

Additional Data 1

Location of ChIP sequences within human genome:

Blat Program UCSC Genome Browser (<http://genome.ucsc.edu/>) was used to search for the homology region in human genome. The alignments of each ChIP sequences and human genome show the exact location of the sequences in human genome.

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

aggctGGAGT	GCAGTgcat	GATCTtgGcT	CACTGCAACC	TCTGCCTCct	50
GGgTTCAaGc	GATTCTCCTg	CCTCAGCCTC	CTGAGTAGCT	GgGacTACAG	100
GtGcccGCCA	cCaCaCcTGG	CTAATTTTTG	TATTTTTAGT	AGAGACAGGG	150
TTTCACCATG	TTGGCAAGTC	TCATCTCAAA	GTCCTGACCT	CAAGTGATCC	200
GCCCCCTCAG	CCTCCCAAAG	TGCTGGGATT	ACAGGTATGA	GCCACCGCGC	250
CCGGCCCCCT	ACAGGGTATT	TTCTATGTCC	TAAAGCCTTC	TTTGAGTGTG	300
AGGCTTCAAT	TATTGTTTTT	ACGAAG			

caggaccctt	ccttccttcc	tctcttctt	ccttcctccc	tcccttcctc	10882238
cctttctctc	tctctctctt	tgagacagtc	ttgctcttgt	caccagacc	10882188
GAGTGCAGT	GatgcGATCT	caGtTCACTG	CAACCTCTGC	CTCCcGgATt	10882138
CAgGgGATTC	TCCTaCCTCA	GCCTCCTGAG	TAGCTGtGAt	TACAGGcGtg	10882088
tGCCAtCgCg	CaTGGCTAAT	TTTTGTATTT	TTAGTAGAGA	CAGGGTTTTCA	10882038
CCATGTTGGC	AAGTCTCATC	TCAAAGTCCT	GACCTCAAGT	GATCCGCCCC	10881988
CTCAGCCTCG	CAAAAGTCGT	GGATTACAGG	TATGAGCCAC	CGCGCCCGCG	10881938
CCCCTACAGG	GTATTTTCTA	TGTCCTAAAG	CCTTCTTTGA	GTGTGAGGCT	10881888
TCAATTATTG	TTTTTACGAA	agtcatggt	ggcagcagag	ggtaccagag	10881838
acctggcagc	tcctgggtctg	ttccccagcc	atggggcatg	ttcatgtgga	10881788
cagaaggaga	gcgggagggc	c			

00000006	ggagtgcagtgccatgatcttggctcactgcaacctctgcctcctgggtt	00000055
<<<<<<<		<<<<<<<
10882187	ggagtgcagtgatgcgatctcagttcactgcaacctctgcctcccggatt	10882138
00000056	caagcgattctcctgcctcagcctcctgagtagctgggactacaggtgcc	00000105
<<<<<<<		<<<<<<<
10882137	caggggattctcctacctcagcctcctgagtagctgtgattacaggcgtg	10882088
00000106	cgccaccacacctggctaatttttgatttttagtagagacagggtttca	00000155
<<<<<<<		<<<<<<<
10882087	tgccatcgcgcatggctaatttttgatttttagtagagacagggtttca	10882038
00000156	ccatgttggcaagtctcatctcaaagtcctgacctcaagtgatccgccc	00000205
<<<<<<<		<<<<<<<
10882037	ccatgttggcaagtctcatctcaaagtcctgacctcaagtgatccgccc	10881988
00000206	ctcagcctcccaaagtgcctgggattacaggtatgagccaccgcgccgggc	00000255

```
<<<<<<< |||||  <<<<<<<
10881987 ctcagcctcccaaagtgctgggattacaggtatgagccaccgcgccggc 10881938

00000256 cccctacaggggtatTTTctatgtcctaaagcTTctTTgagtgtgaggct 00000305
<<<<<<< |||||  <<<<<<<
10881937 cccctacaggggtatTTTctatgtcctaaagcTTctTTgagtgtgaggct 10881888

00000306 tcaattattgTTTTtacgaag 00000326
<<<<<<< |||||  <<<<<<<
10881887 tcaattattgTTTTtacgaag 10881867
```

