

Pancreatic cancer somatic L1 Sanger sequences

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

HKSS_A5nestA55M_A5Pa_069

AATCCATGATCTCTCTTCTGCATTCCAGATCTGAAATTCCAAATTCCCTAAAGAACATT
TCCAAATAAAAGTCCAAACAGCATCTCTAGATCAAGAAATATTACTCTATCCCTATT
CATTTTTCTTCAAACCTTGCTTTTACTTCTGACATTACAATATCTGTAAATTTTACAT
TACTTCCTGTAGTTCATCCTTGGCTTAAACCTTTTGCCCCCTTTTCTTTACCTCACCC
TTTCAGGAAGAGTTCTCAATCCTGTAAATTTCTTTTTGTTCACAGATCATGCATC
CATCATTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	301	342	100.0%	2	-	147424400	147424700	301

HKSS_PAN_A6_M_PANA6_FS_009

GGTCTTTGGCTTTGATAGAATAATAAATAGGATATTAATAGTCAAAGGTGGGAGCA
GATAGTCCAGGTAAATGGCACAAATTAATGCCTAGAGGCAGGAAAGTAAAAAGGA
AGGAATGGGAATAAGAGACTCATTTCGATTTAGTTAGAACACAGAGTAAGCATGAAG
TCATCAGGTGGTAGAATGAACATGCATATACAGCCAGAGGCCAAAGAGGACCGAGAG
GAGGTGTAAGTGGCTCCAGGGAAACCCACCTTTGCTGCTTAACAAACAAATCAAAT
CAAATGTACACTAATGGTGCACCAGAAAAGTGATCTTTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	319	337	100.0%	14	-	80251565	80251883	319

HKSS_A7A55T1_PANC1A7FS_024, HKSS_A7-A55M_A7PanFS_067

TTCTTAGTATTTTCTGAGCCAGCATCATTATGATTAGAAAAATGGAAATGATCCTAAT
GGAAATGACTACAAAGAATTAAATTATAAGAACATTGTAAATGTGTTTCTCTCAATT
ATAATCTCATTTACACTGTACGAAGGTTAGAGGTTTGCATTTTTGCCATCTGAGTCTT
CACAAATTGCTGTTTTTCAAGGGACAAAGGTCTTTTAAAATAAGTATTGAATTTCTA
TCTACAGGAAAAAATTAAATATATGACAGCAGAAAAAGGAGCACTATACCCATAATAC
TATGTTAGTTGCAACATCTTACTATTTTAATGAGTGCAGTAACTCATTCTTCTTAG
AGTAATAAGAATTGTGTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	369	384	99.5%	2	-	51666633	51667001	369

A7-m: HKSS A7A83T2Panc A7FS 078, HKFM A7-A83T1-P A7FS 085

TAAAGACTTTCTCTTTAAATACAGGTTTCAAAAAGATTTTAACAATTTCTTCTCTCTT
TATTTTAAAATCTCATTTAAATTTAGATCTAGACATTTTACCTCTAAGCTATTTGTGT
ACTTACACTCTTCCTTATATTAAGACCAGAAGCATAGGACAGGGATGAATTAAGGA
AGGATGAATCCTGCTGTACTTTGAGTTCACTGATCATCTCAGATGATTTTTCAAATGT
TTTGGGCTCACTGAAATCCAAAACAGGTTTCACCCATGCTTTTACTCTTAAGTTTGGT
GCATGTGCAATTTAAGGGAAATTTAATCCATATGTTTCTGATTCGTTTACACTTAAAT
AGTCAAAATATTGTTTTTAATAGTTATTTGATGCCCAAGTAGCCTTTTGAACCTTTT

HKSS **A8A83T2Panc** A8FS 067, HKFM A8-A83T1-P A8FS 094 (ins. A8-m)

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	350	477	100.0%	18	+	47214067	47214416	350

HKSS **A12A57MG** PNA12FS 088 (A57M, semi-nested)

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	414	445	100.0%	2	-	56127365	56127778	414

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	414	463	100.0%	2	-	12986727	12987140	414

