTTCCTTCATGTGTTTTT
TGGCTGCATAAATGTCTTCTTTTGAGAAGTGTCTGTTTCATGTCCTTCGCCACTTTT
GATGGGGTTGTTGTTTTTTCTTGTAATTTGTTTGAGTTCATTGTAGATTCTGGATA
TTAGCCCTTTGTCAGATGAGTAGGTTGCAAAAATTTCTCCCATGTTGTAGGTTGCCT
GTTCACTCTGATGGTAGTTTCTTTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	423	792	100.0%	11	-	87163755	87164177	423

TSD: 13-16 bp

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	349	413	100.0%	8	+	58567370	58567718	349

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	622	661	99.9%	11	-	84641636	84642257	622

GTATTGTTAATTATTCTTCATGAACTGACAGATTGGTGAGCAGCTGGAAAAAATTA
ATGAAAAACCTCAAAAAGGCTCCAACACTGCCTGATAATCCTACCTGTTCTTTGAA
CAACCTCCTCCATCCTCTTTTGAAGGCGATTGCAAACATTCTCCACTCTCCTCAAC
CTCACACCTTCTCCATCCTCATTCCACTTAGTAGATAGTTGCCTTCTACTAAGAAGA
AAACAAACAGACACTTCTCAAAAGAAGACATTTATGCAGCCAAAAAACACATGAAG
AAATGCTCATCATCACTGGCCATCAGAGAAATGCAATCAAAACCACTATGAGATA
TCATCTCACACCAGTTAGAATGGCAATCATTA AAAAGTCAGGAACAACAGGTGCT
GGAGAGGATGTGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTA
GTTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCTCAGGGATCTAGAACTAGAAATA

CCATTTGACCCAGCCATCCCATTACTGGGTATATACCCAAA**GGAC**TATAAATCATGC
 TGCTATAAAGACACATGCACACGTATGTTTATTGCGGCACTATTACAAATAGCAAAG
 ACTTGGAACCAACCCAAATGTCCAACAATGATAGACTGGATTAAGAAAATGTGGCA
 CATATACACCATGGAATACTATGCAGCCATAAAAAATGATGAGTTCATATCCTTTGT
 AGGGACATGGATGAAATTGG

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	237	265	100.0%	11	+	84641411	84641647	237

In bold/grey: 520/523 or 518/521 bp identity with L1RP (nt. 5215/5217-5737)

TSD: 12-14 bp

HKFM_E4m-32-FS_E4mFS_095

TTTGTTTTATTCTTGTATTATACAGTAAAGTACAACAGATATCATGACTCATTGATAT
 AGCTGGATCCCTCAGTGAGGGGCTCATTAGGTAAGTTAACATACCATATAACCCATA
 GAATGGATTTTACATGCATTCCTCTGTGAACCAATTATACCTTCTTTTTTATAAAATG
 TGTGAATATGGAATATGATAACTCACAGTGAATTATTATACATTGTATTCCATATTCT
 GTTGGCCTCAGGCAAACCTAGGTGATTTCAATTTCTGTTTTATTCCTCTCTACACTAAT
 GTGAAAATAATGATACTTCATATGGGTATTGCTGAGGTTTAGTTAAAATTTATGTAG
 AGTTTTCTATCCAAGCCTATAAAATTATTCATGGGAGTCCTGATTGTTTCTATTACTG
 ATGTGTTATTCCAATAGGTAAAGA**GAATT**TTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	433	488	100.0%	7	+	109320281	109320714	434