Alignment of Clone 2 and chr16:69131743-69132092

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 2

```
GGCGTGTGCC ACCGTGCCCC GCCGAGCCTT CTTAGCTTTT TGGGGTTTTT 50
TTTGGTTGTT TGTTTGTTTA AGACAGAGTC TTAGCTCTGT TCCCAGGATG 100
CTGGAGTGCA GGGGTGCAAT CTCGGCTCAC TGCATCCTCG ACCTCCCAGG 150
CTCAAGGTGA TCCTTCCATC TCAGCCTCCC AAGTAGCTGG GACTATTAGC 200
AAGGTGCATG CCTGGCTAAT ATATGTATTT CTTGTAAAGT CTCAAACCTC 250
TGGACTTAAG CAATCCAAGC AATCCACCTG CCTCAGTCTC CCAATGTGCT 300
GAGATTACAG GCTTGAGCCA TAGCGCCTGG CTGATATTTG TCCCTTTGTG 350
```

Genomic chr16 :

```
acaaaatgag ctggtctcaa accagctggc caagctggtc tcaaactcct 69131692
gacctcaagt gatccatcca ccttggcctt cccgaagtgt tgggactaca 69131742
GGCGTGTGCC ACCGTGCCCC GCCGAGCCTT CTTAGCTTTT TGGGGTTTTT 69131792
TTTGGTTGTT TGTTTGTTTA AGACAGAGTC TTAGCTCTGT TCCCAGGATG 69131842
CTGGAGTGCA GGGGTGCAAT CTCGGCTCAC TGCATCCTCG ACCTCCCAGG 69131892
CTCAAGGTGA TCCTTCCATC TCAGCCTCCC AAGTAGCTGG GACTATTAGC 69131942
AAGGTGCATG CCTGGCTAAT ATATGTATTT CTTGTAAAGT CTCAAACCTC 69131992
TGGACTTAAG CAATCCAAGC AATCCACCTG CCTCAGTCTC CCAATGTGCT 69132042
GAGATTACAG GCTTGAGCCA TAGCGCCTGG CTGATATTTG TCCCTTTGTG 69132092
tctagctcat ttacttggc ataatattta gaaaattcat gtttaaaaaa 69132142
aaaaagaaaag aaaaagattc atgttttggg agcctgtatc agagcttcgt 69132192
```

Side by Side Alignment

```
00000001 ggcgtgtgccaccgtgccagccgagccttcttagctttttgggggtttt 00000050
>>>>>>> |||||>>>>>>>
69131743 ggcgtgtgccaccgtgccagccgagccttcttagctttttgggggtttt 69131792

00000051 tttggttggtttgtttgtttaagacagagtcttactctgtttcccaggatg 00000100
>>>>>>> |||||>>>>>>>
69131793 tttggttggtttgtttgtttaagacagagtcttactctgtttcccaggatg 69131842

00000101 ctggagtgcaggggtgcaatctcggctcactgcatcctcgacctcccagg 00000150
>>>>>>> |||||>>>>>>>
69131843 ctggagtgcaggggtgcaatctcggctcactgcatcctcgacctcccagg 69131892

00000151 ctcaaggtgatccttccatctcagcctcccaagtagctgggactattagc 00000200
>>>>>>> |||||>>>>>>>
69131893 ctcaaggtgatccttccatctcagcctcccaagtagctgggactattagc 69131942
```


Alignment of Clone 3 and chr19:38266193-38266854

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 3

```
TGCAGTgttg tGATccGGC TCACTGcAgc cttgACCTCC tgaGTTCAAG 50
tGgTcCTCCT GCCTaAGTCT CAAGagttcc tgggaccgta ggtgttaatt 100
aaaaaTAATT TTTTTTTTGT AGAGAtgGGG TcTCGCCATA TTGCCAGGC 150
TGGTCTTGA tctcttggtt caaGTGATCC tCCTGCCTCG GCCTCCCAA 200
GgaCTGGGAT TACAGGCGTG AGCCAttgTG CCCAtC
```