HKSS **B7A55T2Panc** B7FS 072, HKFM B7-A55T1-P B7FS 087 (ins. B7m)

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	458	484	99.8%	1	+	172295161	172295619	459

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	328	477	99.7%	1	-	172295624	172295951	328

TSD: 5 bp deletion

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	394	429	93.7%	2	-	229163811	229164204	394

ATTAATATTTACAATTATAGAAATTAGATCCTAAGAAATTTGACAATCTTGAAGGC
AGACAAGAGAATATCTCAGCAAGTTTATTGAAAAGCAGTTTTAAAATTACTTTTAAA

ATGTAAAAAAAAAAGATAGTTTTATAACTGTAATGACTCATAGCAGCACTGTTGGA
 ACAAAGATATGTTTCCCTGAGAAGCTTATGTTAAAGGGAACAGCCTGCTATTTAGTG
 TACAAGTTTTGTCGTGTTCTATATAAAAATATTTTCAAACCCAGTATAATCCTATCT
 CCTAATCATTGCAGTTTAAATGTCTCTAACTCTTCAGAAGTGGTCCAAGAAAATAGA
 TCAGCTATAATAAATAGGCTTATTAACACATTC**TAATTGGGTAAATTGTACCTTTTAT**
TTTGGCCCTAACTGGTCACACTTCTGGGAATATTCTTCCCCTATCAGGAATTTCCATG
TTACCAATATAATTTTGGGATTCAGTCACCTTTATTAGACATGTGGCCCCATGTGAA
GTTTCTTTTCTTCTTTTTTTTTTTTT

Not highlighted:

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN (predicted hit)
1	380	543	100.0%	6	-	129642037	129642417	381

Highlighted in yellow:

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
6	173	173	100.0%	22	-	29065291	29065458	168

HKSS_D7mA33T1FS_D7mFS_007

CTCCTGTGCTGACTTTGGTAAATGTGTACAGGTGAAACCAGCATGTCTTGCTCTCGTC
 TCAGAGTAAATTCCCATCTGCGCAAGACTTGAAGAGCTCAGTGGTAGTAGAGTTTT
 TACTTTAAAACAAAAAGACAACAAGTTTGAGCTTTGAAACTGAACCACCAGGTCCA
 CATTTATTAGTCCTATGGACTTCACCAAATATTTGTCTTCTCTGAGCCTCAGCTTCCT
 GAGCTGTAAAATGGAGATAGTATTCAATTTAGCCTTGAAGGGAGGTTGTCAGGTTTA
 AAGTTAATGTTGTGTGAAAGTAGGCAGTATTCCACCTTTACACTGGTAATGTTTTTTA
 AGTGCTTCAAGGAAGCTCTTATCTAAGTTATAGCCTGATGAAATTTTGTAAATGCAAG
 AAGTTTTACAGGTAAACTCAGCCATGTAGTTCTT**TTTTTTTTTTTTTTTTTTTT**

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	436	459	99.8%	5	-	37823044	37823479	436

HKSS_E5A57Mnn_PANC1E5n_026

AGGCTAATTGTTGAAAGTTCTGTGAGTGTTCCTGATGTGGAGGAGTTGGAGTGA
 ATTATTGCGTGGACCCTGCACTCCGCAGGGGAGCCCCGGGTCTCAAGGCGGGGAG
 TTTGATAAGCCGTCTGTTCTGAGGAGTTTGGATTAGTCCATCTGTTTCTGGTTTTAG
 AAACCTGAGGTGAAGAAAATAAATAACAGAGAAAACAAAAATGAAAAATGCCCCC
 AGTTCCTGAATTGCATGCAGTAAGTCTGCTTGTCTTCT**TTTTTTTTTTTTTTTTTTTT**
TTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	265	294	100.0%	8	-	36416805	36417069	265