SSFM_E4m3-1LR_E4mES_091

TATTGATTATAGAATAAATTCTCTTGAGAACATTTAGATGCATCCCTGCCAACTCATT
 ACACCATCCTCTCTTGGATTGGACTCCTTCATATTCTTCACTTTTGAGAGCTCCCAT
 GTTCCAACCTCTTAATAGCTCCTCAAAATATTTAATTCACAAACACTGCCACATTTTT
 AATTACAGAAAGCCTGTGAAGTTTATATTATTTTATCAGCTTTACAAAAGAAAAAT
 TGAGGTTGCCGGTAAGTGTCAAAACATACTTAGGGGGGATTCCATGGCTTGCCCAAGG
 TCACAAAGATTCAAATGCAGACTTCTAATTTCAAGGTTCAAAATTGTTTTCCCTAAAA
 ACTCAGTTTTGTGTGCGAACTATGATCTCTT**AATTC**CAAAAGCAATGGCAACAAAAG
 ACAAATGACAAATGGGATCTAATTAACTAAAGAGCTTCTGCACAGCAAAAGAA
 ACTACCATCAGAGTGAACAGGCAACCTACAACATGGGAGAAAATTTTCGCAACCTA
 CTCATCTGACAAAGGGCTAATATCCAGAATCTACAATGAACTCAAACAAATTTACAA
 GAAAAAACAAACAACCCCATCAAAAAGTGGGCGAAGGACATGAACAGACACTTC
 TCAAAAGAAGACATTTATGCAGCCAAAAAACACATGAAGAAATGCTCATCATCACT
 GGCCATCAGAGAAATGCAAATCAAAACCACTATGAGATATCATCTCACACCAGTTA
 GAATGGCAATCATTAATAAAGTCAGGAAACAACAGGTGCTGGAGAGGATGCGGAGA
 AATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAA
 GTCAGTGTGGCGATTCTCNGGGATCTAGAACTAGAAATACCATTGACCNAGCCAT
 CCCATTACTGGGTATATACCCAAATGAGTATAAATCATGCTGCTAT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	381	400	100.0%	7	-	109320710	109321090	381

In bold/grey: 570/573 or 569/572 bp identity with L1RP (nt. 4981/4982-5553)

TSD: 4-5 bp

HKSS_E5m31FS_E5mFS_010

ACATGCAATATTTGTTTTTTGTTTCCTGTGTTAGTTCGCTAAGGACAGTGGCCCCATCC
ATGTCCTTGTAAGAACATGATTTTTTTTTATGGCTGCATGGTATTCCATGGTGTATA
TGTACCACATTTTCTTTCTAGTTTCATTTCTTTGTGGTCAGATTAGATACTTGATATTA
TTTCAGGTTTTGTAAATTTTTGGCTTGTTTTGTGAGTTAATGTATAGTTTATGCTTGA
GAATGACCCATTTACTGAGCGGAAGAATGCATATTCTGTAGCCATATGATGAAATGT
TCTCTTAACATCTATTAAGTCCATTTGGTCTATAGTGCAGATTAAGGTCAATGTTTCT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	351	388	100.0%	6	+	49850382	49850732	351

HKSS_C4_F2mFS_F2m_FS_003 (ins. F2-m, normal PCR, sample 11 – normal colon!)

ATGGTCCAGTATGGAAATAGGAAATCCCAGCCTCCCTGCCTCAAGCTAGAACAACC
CAAGAGTTTCCCTGCTAGATCAAGACGAAGCCTATTCTCTGTGGTACTTTTACCTGA
GATCACACTCTTGCTTGGCTTCCTCTTCTCTGCGCTGCTTCTCCCACTCTGTTATT
TGTCTCCTCTATAAGCACTGCTTTAAATGTCATTTGCACAAGTATATTCATCTAGGTC
AGCTTCTAAGGAGTGCAAACCTTAAAAAAATCTAGATGTGATGGTGTAAGTATT
AGTAACCCAGAACAAGGATCGGTAACCTAGTGTTAACAGACAGACTTCT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	336	400	100.0%	2	+	219406734	219407069	336