Genomic chr19 :

```
gttggaatta taggcgtgac tctctacgcc tggccccaac catgtttttg 38266142
tttttttttt ttttctgtga cagagtcacg ctctgttgta caggctggag 38266192
TGCAGTgGcG cGATCtCGGC TCACTGCAAC CTCCgccttc cagGTTCAAG 38266242
cGaTtCTCCT GCCTcAGccT CTCAAGtagc tgggattata ggtacattcc 38266292
actacgcctg gcTAATTTTT gtatTTTTaG TAGAGAcAGG GTtTCGCCAT 38266342
ATTGgCCAGG CTGGTCTTGA agtccttagg tcaagcaatc catctgcctt 38266392
cacctcccaa agtggttgaa ttacaggcgt gagccattgc atgtggcccc 38266442
caaccttgct tttgaagtgg aaggaaagga catggatttg tagactttgt 38266492
ttttctggac taaaaacatt ctttaacttc tcagtaatac aagtttttga 38266542
ggattgattc attgtcttct aagcactttt ttttgagagt ttcgctcttg 38266592
tcaccagggc tggcatgcaa tgggtgcgatc tcggctcact acaacctctg 38266642
cctcccaggt tcaagagatt ctccagcctc agcctcccga gtggctggga 38266692
ttataggtgc ccaccacat gcccggttaa tttttatatt tttagtagac 38266742
acagggtttt accacgttgg ccaggctgga ctcgaacttc tgacctcagG 38266792
TGATCtgCCT GCCTCGGCCT CCCAAAGtgC TGGGATTACA GGCGTGAGCC 38266842
AccaTGCCCA gCcagttttc taagcacttt gaaattttaa tgcactctgt 38266892
ctgtatttta cgatataaca cactagacta ataattattt ttactccctg 38266942
ctttgaagtt tt
```

Side by Side Alignment

```
00000001 tgcagtgttgatcccggtcactgcagccttgacctcc 00000040
>>>>>>> ||||| | ||| ||||| ||||| ||||| >>>>>>>
38266193 tgcagtggcgcatctcgggtcactgca.....acctcc 38266226
```

```
00000044 gttcaagtggctcctcctgcctaag..tctcaag 00000074
>>>>>>> ||||| | | ||||| || ||||| >>>>>>>
38266236 gttcaagcgattctcctgcctcagcctctcaag 38266268
```

```
00000106 taattttt....ttttttagagatgggggtctcgccatattgccaggct 00000151
```

>>>>>>> ||||| ||| ||||| ||| ||||| ||||| >>>>>>>
38266305 taat tttt gtatt tttt tagtag agac aggg tttc gccat attgg ccagg ct 38266354

00000152 ggtcttga 00000159
>>>>>>> ||||| >>>>>>>
38266355 ggtcttga 38266362

00000174 gtgatcctcctgcctcggcctcccaaaggactgggattacaggcgtgagc 00000223
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
38266792 gtgatctgcctgcctcggcctcccaaagtgctgggattacaggcgtgagc 38266841

00000224 cattgtgcccac 00000236
>>>>>>> || ||||| | >>>>>>>
38266842 caccatgcccagc 38266854

