

Additional Data 3

Genomic location of ChIP clones. Blat program (<http://genome.ucsc.edu/>) was used to map the location for 100 ChIP clones in human genome (90 non specific clones are shown below; specific clones are shown in Additional Date 2). Matching bases in input DNA and genomic sequences are colored blue and capitalized. Light blue bases mark the boundaries of gaps in either sequence.

Alignment of YourSeq and chr4:48969215-48969486

Clone 11 YourSeq

```
CTCTCCTAGC TTAATCAGG AAGAATTAGA TACCCAAGC aGACCAATAA 50
AGCAAGCAGC AAGATTGAAA TGGTAATTTT AAAATTACCA GCAAAAAAAG 100
CTGAGGGCCA GACAGATTCA CAGCAGAGTT CTACCAGACA TTCAAAGAAT 150
GTCTTCTTTC ATTCAAGGAA GAAATGATAC CAATCTTTTC ATACTATTCC 200
ACAAGACAGA GAAAGAAGAA ACCCTCCCTT ATTCATTCTA TGAAGCCAGC 250
ATCACCCATA TACCAAAACC AT
```

Genomic chr4 :

```
ccactgaaat attaaagatt attcaagggg actatgaaca ccttttgga 48969164
cataaactac aaagcctaga agagttggat aaattcctgg aaaaatacaa 48969214
CTCTCCTAGC TTAATCAGG AAGAATTAGA TACCCAAGC cGACCAATAA 48969264
AGCAAGCAGC AAGATTGAAA TGGTAATTTT AAAATTACCA GCAAAAAAAG 48969314
CTGAGGGCCA GACAGATTCA CAGCAGAGTT CTACCAGACA TTCAAAGAAT 48969364
GTCTTCTTTC ATTCAAGGAA GAAATGATAC CAATCTTTTC ATACTATTCC 48969414
ACAAGACAGA GAAAGAAGAA ACCCTCCCTT ATTCATTCTA TGAAGCCAGC 48969464
ATCACCCATA TACCAAAACC ATggaaggac ataaccaaaa aagaaaacta 48969514
cagaccaata tccttgatga acgcagatgc caaaatcctt aacaaaatac 48969564
tatctaactg aatccgacaa ca
```

Side by Side Alignment

```
00000001 ctctcctagcttaaatcaggaagaattagataccccaagcagaccaataa 00000050
>>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>>
48969215 ctctcctagcttaaatcaggaagaattagataccccaagccgaccaataa 48969264

00000051 agcaagcagcaagattgaaatggtaattttaaaattaccagcaaaaaaag 00000100
>>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>>
48969265 agcaagcagcaagattgaaatggtaattttaaaattaccagcaaaaaaag 48969314

00000101 ctgagggccagacagattcacagcagagttctaccagacattcaaagaat 00000150
>>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>>
48969315 ctgagggccagacagattcacagcagagttctaccagacattcaaagaat 48969364

00000151 gtcttctttcattcaaggaagaatgataccaatcttttcatactattcc 00000200
>>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>>
48969365 gtcttctttcattcaaggaagaatgataccaatcttttcatactattcc 48969414

00000201 acaagacagagaaagaagaaccctcccttattcattctatgaagccagc 00000250
>>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>>
48969415 acaagacagagaaagaagaaccctcccttattcattctatgaagccagc 48969464

00000251 atcacccctaataccaaaaccat 00000272
>>>>>>> ||||||||||||||||||||||| >>>>>>>
48969465 atcacccctaataccaaaaccat 48969486
```

Alignment of YourSeq and chr13:26617176-26617195

Clone 12 YourSeq

```
ccgcgatcca cgcgcgcatg gcccgcggtg aacgtgctga tcggggcggc 50
ggtatcggtc tggacctgat cgcgcggtg tgcgagcaCC TGGGCTGGAC 100
CCTGCAGCtg cagccctgcg acccgcggtg cagcggggtc accctggact 150
tcgggccttc gcgaccgggc tgaccgacat gccaatcgct ccgcgctgcg 200
gcatgaccgc gcgtgaagac aatgttaatc tcgacctgcg ccgctttatg 250
cggcg
```

Genomic chr13 :

```
tgctgtaat ccagctact cagaaggcag aggtgggaga atcacctaag 26617125
cccaggatgt cgaggctgca gtgagccacg atcgaccac tgcattccag 26617175
CCTGGGCTGG ACCCTGCAGC agagtgcgac cctgcagcag aggggacttg 26617225
aacacaagtc ttgggctctg tatcaaatgt agccatccca ctcttcactg 26617275
aacctcctcc tttcctcca
```

Side by Side Alignment

```
00000089 cctgggctggaccctgcagc 00000108
>>>>>>> |||||>>>>>>>
26617176 cctgggctggaccctgcagc 26617195
```