HKSS_E7A83T2Panc_E7FS_076 (ins. E7-m), HKFM_E7-A83T2-P_E7FS_083

AGTGGAGGGAGAAGCCAGCTTTATAGACTAGTATCCTGTGTGGCCACGTGGCAATG
 AATTTAACTAGTTATCTGTTGATGGAAATGCGGATTATTTTCTGTATGAACTATAACC
 ATGCACCAACAAATAACTGCCTACATGCACATGTGTATCTTAAATTCCCAGAGGTGC
 AACCGTGGCTAGAAATGTGTGCAGTTGCGCACATTCACACTGATGACGTTGATGGCAG
 GGCTGGCTGGGGATGCAGAGTTGCCTGCTTCGAGGTATTCAAGTAGAGGGGACTCTT
 CTAGGAGCCTTTGAATGACCATAACATTGTCAGGCTCTGGACCCAGCTGGCCTGG

TTTCATGGACCCTGACAATGATTTAACCCTTTGGTTCTCAACTTTTTTTTTTNTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	393	452	100.0%	6	-	136535420	136535813	394

HKSS_F5A43M_PANC1C5FS_028 and HKSS_F5A43.22_F5NEST_051 (A43-22: new, independent liver metastasis)

AAACAACACAGGGCCTTCATCCAAGGAGCCATAACTGGACACAGTGTAACCCCAAG
GTCAACAAACCAAGGCAAGATTCTTCAGTCAGGAACACAACCTTCTCAAATGTGAT
ACATGTGAAGAATCTTTATAAGGTCAATTTTCATCTTTGTAGAGTATTTTTTCAACAAG
TTGACAAAATATATGATTGCCAGTGAAAAGCAGAAGAATTTGGTCATTACAGAAA
GATGAGAGTAATACAGAACATTTGGACTCTTACCTCCCACGTACTTGATTACCTTAT
GCCCTCTGAAGGCAAAGATTCCAGAAAATGGACTGGAATCCCAATAGCCCAGACCT
TTGTGCCTTCTAGTGTCCACATTAAAGCCATTAAACAAATGGTTTATTTAAACTTCAG
TTTCTGAGAATGCCTTT
TT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	416	558	100.0%	10	-	78153927	78154342	416

HKSS_G4nestA33Mmw_G4Pa_071

CTTGTTTCATTTGGTTCTTGGGTGAGCAAACCCACAGGAAACCCACTCTTTCTCTTG
ACTTCATAGCGACGTGGAACAGACTTGCTTGCTCTGCTTTATCAGGCTTGGGTGATT
GATTATAAATTGAGGTCTCTTACCCTTGATTATGACAGCAATATATGTATATTATA
GACATTTTCAGAAAAATCATAAAATTATGAAACAAAAGTGACCTGTTTTTTTTTTT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	221	278	99.6%	1	+	158125031	158125251	221

HKSS_G7m_L1ES_G7m_FS_011 (3' junction from the ES L1 PCR product) – within 700 bp and 1 kb of two APAF1 exons

CCAAAGGTTTTTGGTAGCAGAATTTGAGGAAAATAATTTTGTAATTATGGTCTGGA
TTATAAATGAATTGCAAATTCTGCTTTTTCTGTGCTGAAAGAAAAGATCTCTTTAGCA
CTATACCCATTTGATAGCCATTTCCAGTGTGGTTTGTTCAGTCCTCTGTGGACTGCC
TGCCTGTTAAACAGTGCAGAGGTTACATTTCCGTCATTGGGGGCAGCGAAGGGCT
CCTAATTGAGTCACAGTCTGCATGCTAGGCCAGTTTTTATTACCCTGCAGTGCTTAAG
ATATACATACAAACCATGCCAATTTTATTAGAAAACAATCTATTTTTTTTAGATATA
TAATTTTGACTTTTAGAAAACAATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	376	426	99.8%	12	+	99119620	99119995	376