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

TGCTGGGATT	ACAcccCTGA	GCCACTGCGC	CCGGCCTTTT	TTTTTTGAGA	50
TAGAGTCTCG	CTCTGTCGCC	CAGGCTGGAG	TGCAGTGGTc	CGATCTTGGC	100
TCACTGCAAG	CTCCGCCTCC	TGGATTCACG	CCATTCTCCT	GCCTCAGCCT	150
CCTGAGTACC	TGGGACTACA	GGTGCCCGCC	ACCACACCCA	GCTAATTTTT	200
TTCTATTTTT	AGTAGAGACG	GGGTTTCACT	GTGTTAGCCA	GGATGGTCTC	250
GATCTCCTTA	CCTCATGATC	CGCCCGCCTC	GGCCTCCCAA	ATTGCTGGGA	300
TTACAGGGGT	GAGCCACTGC	GCCTGGCACA	GCCTTATTCT	TTAAAATGGA	350
AAAAAAAAAA	aCAAAAAAAAA	AGCTTTTAAA	AATTTTCTC	TTTTAAAAAG	400

cacgcccggc	taattttttg	tatttttagt	agagaagggg	tttctactgtg	49140737
gtctcgatct	cctaacctcg	tgatcgggcg	cccgcccttg	ccttccaaag	49140787
TGCTGGGATT	ACAagCgTGA	GCCACTGCGC	CCGGCCTTTT	TTTTTTGAGA	49140837
TAGAGTCTCG	CTCTGTCGCC	CAGGCTGGAG	TGCAGTGGTg	CGATCTTGGC	49140887
TCACTGCAAG	CTCCGCCCTCC	TGGATTCACG	CCATTCTCCT	GCCTCAGCCT	49140937
CCTGAGTACC	TGGGACTACA	GGTGCCCGCC	ACCACACCCA	GCTAATTTTT	49140987
TTCTATTTTT	AGTAGAGACG	GGGTTTCACT	GTGTTAGCCA	GGATGGTCTC	49141037
GATCTCCTTA	CCTCATGATC	CGCCCGCCTC	GGCCTCCCAA	ATTGCTGGGA	49141087
TTACAGGGGT	GAGCCACTGC	GCCTGGCACA	GCCTTATTCT	TTAAATAGGA	49141137
AAAAAAAAAAAA	cCAAAAAAAAAA	AGCTTTTAAA	AATTTTCTCT	TTTTAAAAAG	49141187
Tgtacacata	acacataatt	gtatatattt	atgggggtaca	tagtgatggt	49141237
ttaataccta	tagtgtattt	ccctcttttt	ttttttttga	gacggagtct	49141287
cg					

00000001	tgctgggattacacccctgagccactgcgcccggcctttttttttt	gaga	00000050
>>>>>>>			>>>>>>>
49140788	tgctgggattacaagcgtgagccactgcgcccggcctttttttttt	gaga	49140837
00000051	tagagtctcgctctgtcgcccaggctggagtgcagtggtccgatcttggc		00000100
>>>>>>>			>>>>>>>
49140838	tagagtctcgctctgtcgcccaggctggagtgcagtggtgcgatcttggc		49140887
00000101	tcactgcaagctccgcctcctggattcacgccattctcctgcctcagcct		00000150
>>>>>>>			>>>>>>>
49140888	tcactgcaagctccgcctcctggattcacgccattctcctgcctcagcct		49140937

00000151 cctgagtacctgggactacaggtgcccgccaccacaccagctaattttt 00000200
>>>>>>> |||||>>>>>>>
49140938 cctgagtacctgggactacaggtgcccgccaccacaccagctaattttt 49140987

00000201 ttctattttttagtagagacggggtttctactgtgttagccaggatgggtctc 00000250
>>>>>>> |||||>>>>>>>
49140988 ttctattttttagtagagacggggtttctactgtgttagccaggatgggtctc 49141037

00000251 gatctccttacctcatgatccgcccgcctcggcctcccaaattgctggga 00000300
>>>>>>> |||||>>>>>>>
49141038 gatctccttacctcatgatccgcccgcctcggcctcccaaattgctggga 49141087

00000301 ttacaggggtgagccactgcgctggcacagccttattctttaaaatgga 00000350
>>>>>>> |||||>>>>>>>
49141088 ttacaggggtgagccactgcgctggcacagccttattctttaaaatgga 49141137

00000351 aaaaaaaaaacaaaaaaaaagcttttaaaaatttttctcttttaaaaag 00000400
>>>>>>> |||||>>>>>>>
49141138 aaaaaaaaaacaaaaaaaaagcttttaaaaatttttctcttttaaaaag 49141187