HKSS_F4m13FS_F4mFS_031

CTAAACGAGCTAGCTTTAAAATTATTGGTGAATAAAAATAGAAATGTTTTCAGAAT
TGTC AACATA TATTTTGGCTGAATTTTATGTTTTCTGTGCTAGATATTTTAAAATGT
CAGTGTTAATTCAAGCTGGAAGCTGCTTAGGGCAAATCTGCCTCCCATTCTATTCAA
AGTCTCACTGAGATAAATACTAATACTAATTGCTTCCTTTGGAAAGGCTAATAAGAAA
CTCAAAAGAATGCAACCCTCTGTCTCCACCTGTGATTGGAAAGCC ACCAGCCTCCT
CGCCTCGAGTTGTCCCGCCTTCTGGGACCAAATCAATGTTTGTTTTACATATGTTATT
TGATGTTACATGTCTCCTTTGTTAAAAGTCAAAATTAAGTACAGTGAGTGGGATAAA
TGTTTTAGGTAACTTTTTGTGTAAATTAATATCTAGAGCTATTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	449	487	99.6%	19	+	28938342	28938790	449

HKSS_F4M13MWLR_4MES_037

TACTACATTGTTTCATAAATACTTTTTCAAATCTGTAATTTGAACTAACTTTTAGAT
AACTTCTGGATTAGACAAAATTATTATCTTTTTTTCTAATAAAAATAACCTTTCCG
GCACATTTTGTGTACAGAATTACATGTTAACTAGAATTTTATCCTTAGTAACCTAAA
ACTTTAGTGAACTCCAAAAAGCAAGAAATCCTGAACCATCAGATATGGGCATTTAT
AGATAAGAACTATCAGATATGGGCATTTTCAGATAAGAAAAAATAGATGGAATTATG
AATTCATAATTTTTGAAACATATTTCTCATATTACAACACTTTCTCAATTGGAAAT
GGCCAGATATCAAATGGGTGTTAAAAATAGCTCTAATCCAGTCTATCATTGTGGCA
CATATACACCATGGAATACTATGCAGCCATAAAAAATGATGAGTTCATATCCTTTGT

AGGGACATGGATGAAATTGGAAACCAT AATTCTCAGTAAACTATC CAAGAACAAA
 AAACCAAACACCGCATATTCTCACTCATAGGTGGGAATTGAACAATGAGATCACAT
 GGACACAGGAAGGGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGGAGGG
 GGGAGGGATAGCATTGGGAGATATACCTAATGCTAGATGACACATTAGTGGGTGCA
 GCGCAC AAGCATGGCACATGTATACATATGTAACCTAACCTGCACAATGTGCACATGT
 ACCCTAAAACTTAGAGTATAAT AAAAAAAAAAAAA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	381	771	100.0%	19	-	28938777	28939157	381

In blue: potential non-templated nt-s (13 bp)

In grey: 363/366 bp identity with L1RP (nt. 5654-6019)

TSD: 14 bp

HKSS_F5m31FS_F5mFS_008

ATGACTAGTGATGCTGAGAATTTTTTTCATATACTTGTTAGCCATTTGTATGTCTTCTT
 TTGAGAAAAGTCTATTTAGATCATTTTCCCATTTTAAAATCAGCTTATTTGTTTGCT
 TGGTGTTGTTTGAGATCCTTGTATATTCTGCATGTTAATCTCTAGTTTGCAAATCTAT
 TCTCCCATTCTGTAGCTTGTATCTACACTCTGTCGATTGCTTTCTTTGCTGTGCAGAAT
 CCTTTAGTTTGATATAATCCCATTTGTCTATTTTCTTTTCACTTGTGTTTTCGAGGT
 CTTATCCATAAAAATCAATGTTCTGAAGCATTTGTCTGTTTCTTCTAGTAGTTTCA
 TAGTTTCAGGTCTTACATTTAAGACTTTATTTT TATTTTATTTTATTTT A TTTTTTAT
 TATACTCTAAGTTTTAGGGTACATGTGCACATTGTGCAGGTAGTTACATATGTATAC
 ATGTGCCATGCTGGTGCGCTGCACCCACTAATGTGTCATCTAGCATTAGGTATATCT
 C

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	410	526	97.8%	4	+	32731413	32731812	400

poly(T) tail might extend further

In grey: 118/118 bp identity with L1RP (nt. 6019-5902)