HKFM_G7-A55T1ESL1_G7ES_090

TAATTTCCCTGGAAAGCCCATCTGATAACACCTCTGTTTCCTGCAAACGTGATACTCTC
 CTAGTCTTCTGCACTATATACCTGTTTCCTGGAGTTTTAGATCCTCCTTTGTAATGAAA
 GGGGGAAAACCCCATCTTCCTCATCTACACTGGTTACCAAAGTAGTCATCCCAATAC
 CCAAACTTTTCCAATCGGCTCCCCAATTCTTCTGACACAACTAGGTCAACTGACTCCT
 TTTCATAATTTCTAATCTTTCAGCATGCAATTCTTTCCATATGGTACTATATTTCCAC
 AGACACAGAGAACAACATTCTAAGCCTCCT**AAAAAGATTGTTTTCT**TAATCCAGTC
 TATCATTGTTGGACATCTGGATTAAGAAAATGTGGCACATATACACCATGGAATACT
 ATGCAGCCATAAAAAATGATGAGTTCATATCCTTTGTAGGGACATGGATGAAATTGG
 AAACCATCATTCTCAGTAAACTATCGCAAGAACAAAAAACCAACACCGCATATTC
 TCACTCATAGGTGGGAATTGAACAATGAGATCACATGGACACAGGAAGGGGAATAT
 CACACTCTGGGGACTGTGGTGGGGTCGGGGGAGGGGGGAGGG

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	336	614	100.0%	12	-	99119980	99120315	336

In bold/grey: 35/36 bp identity with L1RP (nt. 5653-5618) or 29/30 bp identity with L1RP

In dark grey: 252/252 bp identity with L1RP (nt. 5640-5891)

TSD: 10-16 bp

HKSS_G8mA57T2FS_G8mFS_005

TCTAACAGGTGTCCCATAACCAGGACAGATCACCGGGATGCCTGCCTGCCCTGATAA
 CTGATGTTGAAGGTCAGCCACCTCCCCCTACCCGGACTTACTGCTTCCCCACCCCG
 ACCCGCCACGGCTCTAACACACACTGACACATACTGACACACACACTCTCTCTCACT
 CACACACACACCCCTGCAGCCCTCATCTCTTGTCTCTCTTGGGCTGTGAAGTAGGTA
 AAGCTTGGCCTCTGGGGTCCCCTTTTTGTACCTTTTCCATCTTTCTTGGAGGCCTGGC
 TCACGCAGGCAGGGGGCCGAGGCGCTCCTTCTCACTCACTCTGTTGGCAACCCAACC
 AGCCTTTAAACTGTGTCTTTTCATGTATAACAAAAGACCTTTCTTTTTGTCTTTTTTT
 TT
 TTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	397	472	98.3%	6	+	40492018	40492414	397

Comparison with TIP-seq:

HKSS_B2n83NCOMP_B2NEST_001 (N-spec)

AACAGAAATGTTGCAGGAGCTATCTCTGTAAACTATTTGTCTCTGAAACACTTTTGT
 TTGCATCCGAAGCTAAAATAAAAATAATACTTCATATACGGATTTTCCCTACAT
 CAAA**A**CTTTTTTTTTCTTAAATGAATGCAGAGAAGATTAAATCATTTGTCTTAGAAA
 ATCAACATTTCTTCCTATTCAAATATGCCTTTTGGAATAGTTTGTATTCTTGGCC
 ATCTGCCATTACACTTCTATTGAATAATTAGGATAGTTGCTTAATTTAACTACAATTG
 TATATGAGAATAAGCTAGGCAATTTGCATTTGACATTTGGAAATGGGAAAATATTTT
 TT**TTTT**

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	347	351	99.8%	1	-	195892866	195893212	347

HKSS_B7A57MFS_B7FS_085

TTACGGAAAGAAGGGGTTATTTTAAACCAGAAAAAAGTGAATGTCCAGAGAGATA
AGTAAAAAGTGGTGGTAATTAAGCTCTACAGCTAAGACAGGCAGAACAGAGTGATA
ATGTTTATCAAAGAGTGTAATTTAAGAAAAAACTGAAATCAGAGAAAGAGCAGAT
AAAATAAATTTTTGTTTTGTTTTATGATTTTTGAGTTAAATGCTATTTCTAACTCAGA
GAAGACAGATTTTTTAAAATTTACAGGAAAGGCAATGAAGAACAACATTTTAACTA
AGTTACTATATATTTTGTTTAAAAATCCTATAANTCGATTTT

TTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	324	362	100.0%	7	-	53186944	53187267	324