00000401 tg 00000402
>>>>>>> || >>>>>>>
49141188 tg 49141189

Alignment of Clone 5 and chr3:126280985-126281230

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 5

```
AGCCTCCCAA GTAGCTGGGA GTGCACCAGC GTACCCAGCT AATCTTTGTA 50
ATTTTTGTAA AGATGGGATT TTGCCATGTT GTCATGCTGG TCTCGAATTT 100
CTAGGCTCAA GTAGTCCTCC TGCCTCAGCC TCACAAAGTG CTGGGATTAC 150
AGGTATGAGC CACCCCACCC GGCCATGACT AATCTTAATA TGTCTATTTT 200
TGCTCATTGT CACTGAGTGG ACCTGGAGGC TGAGGGCTGG AAGAGC
```

Genomic chr3 (reverse strand):

```
tgaaacatga tcttactctg tcaccaggc tggagtacag tggtgcaatc 126281281
acagctcact gcagcctcaa cctcctgggc tccagccatc ctcccacctc 126281231
AGCCTCCCAA GTAGCTGGGA GTGCACCAGC GTACCCAGCT AATCTTTGTA 126281181
ATTTTTGTAA AGATGGGATT TTGCCATGTT GTCATGCTGG TCTCGAATTT 126281131
CTAGGCTCAA GTAGTCCTCC TGCCTCAGCC TCACAAAGTG CTGGGATTAC 126281081
AGGTATGAGC CACCCCACCC GGCCATGACT AATCTTAATA TGTCTATTTT 126281031
TGCTCATTGT CACTGAGTGG ACCTGGAGGC TGAGGGCTGG AAGAGCaact 126280981
ggaattgctg tagtgccaaa tatatccct ttcattgtga tgccaccctg 126280931
gccaaaggtat catttttgtg tggcagccag agaaatcttt tcaaaa
```

Side by Side Alignment

```
000000001 agcctcccaagtagctgggagtgaccagcgtaccagctaatactttgta 000000050
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
126281230 agcctcccaagtagctgggagtgaccagcgtaccagctaatactttgta 126281181

000000051 atttttgtaaagatgggattttgccatgttgtcatgctgggtctcgaattt 000000100
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
126281180 atttttgtaaagatgggattttgccatgttgtcatgctgggtctcgaattt 126281131

000000101 ctaggctcaagtagtcctcctgcctcagcctcaciaaagtgctgggattac 000000150
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
126281130 ctaggctcaagtagtcctcctgcctcagcctcaciaaagtgctgggattac 126281081

000000151 aggtatgagccacccacccggccatgactaatcttaatatgtctatttt 000000200
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
126281080 aggtatgagccacccacccggccatgactaatcttaatatgtctatttt 126281031

000000201 tgctcattgtcactgagtggacctggaggctgagggctggaagagc 000000246
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
126281030 tgctcattgtcactgagtggacctggaggctgagggctggaagagc 126280985
```

Alignment of Clone 6 and chr2:113102773-113103105

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 6

```
AAAAGAAAAA AACAGAGATG GATGAGATTA GCTACCTGCA GGGCATGGTA 50
GGAACAGGAT GGAAATAAAG GGAATGAGGG GGAATGAGAC TTCTAGGAAT 100
ATCTCTTTTT GTTTATTTTA TTTTATTTTT AGCAGAGATG TGGGTTTCCTT 150
ATGTTGCCCA GCTGGTCTTG AACTCCTGGG CTCCAGCTAT CCTCCTGCCT 200
CCATCTCCCA AAGTGCTGGG ATTACAGGTG TGAGCTACCG CACCCGATCC 250
TCTTTTTGTT CTGAAGTAC TTTTAAAATC ATTTTAATAT TTCACATCTC 300
AAAATAAAT ACAAATAAAA CTCACAAGGA CAGaattcag at
```

