

Stomach cancer somatic L1 Sanger sequences

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

HKSS_A1.2043.T1_A1NEST_025

TTCTTTTGTGTGATATCAGTAGCGTATTTCCAAACATTTAGTTGCACTAGGCCAAAATG
GATGGTATCTCCCCACCTAGAAGACCTCACTAAGTTAGCTTGAAGCTAACACTTCC
TTAACCTGCTGTCTTGTATACTACCTATTCTGACTGATTTTCCCGAGCTTTCCTTTTCC
TACACTCATTTGTAAATACAGCTAATGCCACTGTCTACATTTGCGTATATATAAAATA
ACAAAAGATTATCAGCCCTTTTAAGTCAAATAATTATCATTTGGTTATATTTGGATT
CAGTTTGAAATCACCATTATTTTGTAGACTTTGTTTGAATAATCTTTTTTTTTTTTT

TTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	338	362	100.0%	18	+	23904514	23904851	338

HKSS_A1sFS20432A_A1SFS_061

TTTTCTAAAAACGAAAATTGCCAAAAAGCAAAGCATGCAGGAGACGGATGGATGG
ATGCCATCGCAGCCTCACGCTCCTGCTGATGGATGGTGTGCCCTGAATGACTGGGAG
CACTCACTAACTACTGCCATACCTCCTGCTTTCAGGGAAGCTGGCACAGCCATCCC
TTCCAAGAGCGAATCCCTCCACGCTCACCATCTCTTTAACTGCCTCACTTAGTCATAC
CCGGCCTTTTCCAAAACCAAAGCACCAACAGGCACAGAGACTATCCCAGCCCAGCA
AATGACGAAGCTGAAAGGTGGCGCTAGGACTCTGTCTCTGTCTCTCTTTTATTTT
TACGGTTCTAATGTATACATGTTAGCATTTGATCTCACTTAAATATTTACTTCATGA
TTTGTGGTAGGGGAAATGTCATTAAAAAAAATTTCCTTTAGCTTAATTACAAAAGATG

[illegible]

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	493	556	100.0%	5	-	166988743	166989235	493

HKSS_A1s2034N1UG_A1sES_069 (upper band, GTG primer)

ACATTACATTGCACATTTTCATTCTTTAATATCAAAGAGAGCTAGGTTCTTTGAAATGT
AAAACATCATAAGTGAAAGGATAGGGCCTGCAATTCCCCCAGGAGCCCAAGGTCAT
TGTATAAATAACATTCTGGTTCCCCTATTAATTTCACTCCATTCTGGGATGTGCAGGA
GGCCATAATTGTTAGAGGAAGAGGAGAAGGCTGAACTTTTGCTGCCCATGACGGAG
GTCAGACAGTGTAACTGTGGTCCGTGGTTCAAACAGTTGCCCAAAATGGAGCAAA
ATAAATGTCCTTACAGCTGGTAGAAAGATCAAGATGAAACGTCTA**CGTTGTTTTTCC**
CTTAAAAAATCAGAGATGCTGCAAGAGCTCCCAAGAAGGTATTAATTTCCAGGTA
CTACTGCAAAAATAAGGGTGAGGAGGCGAGTGTTAGGCTTTATTCTCTGCTGTGAATA
GATTAAGCAGACACCAATTTACACCTCATTGTT**AAGAGTAACTTTTTCT**CATTGG
GTATATACCCAGTAATGGGATGGCTGGGTCAAATGGTATTTCTAGTTCTAGATCCCT
GAGGAATCGCCACACTGACTTCCACAATGGTTGAACTAGTTTACAGTCCCACCAACA
GTGTAAAAGTGTTCTATTTCTCCGCATCCTCTCCAGCACCTGTTGTTTCCTGACTTTT
TAATGATTGCCATTCTAACTGGTGTGAGATGATATCTCATAGTGGTTTTGATTGTCAT
TTCTCTGATGGCCAGTGATGATGAGCATTCTTCATGTGTTTTTTGGCTGCATAAATG
TCTTCTTTTGAGAAGTGTCTGTTTCATGTCCTTCA**ACCCACTTTTTGATGGGGTTGTTTGT**

TTTTTCTTGTAATTTGTTTGGAATTGAACAATGAGATCACATGGACACAGGAAG
GGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGGAAGGGGGAGGGATAG
CATTGGGA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	502	987	99.9%	5	+	166988258	166988759	502