Alignment of YourSeq and chr15:53425196-53425231

Clone 13 YourSeq

```
cggtgacccg ggagatctga attccancag ggccggatct cgctcgccaa 50
gaccggtgat gtcgatcacc ccgcagaccc ggccgtcgag atcgtgcagt 100
ggctcgctca ggcagaacac cggcgcgaac cgctgcaggt agtgttcggt 150
gccgcgcacc agtgccggca cgtcGTCAgC CAGGCTGacc gccggcgcgG 200
TGGTGCCGAT CTCGTctctg cccagctgtc gcccgcctg aattcagatc 250
tcccgg
```

Genomic chr15 (reverse strand):

```
ctgggaaaga gagactttga actactaacc ataatgaggg tactgggcac 53425282
agatgaaggt atcaagaaga attttttttt tttagacaga atctcgctct 53425232
GTACCCAGG CTGgagtga GTGGTGCCGA TCTCGctca atgcaacctc 53425182
cacctccagg gttcaagtga ttctcctgtc tcagcctccc aagtagctgg 53425132
cattacaggt gcgtgccacc acaccagct aatttt
```

Side by Side Alignment

```
00000175 gtcagccaggctg 00000187
<<<<<<< |||| ||||| <<<<<<<
53425231 gtcacccaggctg 53425219
```

```
00000200 gtggtgccgatctcgg 00000215
<<<<<<< ||||| <<<<<<<
53425211 gtggtgccgatctcgg 53425196
```

Alignment of YourSeq and chr22:48603526-48603551

Clone 14 YourSeq

```
cgatgagacg atcggcctgc ttgacgaagc tctctgggggt gtgaatcggg 50
gaagtgggtg agcagatggt gacctgggcg tgcttgccgg tcttcttgac 100
ggctgccatc gcgtgctcaa ggttgcgagg atcgttcaga gcgtcgaaca 150
cccggaacac gtccatgccg ttTCGGCCG ACTTCTCGAc aAATTGTcg 200
acgacctcgt cgttgtagtg gcggtagccc agaaggtttt ggc
```

Genomic chr22 :

```
acacggcggg gacgcagtcg cccttgcgct tctcattgac gatctccagc 48603475
caggcatagt cctcctcgtc catgtcatac tccacctcgt tgtccagttc 48603525
CTCGGCCGAC TTCTCGAtga ACTTGT agta cacaggaggc ctcctggggg 48603575
cggacggagg gctgtactcc acgatgcgca ccttgggctc cgggagggca 48603625
ctggccgagg ccggcgtgcc gtgggc
```

Side by Side Alignment

```
00000173 ctcggccgacttctcgacaaacttgt 00000198
>>>>>>> |||||||||||||||| ||||| >>>>>>>
48603526 ctcggccgacttctcgatgaacttgt 48603551
```

Alignment of YourSeq and chr5:53384849-53385118

Clone 15 YourSeq

```
cggtgacccg ggagatctga aTTCCACTCT AGAGCCACTC TTTTATTT 50
TTATTTTTTT TCTTTTTTCA TACTCTACTG TTTGGAAACA GGTCATACTT 100
AGAGAGCCAT ACTTAGAGAG TAGTTATGCT TTACTTTCTT TTGGATAGAA 150
TACCTACACA AATTATTGG AATTATTGG AATTTTCTA CATAGTAGGT 200
TTATCTCTTC TACCCCATTT ATTTGTTGAT TTATTCAATT ATTTACTTAT 250
GTCAGTAGAG ACTCATGGAT ATTTATTTTA TACTTTGTTT Tgaattcaga 300
tctcccgggt caccg
```

Genomic chr5 (reverse strand):

```
cacatcatat caagggtaaa cactgtcaat gtgacttatc actgttgata 53385169
taaactttta tcacctgctt gaggtagtggt ttgtcagggt tctccacttt 53385119
TTCCACTCTA GAGCCACTCT TTTTATTTT TATTTTTTTT CTTTTTTCAT 53385069
ACTCTACTGT TTGGAACAG GTCATACTTA GAGAGCCATA CTTAGAGAGT 53385019
AGTTATGCTT TACTTTCTTT TGGATAGAAT ACCTACACAA ATTATTTGGA 53384969
ATTATTTGGA ATTTTCTTAC ATAGTAGGTT TATCTCTTCT ACCCCATTTA 53384919
TTTGTGGATT TATTCAATTA TTTACTTATG TCAGTAGAGA CTCATGGATA 53384869
TTTATTTTAT ACTTTGTTT ttgtttgttt tggtgtgtgt tggtgtgtgt 53384819
gttgtttttg gagatgcagt ttgtccatat tgctcctagt ctccagggat 53384769
cctcccgggc cccagggatc
```