HKSS_G4m13FS_G4mFS_016

TGTGATCCCATTTGTCTATTTTGGCTTTGGTTGCCTGTGCTTGCAGGTACTGCTCACG
 AAATCTTTGCCAGACCAATGTCTTGGAGATTTCCCAATGTTTTCTTGTAGAAATT
 TCATAGTTTGAAGTTTAAAGTCTTTAATCCACTTTGATTTTATTTTGTATATGGTGA
 TACATAGGGGTCTAGTTTAGTATTTTGCTTATGCATATACAGTTTACCAGCACCAGT
 TATTGAAGACATTGTATTTTCGCCAGTAAGTGTTATAGGCACCTTTGTCAAAAATGG
 GTTCACTGTAGGTGTGTGGATTGTGTTTCGGGGGCCTCTATTCTGCTCCATTTGTCTAT
 GTGTCTGTTTCTATGCCAGTACCATGCTGTTTGGTTACTAGAGTACTGTAAATATATT
 TGGAAGTCAAGTAATGTGATTCCTCTGGTTTTGTTCTTTTGTCTTAGAATAACTTAGA
 ATAACCTTTGGCTATTCTG GGTCTTTT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	490	539	100.0%	5	-	160867637	160868126	490

HKSS_G4m13ESL1_G4mES_025

TCTTTATTTATCAATAATGACATGAATGTAAATGGATTAAACTCTCCAATCAAANCA
 CATNACTGGCTGAATGGATGAAAAACAAGACTCATTGATCTGTTGCCTACAAGAA

ACGCACTTCAACTATAAAGACACATATAGACTGAAAATAAATAAATGAAAGAAGGT
 ATTCCATGCCAGCGGAAACCAAAACAGAGCAGTAGTAGCTATACTTATACCCGACA
 AAATATATTTCAACATCAAACTACAGGAGACAAAGGTTATTATATAATGATAAAA
 GGTCAATTTAGCAAGAGGATATAATAATTGTAAATACATATGCACCCAACATTGGA
 GCACCCNGATACATAAGGCAAATATTATTANAAGCAAACAGAGATATAGGCCCCAA
 TACAAC**AAAANACC**GCANATTCTCACTCATAAGTGGGAATTGAACAATGAGATCAC
 ATGGACACAGGAAGGGGAATATCACACTCTGGGN

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	407	482	100.0%	5	+	160867238	160867644	407

In grey: 73/75 bp identity with L1RP (nt. 5786-5860)

Low quality seq. in the end

TSD: 8 bp

HKSS_H4m61FS_H4mFS_014

AATAGCCATAGGCATGTTGAGATTGCCCCATGCATTGTCTTCTGGGCTGCTTCAGTCT
 AAGTGCTTGTGCTTTGGGAGGTTTTTTCAAGAAGAGACTGGCTGGATGTGGTGGCTC
 ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGAGGGAGCCACCTAGGAGTCAGA
 GACCAGCCTAGGCAATGTGTTGAGATCCTGTCTCTATAAAAATAAAAATAAAATACT
 TAAAATAATTTGTAAAAGAAAAGACTATAAACTGTAGAATTTAGAAGTGAAGGGA
 CACCCCCCCCCCAAAAAAAAAAACTCATCCATATGCCTCATTTAGTGATAAGATATTA
 ACACCCANAAAGATCAAGTTACTTGTCTAGCATCACAGGGTTAGCTAGACAGGTAG
 CTTTCATTATACTTAATAAGGATGTGCTTTANAA**AAAGCCACACTTTTTTTTTT**
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	446	510	99.8%	1	-	223480154	223480599	446