In bold/grey: 378/379 or 376/377 bp identity with L1RP (nt. 5535 or 5533-5157)

In bold/grey: 99/100 or 97/98 bp identity with L1RP (nt. 5805 or 5807-5903)

TSD: 17 bp

HKSS_A2sFS20432A_A2SFS_049

TATCCCCCTTGGTTGTGGTGTAGAGGGATGGAGAATCTGATTTATCATTATTATACA
AACCCAATAAGAACATGATGTGGTGGTTGTTAGCCATGGCTCCTAGAAGACAAACTT
AAACTATAAATGATTATAGATAGGTCTGTCTAGTGGTTAAGAACACAAACATGATT
TTGGACAAATTATTTAACCTCTCTGAATCTGTTTCCTCATTTATAAAATGAGATAATA
ATAACTTGCCTCATTGGATGTACACAGAAACAATGATAACATTTTACTTTAAGGCTA
AACTGCTTTTTGGATACAACAACAACAAAATACAGCTATTTTTATCACATGAGAAT
ATGGAAAAGGGTAATTTTCAGTGATATAGGAAATGAGTTGTCCTCATTATCCAGTGGT
GAGTTGACTTCTCAATAAAATACCAGCTCTACTTATCTTCATTGTTATTATTATATT
TCA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	461	592	100.0%	5	-	11597986	11598446	461

HKSS_A2s20434A_A2sNE_082 (normal)

CTTAAACTATAAATGATTATAGATAGGTCTGTCTAGTGGTTAAGAACACAAACATGA
TTTTGGACAAATTATTTAACCTCTCTGAATCTGTTTCCTCATTTATAAAATGAGATAA
TAATAACTTGCCTCATTGGATGTACACAGAAACAATGATAACATTTTACTTTAAGGC
TAAACTGCTTTTTGGATACAACAACAACAAAATACAGCTATTTTTATCACATGAGA
ATATGGAAAAGGGTAATTTTCAGTGATATAGGAAATGAGTTGTCCTCATTATCCAGTG
GTGAGTTGACTTCTCAATAAAATACCAGCTCTACTTATCTTCATTGTTATTATTATAT
TTTCA

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
4	349	480	100.0%	5	-	11597986	11598331	346

HKSS_B1.2034.T1_B1NEST_021

TTTGTGTAAGGGATCTTCCAATTTTAAAAAGGTAAGTTGGACTATTCTTCACAAA
TTGTCCATTAACCTCATTTTATCTTTTTTCCGGGGGAAAAAAGGTTGAAAGAGTTG
AGGGAGGAAACTGCTCTTTCCTCTTATAATACTTTTTTCAGAAATTCTATTTATATAAT
CAGTTTTAGCCCTACTGGTTGTCTTGCCCTGCATATGGACTCCAGCAGAACTAGTCC
AGGTAGCCAGGAATAAAACAGAACAGACAGTGAAACATGTTATCCTTGCTTTATAT
AGAATATGGCTGCCTGGGTTCTAAGTCCTGGTAACATATGTTGCATAGCTGAGAATT

CATTGTATATTTTGCTGGTTAATTTTCAGAATTGACCTGGCTAAGTGCACATTTCTCT
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	401	458	100.0%	6	-	70793571	70793971	401

HKSS_B1sFS20432A_B1SFS_059 – in the last exon of ELOVL4 (protein coding region)

GAAAATGTAACACCACTGATTTTCAGTCAGTAGATAAGATAATTAGTAATTTATCAAA
ATAATTCATAAAGACCGTTTCTGTGATCGTCTAAAATTTCAGACCGAAGAATGAGTGA
CTATAAGATACATGAAAAATCTCATCCTTTAGACAACCTGGATGTGAACAGGGGGAG
AATCCCCAAAGTCACTTAATGATTGCTTTGGTCTGGAGAATATCAAGGCTAATTTTT
AAAAAAAATGTTTAAAATAAAAACTTCATAAATAAAACATCTGGGTATGGTATTAA
CACTTTACTCAGTCTAAGAGTTACTAGGACATAGAGCACATTTGTCTTTTCTCCCCAC
CCCCAAGCTCTCCTTTGCTTCTGTTTTCCCTGAAATTTTATATGATATGGGAGTTTTTC
CTCACTGTCAACAACAGTTAAGGCCCAGTTCAATTTAATCTCCTTTTGCTTTTCCATT
TTTCTGCTTTTTTCCATTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	480	525	100.0%	6	+	80625891	80626370	480