Side by Side Alignment

```
00000022 ttccactctagagccactctttttatttttatttttttcttttttcat 00000071
<<<<<<<< ||||| <<<<<<<<
53385118 ttccactctagagccactctttttatttttatttttttcttttttcat 53385069

00000072 actctactgtttggaaacaggtcatacttagagagccatacttagagagt 00000121
<<<<<<<< ||||| <<<<<<<<
53385068 actctactgtttggaaacaggtcatacttagagagccatacttagagagt 53385019

00000122 agttatgctttactttcttttgatagaatacctacacaaattatttgga 00000171
<<<<<<<< ||||| <<<<<<<<
53385018 agttatgctttactttcttttgatagaatacctacacaaattatttgga 53384969

00000172 attatttggaatttttctacatagtaggtttatctcttctacccattta 00000221
<<<<<<<< ||||| <<<<<<<<
53384968 attatttggaatttttctacatagtaggtttatctcttctacccattta 53384919

00000222 ttgttgatttattcaattatttacttatgtcagtagagactcatggata 00000271
<<<<<<<< ||||| <<<<<<<<
53384918 ttgttgatttattcaattatttacttatgtcagtagagactcatggata 53384869

00000272 tttattttatactttgtttt 00000291
<<<<<<<< ||||| <<<<<<<<
53384868 tttattttatactttgtttt 53384849
```

```
00000255 attcttcctgatttaagctaggagag 00000280
>>>>>>> |||||
49219541 attcttcctgatttaagctaggagag 49219566
```

Alignment of YourSeq and chr7:8110887-8111075

Clone 17 YourSeq

```
AAGACTGGGT AATTTATAAA GAAATGAGGT TTAATTGACT CACAGTTCCT 50
CATGGCTGGG GAGGCCTCAG GAAACTTACA ATCACGGGGT AAGGCACCCC 100
TTCTCACAAG GCAGCAGGAG AGAGAATGAG TGCCAGCAGG GGAATGCCA 150
GATGCTTATA AAACCTCAG ATCTTGAGAG CACTCACTA
```

Genomic chr7 :

```
gcattcctaa aattagttgc ctctcactg gctggcagag gggggcctgg 8110836
gtgtaagacc ctgtcttagt ctgttgtcac atttctataa ggaaatacc 8110886
AAGACTGGGT AATTTATAAA GAAATGAGGT TTAATTGACT CACAGTTCCT 8110936
CATGGCTGGG GAGGCCTCAG GAAACTTACA ATCACGGGGT AAGGCACCCC 8110986
TTCTCACAAG GCAGCAGGAG AGAGAATGAG TGCCAGCAGG GGAATGCCA 8111036
GATGCTTATA AAACCTCAG ATCTTGAGAG CACTCACTA cacgagaaca 8111086
gcatgggggg aactgcccc tgattcaatt agctcttact aggtccctcc 8111136
caccacatgt ggggattatg gggattagaa ctcaagatg
```

Side by Side Alignment

```
0000001 aagactgggtaatttataaagaaatgaggtttaattgactcacagttcct 0000050
>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>
8110887 aagactgggtaatttataaagaaatgaggtttaattgactcacagttcct 8110936

0000051 catggctggggaggcctcaggaaacttacaatcacgggtaaggcacccc 0000100
>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>
8110937 catggctggggaggcctcaggaaacttacaatcacgggtaaggcacccc 8110986

0000101 ttctcacaaggcagcaggagagagaatgagtgccagcaggggaaatgcc 0000150
>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>
8110987 ttctcacaaggcagcaggagagagaatgagtgccagcaggggaaatgcc 8111036

0000151 gatgcttataaaacccctcagatcttgtgagcactcacta 0000189
>>>>>> ||||||||||||||||||||||||||||||||||| >>>>>>
8111037 gatgcttataaaacccctcagatcttgtgagcactcacta 8111075
```

Alignment of YourSeq and chr7:20814366-20814385

Clone 18 YourSeq

```
agtagtgacag aatcacagcc actgagtaat acagtgcccg caaataatga 50
caaccatccc aaacttttat tgtatttcct gagTCTCATT TAACGACCTC 100
AATtccacgg gagtctggtg gcgtttaaag tgtgggggca ttttacggga 150
aggttacatt actgtaaaca tcattaggtc tgtgtcagga agg
```

Genomic chr7 :

```
ataacataaa aataaaaact tgggtttaat atattgttat aaaaattcag 20814315
aatgaggcca aagtaaatag gattacaaga cctgtagtgt aaatgtcttt 20814365
TCTCATTTAA CGACCTCAAT atcctgtact ccatgtgtgt tactgcagtc 20814415
ttagattgtc aactcttaag acaatctaca ttatttcttt gtatgattcc 20814465
atgtacctat aagaacttgg
```

Side by Side Alignment

```
00000084 tctcatttaacgacctcaat 00000103
>>>>>>> |||||>>>>>>>
20814366 tctcatttaacgacctcaat 20814385
```

Alignment of YourSeq and chr17:2706902-2707021

Clone 19 YourSeq

ACTTAACCTA CCAAGGAGA AAGAGTGATT GATTTCATCA TGGTGCTAAG 50
TGACCTTTGC TTCCTCTCT GTATCTGGAG TTTCTTTGTC TCTTTAAGCG 100
TCTGAAATGA GTGCAGCAAG