Genomic chr2 :

```
tcgtgatcca cctgccttgg cctcccaaaa tgctgggatt acaggcgtga 113102722
gccaccaggc cggccacatt tacctatttg ttcaaggaaa aagaaacaga 113102772
AAAAGAAAAA AACAGAGATG GATGAGATTA GCTACCTGCA GGGCATGGTA 113102822
GGAACAGGAT GGAAATAAAG GGAATGAGGG GGAATGAGAC TTCTAGGAAT 113102872
ATCTCTTTTT GTTTATTTTA TTTTATTTTT AGCAGAGATG TGGGTTTCCTT 113102922
ATGTTGCCCA GCTGGTCTTG AACTCCTGGG CTCCAGCTAT CCTCCTGCCT 113102972
CCATCTCCCA AAGTGCTGGG ATTACAGGTG TGAGCTACCG CACCCGATCC 113103022
TCTTTTTGTT CTGAAGTAC TTTTAAAATC ATTTTAATAT TTCACATCTC 113103072
AAAATAAAT ACAAATAAAA CTCACAAGGA CAGggaaaac gctaaagttg 113103122
aacacaagca gaaacaagca aataaaatgt accctttgac ttctatctta 113103172
ccactttgta gtaaaaataa ctaatccag taa
```

Side by Side Alignment

```
000000001 aaaagaaaaaaacagagatggatgagattagctacctgcagggcatggta 000000050
>>>>>>>> |||||>>>>>>>>
113102773 aaaagaaaaaaacagagatggatgagattagctacctgcagggcatggta 113102822

000000051 ggaacaggatggaataaagggaatgagggggaatgagacttctaggaat 000000100
>>>>>>>> |||||>>>>>>>>
113102823 ggaacaggatggaataaagggaatgagggggaatgagacttctaggaat 113102872

000000101 atctctttttgtttattttattttatttttagcagagatgtgggttcctt 000000150
>>>>>>>> |||||>>>>>>>>
113102873 atctctttttgtttattttattttatttttagcagagatgtgggttcctt 113102922

000000151 atgttgcccagctggtcttgaactcctgggctccagctatcctcctgcct 000000200
>>>>>>>> |||||>>>>>>>>
113102923 atgttgcccagctggtcttgaactcctgggctccagctatcctcctgcct 113102972
```

```
000000201 ccatctcccaaagtgtctgggattacagggtgtgagctaccgcacccgatcc 000000250
>>>>>>> |||||  >>>>>>>
113102973 ccatctcccaaagtgtctgggattacagggtgtgagctaccgcacccgatcc 113103022

000000251 tctttttgttctgaactgacttttaaaatcattttaatatatttcacatctc 000000300
>>>>>>> |||||  >>>>>>>
113103023 tctttttgttctgaactgacttttaaaatcattttaatatatttcacatctc 113103072

000000301 aaaaataaatacaaaataaaactcacaaggacag 000000333
>>>>>>> |||||  >>>>>>>
113103073 aaaaataaatacaaaataaaactcacaaggacag 113103105
```

Alignment of Clone 7 and chr2:113102883-113103072

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 7

```
GTTTATTTTA TTTTATTTT AGCAGAGATG TGGGTTCTT ATGTTGCCA 50
GCTGGTCTTG AACTCCTGGG CTCCAGCTAT CCTCCTGCCT CCATCTCCA 100
AAGTGCTGGG ATTACAGGTG TGAGCTACCG CACCCGATCC TCTTTTGTT 150
CTGAAGTAC TTTTAAATC ATTTTAATAT TTCACATCTC
```