HKSS_B2.2034.T1_B2NEST_017

TTAAAACCTCATTGACTAGGGGGTAGGAGGGGGGAAGACTCAGTTGCAGTGAGCTTT
TTCTTCATTCTTTCCCTCTAAATTTTACCCATCCCGACATTTTCAGTATTGGGCCAGCG
GGTAAAGGGGGTGTGGAGGAGTTTGGGTAGCAAAGAGGGAAGAAAAACAGTGAGA
ATGGAGGAGAAAGGGAGAGAGTCCAAGAGTGGAGCTCAGGGTGTGGGTGCCATGG
GGGCAGCTTCTAAGACTAGCATTAAAGAGGAGGGTTGGTATTTATAGGCACAGGGC
AGGGGGCTATTCTCATGAGCCAGTTAACCAAAAGGTAGGACCATATGAGTTGGTG
GCTACTTGCAATTTTTGAAATTAGATGCTGAATTTGGAAAACCTAGATCTTCTTTTAAAA
AATACGATCCTGGGCCTGGTGCAGTGGCCTGCCACGCCTTCTTGGTGCAGAAGCAT
AGTGGAGCTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	462	511	100.0%	3	-	9087363	9087824	462

HKSS_B6s2043.2A_B6SFS_007 (MIR548I4 and CNTNAP2)

CGTGTGTTGCTTTACTTTTGGATCTTGAGAAGAAAGGACTGTTATCTGCAGGGCACTCT
GGGACAACCTTCTTGGTGATAAGAGTGAAGACTCATATTTGCTTTGTAAATCAATAAA
AAAGAGACCTTTCAGGCAAAAGTGTGATGACTGAGGAGGACAAGTTGTGAATTTT
ATATTGGAATGTAATGTTACCTATGAAATTTTCCACCTATTTTAGGATTTTCATATTT
TCAGATCAATCAAAATTTGTTGTGAACAAGGTTTCTCCTCCGTGTCCTACGAACCTAC
AAAAAAATGAGTGCCTGTGGGTGTTTTCAAACCTGCCTGTGGGTAGACAGAGCTATGT
TACTACCTGGAACCTCTGTGAATGTCTAAAAGAAAGTCAAATATCAAAATCGAAAA
GGAACCTATTTTCTTTGATATGTCTTGTGTATGACCTTGGTAGGAACAATGACAAA
ATTTTGACATGTTTCAAGATGTCTTAGAACAATGAAATTAGTATATATTAATAATAGCAG
TGCTTTGTTGTCCTTTTAAATAATACATGCATTTTANTTTTTTTTTTTTTTTTTINCCC
TTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	549	581	100.0%	7	+	147130508	147131056	549

HKSS_C1sFS26704A_C1SFS_057 (RIMS2 gene, intronic)

TCTTTCCCTTCCATATGGTGCTAGCTGTAGGTTTGTCAAATATGGCCTTTTTTATTTTC
 AGGCATGTTTCTTTTATATCTAGTATGTTTCAAGATTTAAAAATCATTATTAAATGCTTT
 TATTGGAATGTACTAACATGGCTGTATGGTTTTGGTCTTTATTTCTATTATTGTGGTG
 TGTCACATTTATTGAATTGTGAATGTTGAACCATCTTGCATTCTGGGATGATTGTG
 GTGATTGATCTTTATAATGTTTTATTTCAGTTTCAGTTTGCTAGAATGTTTTTGAAGATT
 TTTGCATCTATGTTTCGTTTCATCAGAGATAATGGCCTCTAGTCGTCATTGTTGTTGTTT
 CTGTGTCTTTGCCTGTTTTTATTCTCAGGTTAATACTAGCCTCATAGAATGAGTTTGG
 AAGTAGTCTCTCCTCTTCAAACTTGTTGGCAGAGTTTGAGTAGGATTGGTATTAATT
 CTTCTTTTAAATATTTGATAGAATTCAGCAGTGACTCCATCATGTCTTGGGCTTTTGT
 TTGATGACAGACTTTTTATTATGGCTTCAATCTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	560	586	100.0%	8	+	104716316	104716875	560