Genomic chr17 :

ttaagagcct gcaatgcagg cagacattgg tggccttcct agcccctggc 2706851
ttcatcccg tcttctgtcg ctccaacccat cctgggtggct ttggccatgg 2706901
ACTTAACCTA CCAAGGAGA AAGAGTGATT GATTTCATCA TGGTGCTAAG 2706951
TGACCTTTGC TTCCTCTCT GTATCTGGAG TTTCTTTGTC TCTTTAAGCG 2707001
TCTGAAATGA GTGCAGCAAG cactattgac ccttgctctg caggtgctgg 2707051
tggccacggg aggcctggag caggctgcag ctgccagcct ctcttaagca 2707101
tcccccatat tccatgctgg

Side by Side Alignment

0000001 acttaacctacccaaggagaaagagtgattgatttcacatcatggtgctaag 0000050
>>>>>> |||||>>>>>> >>>>>>
2706902 acttaacctacccaaggagaaagagtgattgatttcacatcatggtgctaag 2706951

0000051 tgacctttgcttcctctctgtatctggagtttctttgtctctttaagcg 0000100
>>>>>> |||||>>>>>> >>>>>>
2706952 tgacctttgcttcctctctgtatctggagtttctttgtctctttaagcg 2707001

0000101 tctgaaatgagtgagcaag 0000120
>>>>>> |||||>>>>>> >>>>>>
2707002 tctgaaatgagtgagcaag 2707021

Alignment of YourSeq and chr2:47043372-47043407

Clone 20 YourSeq

```
aggctaaggg cctttggaag ccgttgagcg aacggggcgt tgcgatcaac 50
accctcctaa ctgcagaact GCCTTTCTG GTGGCCAAAg GGCCAAGGC 100
taagcagctc ttcctggagc cactgactga ccaaccgatc accgatgcgc 150
taattcgccg gctccaagca ttgggcgcgc agatcgggct tgggattcgg 200
gtctgcacgc tgaccgaggc attcg
```

Genomic chr2 (reverse strand):

```
ccttgactg ttcaacctat caggtaggct caagtgttc actcccatca 47043458
gggggtgggc tgcccagaag cagcagccca gaggggactc ttcacaaatg 47043408
GCCTTTCTG GTGGCCAAa GGCaagagt CAAGGcagag cttcccatgg 47043358
gacagaacta gagacagcca tatggccgag acaccatggc caggcaggaa 47043308
gtctgccata ctgcccgaat gagccatggc aggagc
```

Side by Side Alignment

```
00000071 gccttttctggtggccaaagggcc.....caaggc 00000100
<<<<<<<< ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| <<<<<<<<
47043407 gccttttctggtggccaaaggccaagagtcaaggc 47043372
```

Alignment of YourSeq and chr1:208814512-208814586

Clone 21 YourSeq

```
cgaatgcctc  ggtagcggtg  cagacccgaa  tccaagccc  gatctgcgcg  50
cccaatgctt  ggagccggcg  aattagcgca  tcggtgaTCG  GTTGGTCAGT  100
CAGtggctcc  aggaagagct  gcttagcctt  gggccctttg  gccaccAGAA  150
AAGGCAGTTC  Tgcagttagg  aggggtgtga  tcgcaacgcc  ccgttcgctc  200
aacggcttcc  aaaggccctt  agcctgaatt  cagatctccc  gggtcaccgc  250
gggcggatcc  cccgggctgc  ag
```

Genomic chr1 (reverse strand):

```
catggagagg  gcctcagagg  cagggcccat  ggcccatggc  cctgataggt  208814637
gtatactcta  ggttttcaaa  gcaaccagtg  actgcacaca  caaagtctgg  208814587
TCGGTTGGTC  AGTCAGcaaa  aacaaaaatc  aacagatgac  aagggttaata  208814537
taaaggaaaA  GAAAAGGCAa  GTTCTttgtt  gtcaggaagc  atttagtgta  208814487
acaaggggtg  gcaagtcctt  accttcaggg  ggtcccactt  gcagtggatt  208814437
cccattgtgt  tatggcctaa  attaa
```

Side by Side Alignment

```
000000088  tcggttggtcagtcag  000000103
<<<<<<<<  |||  <<<<<<<<
208814586  tcggttggtcagtcag  208814571
```

```
000000147  agaaaaggca.gttct  000000161
<<<<<<<<  |||  <<<<<<<<
208814527  agaaaaggcaagttct  208814512
```