Potential polymerase slippage on poly(A) stretch

HKFM_H4m64mwLR_H4mES_059

GTGGCACAATCTCAGCTCACTGCAGCCTCTACCTCCTAGGCTCAAGCGATCCTCACA
 CCTCATCCTCTTGAGTAGCTGGGACTACAGGTGTGTGCCACCATGCCTGGATAATTT
 TTTATGTTTTTGGTAGAGACAGAATTTTGTTCATGTTGCCCAAGCTGGTCTTGAAGTCC
 TGAGCACAAGCGATCTGCCCATCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATAA
 GCCACCAGATAATTTTTTAAGTATTAATATGGTCA**AAAGATGTGGCTCTT**CCTGTGT
 CCATGTGATCTCATTGTTCAATTCCCACCTATGAGTGAGAACATGCGGTGTTTGGTTT
 TTTGTTCTTGCGATAGTTTACTGAGAATGATGGTTTCCAATTTTCATCCATGTCCCTAC
 AAAGGATATGAAGTCATCATTTTTTATGGCTGCGGGAGATATACCTAATGCTAGATG
 ACACATTAGTGGGTGCAGCGCACCAGCATGGCACATGTATACATATGTAAGTAACTAACCT
 GCACAATGTGCACATGTACCCTAAAGCTTAGAGTATAATAATAAAAAAAAAAATATG
 CTAT**AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA**

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	279	606	100.0%	1	+	223479890	223480168	279

In bold/grey: 158/159 or 155/156 bp identity with L1RP (nt. 5841/5844-5683)

In grey: 120/120 bp identity with L1RP (nt. 5900-6019)

TSD: 12-15 bp

TTTTTGTTTGTGAATCCATAAGATCCCTTAACAGATATGATTCTCAAGTATTTTCTTTC
ACTCAATAGGCTTTTTTAAACTTTCTTGATGATGTCTGTTACGTGCAGACATTTCA
AATTTTGATAGTCATTAATCTTTTTTGCAGTCACAAAGATTTATGTCTATGCTTCTT
CTAAAAATTTTATAGTTTTAGCTCTTATATTTAGTGATTCTATTTTGAGTTAATTTTAG
ATACAGCATATGCCAGGAGTCTATTTTTATTCTTTTGCATGTAGATACCTAGTTTTCC
CAGCACCATTTGTGGAAAAGACTATTCTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	323	394	100.0%	8	+	43352935	43353257	323

TGGTGTCTCCTCTGAAGGTTTGGCCATGCCTCAGCATTGTTTCTGCTACAGTCAGCTCTT
TCCTCCGGAAAGCACTGGAGAGTCCAGGTCTGTTAAGAAATGCTCACTCAGCACCA
AGAAAAATGGGTTTCATCATTTCTAAGCATCTGCTTAGAAATAAAACCAGATGCTCAG
ACCTAGGAATCAATAGAGTAAATATTAATTCAGTATAAGAGAAAGAAGGTCCTACA
TCACCTCCAAATAAGAAAAAATATGGAGGCCAACAATTAAACTGAAGGAAAAATA
TTTTTAAAAAGAAAGAAAAAGGAGTGACTAACCAATTAGACTGTGAGCTCCTTAAG
GGCATAAATGATAAGCACTTAATATGTATTGTTAGTTCAGTAAAAGAGTTTAAAAGG
AATCAACTTAATTCTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	412	459	100.0%	1	+	119624466	119624877	412

CTGGTCTCTCTCCCTCCTTCCTCTTGCTGCCTCTCTCAGCTCTTTAATATATACACAAA
CGGGGATTTCTCCACTCTTCTGTTTTCCCTCTATTTGCTCATTATTTAGATTCTGAGCA
ACAAATGAGAGTCCAAGAGCAACCTGAGCAGGTGAGACATTTTCCCTATTAGACAT
GAAAAAGAGGCATGGATGTGAAGTCCACACCTAAATATTCTTTTAAATTTCTATTG
CCCTATGGGCACACCGTGACTTACTCTTCCACTTGTTCTTCTCCTCTGGGCAGTTCCAGT
CAGCTTTGCCATTGTGCATAACAGGAAGTGGAGTGCTCTTGCAAGGAAGGCCTAGA
GTTTCAGGAGACAAACCATTGAGTTAATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	377	419	100.0%	4	+	129276219	129276595	377