HKSS_C1s26702A_C1sNE_086 (normal, detected only by nested PCR)

TTTTATTCAGTTTCAGTTTGCTAGAATGTTTTTGAAGATTTTGCATCTATGTTTCGTTCA
 TCAGAGATAATGGCCTCTAGTCGTCATTGTTGTTGTTTCTGTGTCTTTGCCTGTTTTCA
 TTCTCAGGTTAATACTAGCCTCATAGAATGAGTTTGGAAGTAGTCTCTCCTCTTCAAA
 ACTTGTTGGCAGAGTTTGAGTAGGATTGGTATTAATTCTTCTTTTAAATATTTGATAG
 AATTCAGCAGTGACTCCATCATGTCTTGGGCTTTTGTGTTGATGACAGACTTTTTATTA
 TGGCTTCAATCTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	308	335	100.0%	8	+	104716568	104716875	308

HKSS_C1s2670.4A_C1sES_088

ACCAAATAATGCATGTTAAAGAACTAGAAAAGCAAGAATAAATCAAGCCCAATATT
 AATAAAAGAAAAAATATAATAAAAAAGCAGGAATAAATAAATGAGTCAAAAAA
 CACAAAAGAAAAATGAAAGGAAAAGTTGGCTTTTTGAAAATGTAAACAAAATTAAC
 AAACCTCTCACTAGGAACTAAGAAGAGTCCAAAATAAATAAATCAGAGATAAAA
 AAGAAGACATTAAAACTGATACCATGAAAATACAAAGGATCATTAGAGACTACTGT
 GAACAAATATATGCAAAAAAATTGAAAAATACACAAGAAATGGATACATTTCTAGA
 CACATACAACCTACCAAGATTGGATCATGATTAAATGGAAAACCTAAACAGACCAA
 TGCTAGATGACACATTAGTGGGTGCAGCGCACCAGCATGGCACATGTATACATATGT
 AACTAACCTGCACAATGTGCACATGTACCCTAAAACCTTAGAGTATAAT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	392	496	100.0%	8	-	104716882	104717273	392

In grey: 107/107 or 104/104 bp identity with L1RP (nt. 5913 or 5916-6019)

TSD: 5 bp deletion

HKSS_C2s2812.2A_C2SFS_011

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	569	612	100.0%	14	+	79473243	79473811	569

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	311	424	99.1%	2	+	120064353	120064662	310

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	435	474	99.8%	7	-	88873944	88874378	435

AATCCAGAATATAGATGTGTAGCTGAGGTCTGAAGAGACTTGGGGATTTTGAATACT
GGGCAAAGACATTGGAAGGAAATGGAGCTCGAGAGTGGGGCACAGAGGGTAGTGA
TAAGCAAGCAGACAATTGTAATGGATCACAGACTATGGGATTTTATTCACCAGAAG
ATGACTGAAAATTCTGAGTTTTAAAAATAGCAACGCAGTGAAGATTGATGACTATTT
CATACTATACATATGAAGAGATGAAATTTTATTTT **TTTTTTTTTTTTTTTTTTTT**
TTTTTTTTTTTTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	491	535	100.0%	11	-	84409927	84410417	491

HKSS_D2.2043.T2_D2NEST_061

GTGCCNTACAGAATCTGAGCGTTACATGGCATTCTCTAGAAGGAGTTGTGCAGGGTTT
CAACCCTGGGCACTTCCCCTCACACTCCTAAGACAAGGGACAACCTGACCCAGCAC
ATGAGGGAGTAAGACATGAAACTCTGCCAGCTTTGGCAGAGGCAAAGCAGGAAGG
GGCCTGAGTAAGGAAGTAGAAAGGGAAGGTAGAAGATCAAGCTTTAAGACAGGAG
GATGAATATGGACTTTGAAGAAGATGTGAAAAGTGAGAGTGGGAGGAAAAGGCTAT
CTATGAATAAGGGGAGGCTTAGGGCTCAAGCAAGGAAGGGCCATTGTGGACTGGCT
GGAAGAGAGAACTGTAATTGGAAGGGGAATTTTTTTTT **TTT**

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	375	378	100.0%	6	+	125612997	125613371	375