00000001	agtaatttgcagtggaaggaagattataataggaaaaacaacaaaaaga	00000050
<<<<<<<<		<<<<<<<<
23802689	agtaatttgcagtggaaggaagattataataggaaaaacaacaaaaaga	23802640
00000051	cccagacagacagtgatatccctttgttcaaaaagcggttaataacatgata	00000100
<<<<<<<<		<<<<<<<<
23802639	cccagacagacagtgatatccctttgttcaaaaagcggttaataacatgata	23802590
00000101	atttattcagtaaaaacaagtatatattattctgttaacttttctaatacagc	00000150
<<<<<<<		<<<<<<<
23802589	atttattcagtaaaaacaagtatatattattctgttaacttttctaatacagc	23802540
00000151	agatcctgtgaatagtttcattcagtttctttttacctttttaggaaacg	00000200
<<<<<<<<		<<<<<<<<
23802539	agatcctgtgaatagtttcattcagtttctttttacctttttaggaaacg	23802490
00000201	tactccaaactaagcccaagatgcaaagttt	00000232
<<<<<<<<		<<<<<<<<
23802489	tactccaaactaagcccaagatgcaaagttt	23802458

Alignment of YourSeq and chr21:40443401-40443559

Clone 24 YourSeq

```
cggtgacccg ggagatctga attccgatgg acctcgggga gcgccgcaac 50
tcggggggca ATGGAGCGAT GGAactcggg gagcgatgga actcggggag 100
cgatggaact cgggggagcga tggaaactcg ggagcgatgg aactcgggga 150
gcgatggaac tcgggggagcg atggaactcg gggagcgatg gagcccgggg 200
agcgatggaa ctcgggggagc CATGGAGCGA TGAaactcg gggagcgatg 250
gaactcgggg agcaATGGAG CGATGGAact cgggggagcga tggaaactcg 300
ggagccaat
```

Genomic chr21 (reverse strand):

```
gatggagtga tggatgttgt ggtgacagtg gtgttgggtg tgggattgtg 40443610
atggagtgat ggatggttgt ggtgacagtg gtgttgggtg tgggatatgt 40443560
ATGGAGCGAT GGAgttgtg acagtgggtg tgggtttggg atagtgaaga 40443510
agtaatggat ggtggttgtg atagtgatgg tgggtttggg atagtATGG 40443460
AGCGATGGA t ggtggttgtg atagtacgg tgggtttggg atagtATGG 40443410
AGCGATGGA t ggtggttgtg acagtgggtg tgggtttggg atagtgatgg 40443360
agtgatggat gttgtggtga cagtgggtgt ggtgttggga tagtgatgga 40443310
gtgatggat
```

Side by Side Alignment

```
00000061 atggagcgatgga 00000073
<<<<<<<< |||||<<<<<<<<
40443559 atggagcgatgga 40443547
```

```
00000221 gatggagcgatgga 00000234
<<<<<<<< |||||<<<<<<<<
40443464 gatggagcgatgga 40443451
```

```
00000265 atggagcgatgga 00000277
<<<<<<<< |||||<<<<<<<<
40443413 atggagcgatgga 40443401
```

Alignment of YourSeq and chr5:53384849-53385115

Clone 25 YourSeq

```
CACTCTAGAG CCACTCTTTT TTATTTTAT TTTTTTCTT TTTTCATACT 50
CTACTGTTTG GAAACAGGTC ATACTTAGAG AGCCATACTT AGAGAGTAGT 100
TATGCTTTAC TTTCTTTTGG ATAGAATACC TACACAAATT ATTTGGAATT 150
ATTTGGAATT TTTCTACATA GTAGGTTTAT CTCTTCTACC CCATTTATTT 200
GTTGATTTAT TCAATTATTT ACTTATGTCA GTAGAGACTC ATGGATATTT 250
ATTTTATACT TTGTTTT
```

Genomic chr5 (reverse strand):

```
atcatatcaa gggtaaacac tgtcaatgtg acttatcact gttgatataa 53385166
acttttatca cctgcttgag gtagtgtttg tcaggtttct ccacttttct 53385116
CACTCTAGAG CCACTCTTTT TTATTTTAT TTTTTTCTT TTTTCATACT 53385066
CTACTGTTTG GAAACAGGTC ATACTTAGAG AGCCATACTT AGAGAGTAGT 53385016
TATGCTTTAC TTTCTTTTGG ATAGAATACC TACACAAATT ATTTGGAATT 53384966
ATTTGGAATT TTTCTACATA GTAGGTTTAT CTCTTCTACC CCATTTATTT 53384916
GTTGATTTAT TCAATTATTT ACTTATGTCA GTAGAGACTC ATGGATATTT 53384866
ATTTTATACT TTGTTTTttg tttgttttgt tgttgtttgt tgttgtttgt 53384816
gtttttggag atgcagtttt gccatattgc tcctagtctc cagggatcct 53384766
ccggggcccc agggatc
```