Genomic chr2 :

```
aacagagatg gatgagatta gctacctgca gggcatggta ggaacaggat 113102832
ggaaataaag ggaatgaggg ggaatgagac ttctaggaat atctcttttt 113102882
GTTTATTTTA TTTTATTTT AGCAGAGATG TGGGTTCTT ATGTTGCCA 113102932
GCTGGTCTTG AACTCCTGGG CTCCAGCTAT CCTCCTGCCT CCATCTCCA 113102982
AAGTGCTGGG ATTACAGGTG TGAGCTACCG CACCCGATCC TCTTTTGTT 113103032
CTGAAGTAC TTTTAAATC ATTTTAATAT TTCACATCTC aaaaataaat 113103082
acaaataaaa ctcacaagga cagggaaaac gctaaagttg aacacaagca 113103132
gaaacaagca aataaaatgt accctttgac ttctatctta
```

Side by Side Alignment

```
000000001 gtttattttattttatttttagcagagatgtgggttccttatgttgccca 000000050
>>>>>>> |||||  >>>>>>>
113102883 gtttattttattttatttttagcagagatgtgggttccttatgttgccca 113102932

000000051 gctggtccttgaactcctgggctccagctatcctcctgcctccatctccca 000000100
>>>>>>> |||||  >>>>>>>
113102933 gctggtccttgaactcctgggctccagctatcctcctgcctccatctccca 113102982

000000101 aagtgtctgggattacaggtgtgagctaccgcacccgatcctctttttgtt 000000150
>>>>>>> |||||  >>>>>>>
113102983 aagtgtctgggattacaggtgtgagctaccgcacccgatcctctttttgtt 113103032

000000151 ctgaactgactttttaaatacattttaatatatttcacatctc 000000190
>>>>>>> |||||  >>>>>>>
113103033 ctgaactgactttttaaatacattttaatatatttcacatctc 113103072
```

Alignment of Clone 8 and chr16:45169084-45169213

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 8

```
CATGTTGGCC AGGCTGGTCT CGACCTCCTG ACCTTAGGTG ATCCACCTGC 50
CTCGGCCTCC CAAAGTGCTG GGATTATAGG CATGAGCCAC TGTGCCTGGC 100
CTGTGATTTT TTTTTTTAAG AGACAGGGCC
```

Genomic chr16 :

```
aagtgattct cctgccacag cctccctact agctgggatt acaggcgcct 45169033
gccaccatgc ctggctaatt tttgtathtt tagtagagac agggtttcac 45169083
CATGTTGGCC AGGCTGGTCT CGACCTCCTG ACCTTAGGTG ATCCACCTGC 45169133
CTCGGCCTCC CAAAGTGCTG GGATTATAGG CATGAGCCAC TGTGCCTGGC 45169183
CTGTGATTTT TTTTTTTAAG AGACAGGGCC tcactctgtc acccaggctg 45169233
gagtgcagtg gtgcaatcat agctcactgc agcctgtaac tcctgggttc 45169283
tagcaatcct cctacttcta cctcctgagt
```

Side by Side Alignment

```
00000001 catgttggccaggctggtctcgacctcctgaccttaggtgatccacctgc 00000050
>>>>>>> ||||||||||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
45169084 catgttggccaggctggtctcgacctcctgaccttaggtgatccacctgc 45169133

00000051 ctcggcctcccaaagtgctgggattataggcatgagccactgtgcctggc 00000100
>>>>>>> ||||||||||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
45169134 ctcggcctcccaaagtgctgggattataggcatgagccactgtgcctggc 45169183

00000101 ctgtgatttttttttttaagagacagggcc 00000130
>>>>>>> ||||||||||||||||||||||||||||||| >>>>>>>
45169184 ctgtgatttttttttttaagagacagggcc 45169213
```

Alignment of Clone 9 and chr16:45169083-45169213

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 9

```
aagctggaan ctccaccggc ggggtgggcgg gcccgcttct taagccccgg 50
cgggtgaccc gggagtatct gaattCATG TTGGCCAGGC TGGTCTCGAC 100
CTCCTGACCT TAGGTGATCC ACCTGCCTCG GCCTCCCAA GTGCTGGGAT 150
TATAGGCATG AGCCACTGTG CCTGGCCTGT GATTTTTTTT TTTAAGAGAC 200
AGGGCC
```