ACAGTTCCTGGCTCTCTTGAACACTGGTTTCGCAAAGTGGGGCCACTGGACCAGCAGC
ATCCACATCACCTGGGAATTTATTAGTAATGCAGATTTTCAGACTCTACTTCAGACCT
ACTGAAGCAGAACTCAGAATGGGGCTTGCAATCTGTTTTAACAAATCCCTGCAGGTG
ACTGCAGATGCACACTGAAGTTTGAACACCACTGCCTTAGAACAGGGGTCAGCAAA
CCCTTTCTTTAGAGGGCCACGTAGTAACTATTTTAGGCTGTGTGAGCTACATGGCCTC
TGTTGCAACTCTTCAACTCTGTTGTATGAGAACAGCCACAGAGAGCTGTGTTCTAAT

AAAAATGTTACTTATGAGCATTAATATTTGAATTTCA**TATAATTTTC****TTTTTTTTTTTT**
TTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	389	422	100.0%	13	-	43328787	43329175	389

HKSS_61A8NLRMW_E8NES_005

TCAAGGTTGATCTGAGCCGTAGTCAGTTGTCCTGCTGGGGAAGGTAGGCCCTGGCTG
AAGGGACACATACAGGCCTCCTTAGGTCAGATCCAATGTCCCAGCTGAGCCATTTCC
TCAAGATAAAGCTTTAAGGGAAACCAATGGCCTGAGGAGTGTAGGAGATCATGTGG
GGGCCTCAGAAAGAAAAGGCTGCTGAATTAAAGATGGATTCTTCAGCAAAATGTGT
CCTCAGTAAGAGCAAACCAGAGATGTTCTAGAGCAGGGGTCTGCAAACCTGAGGCCT
GTGGTTCACATACAACCCACTGCCAGCTTTTATGCAGCTGGTGAGCTAAGATTAGTT
TTCACATTTTTTTAATGGTTAGGGAGAAAAAAGCAAAAGAATGACAATATTTTGTA
CACAT**GAAAATTATA**CCATTTGACCCAGCCATCCCATTACTGGGTATATACCCAAAG
GAC**T**TATAAATCATGCTGCTATAAAGACACATGCACACGTATGTTTATTGCGGCACTA
TTCACAATAGCAAAGACTTGGAACCAACCCAAATGTCCAACAATGATAG**T**CTGGATT
AAGAAAATGTGGCACATATACACCATGGAATACTATGCAGCCATAAAAAATGATGA
GTTTCATATCCTTTGTAGGGACATGGATGAAATTGGAAACCATCATTCTCAGTAACT
ATCGCAAGAACAAAAAACCAACAC**T**GCATATTCTCACTCATAGGTGGGAATTGAA
CAATGAGATCACATGGACACAGGAAGGGGAATATCACACTCTGGGGACTGTGGTGG
GGTCGGGGGAGGGGGGAGGGATAGCATTGGGAGATATACCTAATGCTAGATGACAC
ATTA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	411	440	100.0%	13	+	43328386	43328796	411

In bold/grey: 440/444 bp or 437/441 identity with L1RP (nt. 5488-5931 or 5491-5931)

TSD: 7-10 bp

HKSS_A11n31FSHW_A11nFS_063

CAAATTTTCAATTTTCAGTTGCAAAGTTCTTCGCAGGAACTTTAAAAAACCACATGAA
ACTTTCAGAGTAAATTAGAATCAAGAAAACTTCACCAAAACTGATACTAGTAAAA
AAAGAAACCACTTATAAAGCTATCTTTCTAGAATAACACTATATATATGTGGACAAA
GATATTTTCTTATTTTACAAGGACTACATAATACTTTATGCAATTGCCCTCACATTTG
GCAATATCAATAAATTCTCAAATAAATTTTAAATGTCTTTATCATGACATTTATTATT
ACTAATAATGAGCCAATATTTATTAAGAATTGTTTATCTGTCAAAAACCACAAAACA
CTTTTATTATTATTTATGAACACTTTTATATTTATATTTATATAATATATTTATAA
ATACTTT**TT**
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	410	504	100.0%	5	+	104745470	104745879	410