HKSS_E5nA43T1CO_E5NEST_088 and HKSS_E5nA43T2CO_E5NEST_086

GCCTTGGGGCATAACTCAGGTGATCACTTTAATACATACTTTTCATGCTGGAAAGAA
TTGATAAACAATGTCTGTAAAAGTAAAATATTCTGATGTAAGTGAAGCTGGGATCAA
CAGAGATAAAAGTTGTGGAAACAGATAAGTCCTGTTGGAGGTTTCCCCTGAGGGAT
TTTTGTATTACTTTGTGTAAGCGGGGAAAATGAAGGGATTTTCTGGATTCTTCATA
ATCAGATTCAAATCTCCCCTTTGCACAGGTGAGCAGTAAGTAGATATTTGAAAAGCT
ACTATTGTGGATGGACTTTTGCTCCTGCTGGACGTTTTCTTTTTTTTTTTTTTTT

TTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	324	358	99.4%	11	+	96689105	96689428	324

HKSS_E5A43T1COMP_E5ES_009 (PANC1 comparison 5' junction long range FS product with ES and GTG primers)

ATTAACATATGAGAGGGGAACAGGTAGCATTAGAAGATCTGGCTGGGTAAGGTTTGA
AGCTCTTGTTCTTCCTCATCAAAATATTGTGGTCCCCAGTGTCGCCTCTCTGATACCA
GTTCCCAGTCAGATGTGCCCCAGAGGGTGCTTCCCTCTCCACATCCTCTCCTTCTGCC
TAAACAGTCTGAGCATCTAACCCTCAGCACTGAGACTGCTCAAGTACAATTTAAAAA
AAAAGGTTCAATTGATCTCTTCATAGTTGATGTGTTGTCTTCTGAAGTTACTTTAAA
TTATTATTACTCTGGACCCTTTTTACCCCTGCCTTTCAGCATGCATCACTCTTCACAT
TGATTTTCATCATTTCAATGTAATTGGAAGTAAAAACGTCCAGCAGGTTTTGATTT
GCATTTCTCTGATGGCCAGTGATGATGAGCATTTCTTCATGTGTTTTTTGGCTGCATA
AATGTCTTCTTTTGAGAAGTGTCTGTTCATGTCCTTCGCCCACTTTTGTGAGGGTTG
TTTGTTTTTTTCTTGTAATTTGTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTT
GTCAGATGAGTAGGTTGCAAAAATTTTCTCCCATGTTGTAGGTTGCCTGTTCACTCTG
ATGGTAGTTTCTTTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCATTGTCAA
TTTTGTCTTTTGTTGCCATTGCTTTTGGTGTTTTGGACATGAAGTCCTTGCCACGCCT
CATCTCACACCAGTTAGAATGGCAATCATTAAAAAGTCAGGAAACAACAGGTGCTG
GAGAGGATGCGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAACTAG
TTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCAGGGATCTAGAACTAGAAATAC
CATTTGACCCAGCCATCCCATTAAGTGGGTATATACCCAAATGAGTATAAATCATGCT
GCTATAAAGACACATGCACACGTATGTTTATTGCGGCACTATTCACAATA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	394	492	99.0%	11	-	96689412	96689804	393

TSD: 15-17 bp

In bold/grey: 361/361 (or 359/359) bp identity with L1RP (nt. 5310-4950)

In bold/grey: 277/277 (or 276/276) bp identity with L1RP (nt. 5322-5598)

HKSS_E11nA43T1CO_E11NE_024 (in SOX6 3'UTR, T1 only)