Genomic chr16 :

```
caagtgattc tcctgccaca gcctccctac tagctgggat tacaggcgcc 45169032
tgccaccatg cctggctaatt ttttgtatct ttagtagaga cagggtttca 45169082
CATGTTGGC CAGGCTGGTC TCGACCTCT GACCTTAGGT GATCCACCTG 45169132
CCTCGGCCTC CCAAAGTGCT GGGATTATAG GCATGAGCCA CTGTGCCTGG 45169182
CCTGTGATTT TTTTTTTTAA GAGACAGGGC tcactctgt caccagggt 45169232
ggagtgcagt ggtgcaatca tagctcactg cagcctgtaa ctctggggtt 45169282
ctagcaatcc tcctacttct acctcctgag t
```

Side by Side Alignment

```
00000076 ccatgttggccaggctggtctcgacctcctgaccttaggtgatccacctg 00000125
>>>>>>> |||||>>>>>>>
45169083 ccatgttggccaggctggtctcgacctcctgaccttaggtgatccacctg 45169132

00000126 cctcggcctcccaaagtgctgggattataggcatgagccactgtgcctgg 00000175
>>>>>>> |||||>>>>>>>
45169133 cctcggcctcccaaagtgctgggattataggcatgagccactgtgcctgg 45169182

00000176 cctgtgattttttttttaagagacagggcc 00000206
>>>>>>> |||||>>>>>>>
45169183 cctgtgattttttttttaagagacagggcc 45169213
```

Alignment of Clone 10 and chr11:91127838-91128028

Click on links in the frame to the left to navigate through the alignment. Matching bases in cDNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence (often splice sites).

Clone 10

```
AGCCTCCCAA AGTGCTGGGA TTACAGGTGT GAGCCACCAT GCCCCAGCCT 50
CCTTTCCTTT TGAATACTAC AAAATACCCT TTTCCAAGCT ATCTCTTTTG 100
AGCCCTAAAC TTGTATTCCA ACTTACCTCC TTGACAAATC AGTGGCATCT 150
CAAATTCAAC ATGATGAGCA CTGAATTTGT CTTCCACTTA A
```

Genomic chr11 :

```
ccaccatgcc cagctaattt ttgtattttt tgtagagatg gggttttacc 91127787
atgttggcca ggatggcctc gatacttga cctcgtgatc cgcctgcctc 91127837
AGCCTCCCAA AGTGCTGGGA TTACAGGTGT GAGCCACCAT GCCCCAGCCT 91127887
CCTTTCCTTT TGAATACTAC AAAATACCCT TTTCCAAGCT ATCTCTTTTG 91127937
AGCCCTAAAC TTGTATTCCA ACTTACCTCC TTGACAAATC AGTGGCATCT 91127987
CAAATTCAAC ATGATGAGCA CTGAATTTGT CTTCCACTTA Aaacctagtt 91128037
ctcattattt tccatctcag aaaggtcagg attatctatc tatcccatg 91128087
cccaagtcac gaatctagaa gtttttttaa ttacctttc t
```

Side by Side Alignment

```
00000001 agcctcccaaagtgtctgggattacaggtgtgagccaccatgccccagcct 00000050
>>>>>>> |||||  >>>>>>>
91127838 agcctcccaaagtgtctgggattacaggtgtgagccaccatgccccagcct 91127887

00000051 cctttccttttgaatactacaaaatacccttttccaagctatctcttttg 00000100
>>>>>>> |||||  >>>>>>>
91127888 cctttccttttgaatactacaaaatacccttttccaagctatctcttttg 91127937

00000101 agccctaaacttgattccaacttacctccttgacaaatcagtggcatct 00000150
>>>>>>> |||||  >>>>>>>
91127938 agccctaaacttgattccaacttacctccttgacaaatcagtggcatct 91127987

00000151 caaattcaacatgatgagcactgaatttgtcttcacttaa 00000191
>>>>>>> |||||  >>>>>>>
91127988 caaattcaacatgatgagcactgaatttgtcttcacttaa 91128028
```