Side by Side Alignment

```
00000001 cactctagagccactctttttatttttatttttttctttttcatact 00000050
<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<
53385115 cactctagagccactctttttatttttatttttttctttttcatact 53385066

00000051 ctactgtttggaacaggtcatacttagagagccatacttagagagtagt 00000100
<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<
53385065 ctactgtttggaacaggtcatacttagagagccatacttagagagtagt 53385016

00000101 tatgctttacttttcttttgatagaatacctacacaaattatttggaatt 00000150
<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<
53385015 tatgctttacttttcttttgatagaatacctacacaaattatttggaatt 53384966

00000151 atttggaatttttctacatagtaggtttatctcttctacccatttattt 00000200
<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<
53384965 atttggaatttttctacatagtaggtttatctcttctacccatttattt 53384916

00000201 gttgatttattcaattatttacttatgtcagtagagactcatggatattt 00000250
<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<
53384915 gttgatttattcaattatttacttatgtcagtagagactcatggatattt 53384866

00000251 attttatactttgtttt 00000267
<<<<<<< ||||||||||||||| <<<<<<<
53384865 attttatactttgtttt 53384849
```

Alignment of YourSeq and chr17:38529244-38529641

Clone 26 YourSeq

```
GAAGAAAAGC CAAATGCTt gtataatata acaggGATTCTGCCCCAGg 50
GCAGagCCAA TCAAGACAGA GTCCTTGTCT TTggCCGGAC CACAGGATca 100
GTGTTGAAAA tGgGAGGAGg GGTAGAGGtA GAGcGGATGG AGAACacGGA 150
ATCATTTCCT ATATTgTAA AGTTaTTCAG gTAAGAAAAT CAGCAATTAC 200
cAgAGCCTAA TgTTATAGA CATGTCTTTT CTTCcGTAGT ATGaAAGGTC 250
AATTCTGTTT ATTgaCcTtG GcGATAATCA TAGtAATCgg AAAagAATAC 300
AaTCcTGgGa cGagTTACCA GAgGGGACAC Taccgatcctt gTGCATAGCA 350
TaAATGACac cagcgAactt TTTAAataGA AGAGCAcAcA AATCCATTg 400
tctcggatcc aaagaactgt
```

Genomic chr17 :

```
gcctcccaa gtgctgggat tacaggcata agccaccgcc ctcggcctca 38529193
tccatgattt tatTTtgcca tttcaagtga tggagcttgt tttagagctg 38529243
GAAGAAAAGC CAAATGCTa gttaatctaa actaGATTCC TGCCCCAGtG 38529293
CAGaCCAACT CAAGACAGAG TCCcTGTCTT TcCCGGACCA CAGGATttGT 38529343
GTTGAAAAGg aGAGGAGtGG gAGAGGcAGA GtGGATGGAG AACaAGGAAT 38529393
CATTTTCtat ATTTtTAAAG TTcTTCAGtT AAGAAAATCA GCAATTACaA 38529443
tAGCCTAATc TTAcTAGACA TGTCTTTTCT TCCcTAGTAT GtAAGGTCAA 38529493
TTCTGTTcAT TtgCaTaGGA GATAATCATA GgAATccAA AttAATACAc 38529543
TcTGTgctG AcTTACCAGA tGGGACAcTc taagattttc TGCATAGCAT 38529593
tAATGACAtt ttgtActTcT TcAAcgcGAA GAGCAgAtAA ATCCATTtct 38529643
ttctgttcca atgaacttta acacattaga aaaacatata tatatatcctt 38529693
tttaaaaggT ttataaaatg acaacttcatt tttatcattt taaaataa
```

Side by Side Alignment

```
00000001 gaagaaaagccaaatgcc 00000019
>>>>>>> |||||>>>>>>>
38529244 gaagaaaagccaaatgcc 38529262
```

```
00000036 gattcctgccccagggcagagccaatcaagacagagtccttgtcttt 00000082
>>>>>>> |||||>>>>>>>
38529278 gattcctgccccagtgagaaaccaatcaagacagagtccttgtcttt 38529324
```

```
00000085 ccggaccacaggatcagtggtgaaaatgggaggaggggtagaggtagagc 00000134
>>>>>>> |||||>>>>>>>
38529326 ccggaccacaggatttgtgtgaaaaggagaggagtgggagaggcagagt 38529375
```

```
00000135 ggatggagaacacggaatcattttctatatatttgtaaagttattcaggtaa 00000184
>>>>>>> |||||>>>>>>>
38529376 ggatggagaacaaggaatcattttctatatatttttaaagttcttcaggtaa 38529425
```

```
00000185 gaaaatcagcaattaccagagcctaattgttattagacatgtcttttcttc 00000234
>>>>>>> |||||>>>>>>>
38529426 gaaaatcagcaattacaatagcctaattcttactagacatgtcttttcttc 38529475
```

```
00000235 cgtagtatgaaagggtcaattctgttcattgaccttggcgataatcatagt 00000284
>>>>>>> |||||>>>>>>>
38529476 cctagtatgtaagggtcaattctgttcattgcataggagataatcatagg 38529525
```

```
00000285 aatcggaagaataacaatcctgggacgagttaccagaggggacact 00000331
>>>>>>> |||||>>>>>>>
38529526 aatcccaaatatacactcttgtgtgacttaccagatgggacact 38529572
```

```
00000342 tgcatagcataaatgacaccagcgaactttttaatagaagagcacacaa 00000391
>>>>>>> |||||>>>>>>>
```