HKSS_E1.2043.T1_E1NEST_031

TTCTAGTCTATTGTTGAAGTTTTCAAATGTTGAAATTTAAAAAAACCAATGTTTTGAA
TTATTTTTCTAGGATTTTGTAAATTTCTTTTTTCATTGATATCTATTGCTGAAGAATTAT
TGTGTTCCTTTGGAGGGGTCATATTTTCTTATTTTTTCATATTTCTTGTTTACAT
CGATGTCTGCACATCTGGTGTAAACAGTTGCTTCTTCCAATTTTTGAATTTACTTTTGT
AGGGGAAGACTTTTTCTGAAGATGTTTCTATGGTATTGTTTAGATAGGGCACTTTG
GCTTTGATACTGAATGCACATAGTAGTCTAGTCTTTGTATGATTCTTT **TTTTTTTTT**
TT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	341	406	100.0%	11	+	83036467	83036807	341

HKSS_F1.2812.T1_F1NEST_019

CTAAATTTAATTTCTGAAAGGGCAATAACCATCAGCTATGATTCTTTTTACACCTCCA
GTTGTAAGTATTACCAATGTTTGTAAATGTTGATCAGGAACAACCTCCCCACCCCA
CCCATGTCTCACAAGGATAATAAAATTGATGCAAATCTAATCTGGGAGACTTGATAT
CTCGTAAACTAGATTTTAATCATTTTCAGAAATGTATTCACCTCTTAATGATTTTTAAG
TCACTCAGAATTTTGTAGCTTTCCTCATATAGATGACATATATTTCTGGCCAAGTTTA
TTCTTTGTTACTGTAGTAAATGGTTTTATTTTTTTCCATTGTTTTCTAACAAATTTGTC
TTGGCATATATTAATAATTATTTCTCTTTAATAATTTGATAATTAGGCTTCTTATAAAA
CTCTTACTAGACAGGTACTTTCAGCTAATTCTTTTTGGGTTTTCCATTTAACACTAAT
ATAATTTGTAAGTTATTTTATTTTGCCTCCTTTTTTTCTGTGTCTCATCTTATTTCAAC
CTTGCCTCCCTTCTAATTGCTTTGGTTAGAATTTCTTTGGGCAATAGTTTTTTTTTTTT
TTTTTT **TTTTTTT**

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	588	596	100.0%	4	+	120467693	120468280	588

HKSS_F1sFS20432A_F1SFS_053

TTCCAACAAGATCCCCAGGCAACTCAAATGTGCCCTTTTAAAGCACAGTAAACCTTC
ACATGAACAGGATGTGACCAACCCTTGGTAGATGCTCCTCCTCCTGTTGGGAGGAGT
GAACCATCAAGGGGAAAGGAAAACAGTGAAAGCAATGATTCTCCCTTTAAGTACAG
ACAGAAGCCAGCAGGAGGAGGCAGGAAAACACTCCCTTTCCCCAACATGCCTGTTT
CCTCCAAACTCGATCATGATTTTCCAGGGCCACAGATTAGAATGTCAGTGTATAATT
TAGTTACATACACATCTGATATAGTTGTTCCCTTCCAGTTCTCTTAAACCTCATCCCAG
CCTCTTAGATCCTATATAAAGGCCAAACTGGTAACAATTCTTCCACTCCCCGGTGCC
CAAAAGCCTTCTTTATTCTTTTATAGCACAGGATAAGCAAGAAAAAATAGGTTTTGAC
AGGAGATATGGAGGAAAGAGAAAGGGAGCTTATTTTTCTCCAAAGAAAAAAAGG
GCACTCTTCTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	524	546	100.0%	10	-	78702205	78702728	524

HKSS_F2s2043.2A_F2sNE_089

AAAGGAAACTCTAGCTAAATGAAGAGAGTATGAACACATCATCCTCTGGAAGGGGA
AACCTCATAATCATTAAACCTGGACTGAGAGAATTAAGGGGTCTAAAAGTTTATACC
TCATTTTAGACTGTTCTGAGCACAACCTTGTTGCTTCCTGGTGCCTGTGAGGATCATCT
ATGCCAAGGATGGATTTTGGCCTTCCTAGAAAGTCCTTGAAACTGTTGTAAACTTCC
TGGAGTGCTTACAATGTCGGGCTCTCCGTGTCATTTCATGGGTTTATTTCAAATGAAT
CTCCATTCTTTCAAGGTTGGGTGGAGTTGGCCTAAGTCTTGCTAACTGTTTACATTGT
AGTAGTTCAGTTGTTTATGGACCTCCACCCATGGTGACTTGTCCTTTTAGACCAGTA
CACCTAGAATAGAAAACGTACACTGTTTTGTTTCTCTCCATTTTCAGCTTTTGTTTG
TTTTGCTTTTAAGCTAACTTGAGCTTAAATTAATAAATGTAAAGTGAGATTCTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	515	552	100.0%	5	+	15526796	15527310	515