CAAAAAACACACACACTCACAGATGTTGTTTCGTAAGTGTTATAAGCACTGGATATA
AATGGTATTTTTTATCACTTCTGACTAATGTGAAACTGTTGTACGAAACTACATGA
ACAAAAGTCATCTGTTTCGACTCGTGTGGGCTTGCCTCACAGTTGCCGGATTTGAGT
CATTTTTATGTCTTGTTATTTCATTTATTTATGCAAATACATGTGTGTATGAACACTT
TGTTTTAGCTCCAGCTCTGCCTCAGTACTGGGGTTCATTTACTTTTAGCCATGTTCTT
AAAAATGAAAGGCTATTCAGGAATGATCTGATTGTAAACGTCTTTTTTCATTGGATCA
AACAGTAATGCTGTATTTGAATCTAAATTTTGTGTATAAGCAGTTTATTTATTAGCCA
AGTTTGGCTCTAAATATCCATGGAAATTAAGAATGACAATCATAGGGATCAATTTCAT
TTTATTTTCAGTGGGGCTTAAACAAAGTTTATATGACTTTACCATCTCATTTTAGATT
TTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	521	536	100.0%	11	-	15991265	15991785	521

HKSS_F6nA43MCMC_F6NST_094 and HKSS_A43T1COMP_F6NEST_005

AATTCCTTGCTGGTTATAAAGCTAATTTATTATGATTTTTCTTTTTAATCTGCATACATT
ATGCTTAACTGAAAATGAGAATCTGAACTCCTAGTGACTAGGCTCATTTTTATTTT
ATCTATCATTTTTGCAAATGTCATTAATCTGGCAAAAAGTCTTATACAATCTTCTCTT
GCTTTGATATTGCAAGAAAATCCACATAAGACATATTCTTAATGGTGAAGAAATCT
TCAAAAAGGTAAAAGTTTAAAATGTGGAAGGACAGAACTGGTGATTCATCCTGGA
GAGTTATCTATTTAATTTAAAATTATCTTTTTCAAAATAATTTAATACATTTGGAAAA
AAATCCAGACTTGAGAGAAAATGGGCAGTTTTCATAACATTAGAATCTTATTA AAAAT
CTGTTTTT TTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	410	427	100.0%	6	+	98573583	98573992	410

HKSS_F10nA55T1CP_F10ST_059

GACACATGATGGGGAAAAAGACACGTTGGAGCCAGCTGAGGTGGTGGTGGGAGGG
AGAGCATCAGGAAGAATAGCTGATAAATACTGGGCTTAATACCTAGGAAATGGGT
GACCTGTGCAGCAAACCTACCATGGCACACACTTACCTATGTAACAAACCTGCATATC
CTGCACGTGTATCCCGAACTTAAAATAAAAGTTGAAGAAAGAAAATAAAGAAAA
ACACATGAAATTTTAAAAATTACATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	254	322	100.0%	1	+	73472711	73472964	254

HKSS_F10A55T1CMP_F10ES_007 (PANC1 comparison 5' junction long range FS product with ES and GTG primers)

CTTACTCCCCAGAGGAAAATTACATTGAATTATTTCAACGGTTTATGTTTTCTAAGAG
ATGACCTCATAGCTGCGTATAATATGCTTATGTCATTGTTTCTTGAGATTTTTTAAGA
CATTAGAAATTGTTTTTTTGAATAATAGATCAAAATTTAGCTTGACTCAACCCATCT
TTTCATTTTCCTTACATTTATATTTAACATCATATTTAAACTTCTGTAATTTTTTAAAA

AGTGCTTTGGCTCACCAAACATTTTTTGTATCTCATAGACCATAAAAAATAACTTTTAA
 AATACTCCCTCATACCTTGTAAATTAGAAACTGAAAGCTTTAACTATATGTTTAAA
 TGGTCGCAAAGGTCATACTCTAAAGCATATTATAAATATTTAATTTTTTAAAATTAAA
 AATATTTTCATCCTTTC**AAAAAATGTAATTTT**ATAGCAGCATGATTTATACTCATTG
 GGTATATAACCCAGTAATGGGATGGCTGGGTCAAATGGTATTTGCACAT**T**GTATGTTTA
 TTGCGGCACTATTACAATAGCAAAGACTTGGAACCAACCCAAATGTCCAACAATG
 ATAGACTGGATTAAGAAAATGTGGCACATATACACCATGGAATACTATGCAGCCAT
 AAAAAATGATGAGTTCATATCCTTTGTAGGGACATGGATGAAATTGGAAACCATCAT
 TCTCAGTAACTATCGCAAGAACAAAAAACCAACACCGCATATTCTCACTCATAG
 GTGGGAATTGAACAATGAGATCACATGGACACAGGAAGGGGAATATCACACTCTGG
 GGACTGTGGTGGGGTCGGGGGGANGGGGGGAGGGGATAGCATTGGGAGA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	437	847	100.0%	1	-	73472948	73473384	437