38529584 tgcatagcattaatgacattttgtacttcttcaacgcgaagagcagataa 38529633

00000392 atccattt 00000399

>>>>>> ||||| >>>>>>

38529634 atccattt 38529641

Alignment of YourSeq and chr4:57025056-57025303

Clone 27 YourSeq

```
TCACAATACC CTATTGTTAA TTCCATATTA AGACTATATA CGGTGTTTTG 50
AAATTGTCTG CCTCTGGAGA CTTCCAAGAT TCATTGAGAG CAGAAGGTTA 100
ATTTTGTTCA TCTTTGCATT CCCAGGGTCT TATATATACA TAATAGGCTG 150
TATTTGTTCT CTA AAAAATA CAGAACCAAT AGGATATGTA CAGATTATGA 200
GAAATTGGCT CTGCAAAATG GAGGTGAAGT CCCACAGTCT GCCTTCTG
```

Genomic chr4 (reverse strand):

```
aggtaaagaga gattgagtat agactgtgga gaattagtct ttttcattca 57025354
cagtatacaa ttgttttcta gagatcagag tccttcctac ttttgtgtat 57025304
TCACAATACC CTATTGTTAA TTCCATATTA AGACTATATA CGGTGTTTTG 57025254
AAATTGTCTG CCTCTGGAGA CTTCCAAGAT TCATTGAGAG CAGAAGGTTA 57025204
ATTTTGTTCA TCTTTGCATT CCCAGGGTCT TATATATACA TAATAGGCTG 57025154
TATTTGTTCT CTA AAAAATA CAGAACCAAT AGGATATGTA CAGATTATGA 57025104
GAAATTGGCT CTGCAAAATG GAGGTGAAGT CCCACAGTCT GCCTTCTGca 57025054
ggctgaaggc ccaggaaagc cagtgtagtt ccaaaccga gggcttgaga 57025004
atcaggggag gcaataacgt taagtcctag tctgaaggcc tgaggacc
```

Side by Side Alignment

```
00000001 tcacaataccctattgttaattccatattaagactatatacgggtgtttg 00000050
<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<
57025303 tcacaataccctattgttaattccatattaagactatatacgggtgtttg 57025254

00000051 aaattgtctgcctctggagacttccaagattcattgagagcagaaggta 00000100
<<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<<
57025253 aaattgtctgcctctggagacttccaagattcattgagagcagaaggta 57025204

00000101 attttgttcatctttgcattcccagggctttatatatacataataggctg 00000150
<<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<<
57025203 attttgttcatctttgcattcccagggctttatatatacataataggctg 57025154

00000151 tatttgttctctaaaaaatacagaaccaataggatatgtacagattatga 00000200
<<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<<
57025153 tatttgttctctaaaaaatacagaaccaataggatatgtacagattatga 57025104

00000201 gaaattggctctgc AAAATGGAGGTGAAGTCCCAGTCTGCCTTCTG 00000248
<<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<<
57025103 gaaattggctctgc AAAATGGAGGTGAAGTCCCAGTCTGCCTTCTG 57025056
```

Alignment of YourSeq and chr16:24411988-24412236

Clone 28 YourSeq

```
cggccgctct agcccgcggt gacccgggag atctgaattC CTTGGCATCC 50
gtcgcaatga acTGAAGGTG GAGGAGATcc cacgggatga catcatacgg 100
gcagcggcat atttcagaga cagtccggaa aaagcacgaa agcgatttgg 150
tgaagaggga tggtagctca ataagggtga tgacgcgccg caggccgtaa 200
tggcgctcct gtgccacgga aaaaacctcg gctgggacaa atcgctaagg 250
gagggtgctgc acgtgtttta gaattcagat ctcccgggtc accg
```

Genomic chr16 :

```
cgggcttgag ccaccatgcc cagctattta tttatttttg tggagacagg 24411937
gtctcaccat ttgacctagg ctcatcttaa acggctcaag caatctccca 24411987
CTTGGCATC Ccaaagtgtc gagattacag gcatgtccca ccacgccggc 24412037
ctctctttac ctttctaata tggctagcag aaagtttaaa attacatgtg 24412087
tgggtcagat gacatttctc ttgggcagca cttccctgga caggcagtgt 24412137
atcccagaaa ggcagacctg ggctagccac agaattctca acccatccc 24412187
caagacttga ggctgacaag aagtaaaaca aagTGAAGGT GGAGGAGATg 24412237
aaaaatggga tgcaaagaaa cagatgtgat atagtccatc tttctctctc 24412287
ttttttaaaa tatagactgg gtctcactgt gttgccagg ctggtctca
```

Side by Side Alignment

```
00000040 ccttggcatcc 00000050
>>>>>>> |||||>>>>>>>
24411988 ccttggcatcc 24411998
```

```
00000063 tgaaggtggaggagat 00000078
>>>>>>> |||||>>>>>>>
24412221 tgaaggtggaggagat 24412236
```