HKSS_F4.2043.T2_F4NEST_002 – CNTNAP2 gene (second hit in gastric cancer)

AGGGCTTCACCTTCTCGGGTCCTAGGGAGGGCTGGTGGCTTGAGCTGAGAGAACCC
ATGCTAAGCTTGGGCACCTGAGACAGCAGAAGCATGGACCTGATATTCCTTGCAATG
GGACGGCACTCTCAGCTGCAGCCCAGCATCACTGCTGCATATCAAGGAACATGACA
TTGACAGGTATTGCTGGCTGCTCAGTTTCCCTGCATGCCTGGCCCCATTTTCTGGGAT
CTTGTGTTGGTTTCTGAGCTTTCCCATGCTCTAGTTTACTTATTCTTAATTGATTTAAC
AAGTAAATATTTGTTCAAAAAAATACCATGAAAAATGTATTTAATTATGTATACTTA
ATGTATATATTGTGTATGTGTGTATACTTACATATAAGTAAAAATGAATGACATTA
ATGATACAAGGGATGGGAGGAAGAAATTAAGAGTTTTTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	442	474	100.0%	7	-	146918230	146918671	442

HKSS_F4s2043.2A_F4SFS_009 (KLF12 gene, intronic)

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	522	547	99.7%	13	-	74488520	74489042	523

CACATACATTCCAAGCCCACACTCATTTTGTTTTGTTCCTTTTGTATTTTCCTTTT
TTCTTTTACCTTTTTATTTTACCTAATTCAGACTTAAAAAGAAGTTGCAAGAAAAA
AATCCTGTATACTCTTTTCACCCAGATTTCCCAAATGTTAACATATCACCATATTTGC
TTTATCAATTTTGTCTCTCTCTATTTTGTAGTTGTGAGATACCTCTTTGCCCTAAAT
ACTTCAGTGTATTTTCTAAGAATAAGGTTTTCACTTACATAACTATCATATAATTAAA
ATCACGGTATTACTATTGTTGCAATAGCTAATCTAATCCACAGACTTTATTGAGATTT
ATATATTC

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	358	434	99.5%	18	+	39963935	39964292	358

GTGATCCAACTTTTGGCATATCATTTTTCATTGTATTCTCATAATTATTTCTGTAGAA
TCAATAGTAATGTCCTCACTTTAATTTCTGATCATAGTAATTTGTGTACTCTTTCTTAT
TTTCTTAATCAATACAGCTAAAGGTTTGTCAATATTGTTGATCTTTTTAAAGAACTAA
AATTTTGTTTGTGATTTCCTTTATTTTTTTTTTNCTTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	211	219	100.0%	20	+	13998704	13998914	211

[illegible]

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	477	555	99.0%	18	-	25142102	25142577	476

HKSS_H2s2043.2B_H2sNE_087

AAATAAAAGTTAGAGGGCATCAGCCAAGAGAAAAGTGGCACTACTGTGAAAATATG
TGCATCCTTGGTGTCTTAGGCTGTTTGGGCTTCTGTAAACAAAATTCTGTAGACTGGGT
AGCTTATGAATTATAGAAATTTATTTCTTACAGTTCTGGAGGCTGAGGAGTCCAAGA
ACAAAGCACTGACAGATTTGGGAGCCAGTTGGCCTCCCAGAGTTAAAATGATAGAG
GGAAATAGAAATGATTATAGTCCTACTTGTCTCTATATTTTCTGGTGAGGGCCCATT
TCCTGGTTCACAGTTGGTGTCTTCTCACTGTATCCTCACATGGTGGAAGGGGTAAGA
GATCTCTCTCAGGCTTCTTTT

START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
1	363	398	100.0%	8	-	94494537	94494899	363