TSD: 13-17 bp

In bold/grey: 71/71 (or 67/67) bp identity with L1RP (nt. 5556-5486)

In bold/grey: 342/344 (or 341/343) bp identity with L1RP (nt. 5563-5905)

HKSS_G6nA43T1CMP_G6NST_053

TCTCTCTCCGTGCCTCTCTCACTCCTGCTCTGTTTGCTTATCCCAAATCCTCTTAATCT
 CTGTCTAATCTCTTTCTTCTTATACTGACTGCTTCTTTTTCTTTTATTTTCATCC
 TGTTTCTTCTGCCAGCTCATGTTTAAACAAGAATAACCCCTGTAACATGACATTCTTT
 ATAAGTGAAGTGATTTAAAAAAACTTTCTTAGATGTAGCTCATTATTTTGGGAAAT
 CATGTCTATAACTCGCAATTCAACAAGGATTGAGTTTGTGCAGTATGACAGAGACCA
 TGTTGAGTGCTGAAGTTTTATGAAGACAAATAATTCACAGCCCTCTATTAAGAATCT
 GAAGCAGGTGGCTGGGGGGACATATGTAAGTGTGTTTATTGAGGAGTCGAAGTGTG
 TGATGGATAATTTTGAAGAGTTTTTATTTTTTT**ATTATACTCTAAGTTTTA**

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	437	455	100.0%	2	+	126511550	126511986	437

In grey: 18/18 bp identity with L1RP (nt. 6019-6002)

No new poly(A) tail - endo-independent insertion?

HKSS_H6A55T1CMP_H6FS_064

TGATNAATTTTCAGTTTACCAGATTAAAAACTCATGCTCATCAAAATAGACACTGTTA
 AGAAAATAAAAGAGTAACCCCAAGACTGGAATAAAATATTTGTATTATATAAATCT
 GACAAATGACTTGTATCAAATAAATAAAGAACAACACTACATATCAACAACAAAGAA
 GATAAAGAACCCAATCAATAATTGGTAAAAGACTTTCTCAGGTACTTCATAAGATAT
 AGGAATAACCAATAATTATATAAAAAATGTGCTCAACAGCAGTCATCAAAGAAATTT
 AAATTAAAGCCACAAGATACACACTCACCAGAATGGCTAAAATTAAAAACACAGAC
 AATTGCAAGTGATAGCAGAGTGGAGAGCAACTGAAACTCTCATAAATTGTTGGATG
 AAATGTAAAATGGCATAAACACTTTAGAAAAGTGTGTTAGATACTTC**TTTTTTTTTTT**
TTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	442	470	100.0%	14	-	93973639	93974080	442

HKSS_A55T1COMP_H6ESL1_009

TTTGTTTATCAACCTTCCTATTGATGTATATTTGGGTTGTTTTTCAGTTTTTAGCCAATA
TACATAAAGCTGCTATGAATATCTTATACAAGTTTTTTTGTGGACTTATGCATTTATT
TCTCTTGGGTATATACCTAGGACTGGAATTGCTGGGTCATAGAGTTTATAAACTATC
GCAAGAACAAAAAACCAAACACCGCATATTCTCACTCATAGGTGGGAATTGAACAA
TGAGATCACATGGACACAGGAAGGGGAATATCACACTCTGGGGACTGTGGTGGGGT
CGGGGGAGGGGGGAGGGATAGCATTGGGAGATATACCTAATGCTAGATGACACATT
AGTGGGTGCAGCGCACCAGCATGGCACATGTATACATATGTAACCTAACCTGCACAA
TGTGCACATGTACCCTAAACTTAGAGTATAATAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	168	200	99.5%	14	+	93973473	93973640	168

In bold/grey: 266/266 bp identity with L1RP (nt. 5754-6019)

Potential TSD: 1-2 bp