00000001	acatgtgctgtgattttataaggcagcggttatgatatacagcattttcta	00000050
<<<<<<<<		<<<<<<<<
39189451	acatgtgctgtgattttataaggcagcggttatgatatacagcattttcta	39189402
00000051	tagttactcaaacagaaccttgctttcaagatttagctaagttagactag	00000100
<<<<<<<<		<<<<<<<<
39189401	tagttactcaaacagaaccttgctttcaagatttagctaagttagactag	39189352
00000101	aatttgtggaatatacttggactacttgaactaagagaaatgacccatgg	00000150
<<<<<<<<		<<<<<<<<
39189351	aatttgtggaatatacttggactacttgaactaagagaaatgacccatgg	39189302
00000151	agtaaaatcttcccagtcagaataattccctagtagcccatcagtccta	00000200
<<<<<<<<		<<<<<<<<
39189301	agtaaaatcttcccagtcagaataattccctagtagcccatcagtccta	39189252
00000201	tcactcagtgataataatctctgtctcccacttagaacaacagaataaa	00000250
<<<<<<<<		<<<<<<<<
39189251	tcactcagtgataataatctctgtctcccacttagaacaacagaataaa	39189202
00000251	acattgtatcaaattgaggctggtgtgagtgaagtgggttcacaactaa	00000300
<<<<<<<<		<<<<<<<<
39189201	acattgtatcaaattgaggctggtgtgagtgaagtgggttcacaactaa	39189152
00000301	ttgatcacaaccagttatagatttacttgtccttttccactcccaccgct	00000350
<<<<<<<<		<<<<<<<<
39189151	ttgatcacaaccagttatagatttacttgtccttttccactcccaccgct	39189102
00000351	tcacttcacta	00000361
<<<<<<<<		<<<<<<<<
39189101	tcacttcacta	39189091

Alignment of YourSeq and chr18:52432512-52432915

Clone 30 YourSeq

```
TTATCCCATT AAtCgTTTTA gTCATTTCAg ACTGAGTGAA TtAATACCAC 50
TTaAAAGAAT CACTTATACT TACCTAGGAT ACTGAcAATA GcATTGTTAC 100
TCACAAACCT ATTAATACATA TATGAACGAA ATACTACTTA CAGTTACgCT 150
GTTAACATTc TGAAACTTAA CATAACGAac TGGAACAATG CCATCTTCTT 200
TAATATCATC CTCTGTcAGT TCCAGAGCTc GAGTTGGTTC ACTTCTTTCT 250
GCCTCTTCAA AATCCATAGA TCGGGGTAGG TTGATAAAAA TTTTACATA 300
TTTAGGGCCC TGACCTATAC AATGGTAGAA TAAATAAAAA TGcTTAAAAA 350
CCTCAAATAT ACTATACTCC CTTTACCACT ACACTCACAC TATACACAGA 400
CACa
```

Genomic chr18 :

```
acttaccata tacatataaa ataactgaca aaaccccaca aatattcaaa 52432461
aatcaatctg tccttcctct ttaggttaca taaattaaaa agaagaaaat 52432511
TTATCCCATT AAaCaTTTTA cTCATTTCAa ACTGAGTGAA TaAATACCAC 52432561
TTtAAAGAAT CACTTAgACT TACCTAGGAT ACTGaaATA GtATTGTTAC 52432611
TCACAAACCT ATTAAATACA TATGAACGAA ATACTACTTA CAGTTAcACT 52432661
GTTAACATTc TGAAACTTAA CATAACGAag TGGAACAATG CCATCTTCTT 52432711
TAATATCATC CTCTGTcAGT TCCAGAGCTt GAGTTGGTTC ACTTCTTTCT 52432761
GCCTCTTCAA AATCCATAGA TCGGGGTAGG TTGATAAAAA TTTTACATA 52432811
TTTAGGGCCC TGACCTATAC AATGGTAGAA TAAATAAAAA TGtTTAAAAA 52432861
CCTCAAATAT ACTATACTCC CTTTACCACT ACACTCACAC TATACACAGA 52432911
CACacacaaa tcaatacaca tataactcaa ataactccat tattagaact 52432961
tgtacaaaag tctgagtatt caggtagcca atcctttatt ttccaaaaca 52433011
catt
```

Side by Side Alignment

```
00000001 ttatcccattaatcggttttagtcatttcagactgagtgaattaataaccac 00000050
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432512 ttatcccattaacattttactcatttcaaactgagtgaataaataaccac 52432561

00000051 ttaaaagaatcacttatacttacctaggatactgacaatagcattgttac 00000100
>>>>>>> || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432562 tttaaagaatcacttagacttacctaggatactgaaaatagtagtattgttac 52432611

00000101 tcacaaacctattaaatacatatgaacgaataactacttacagttacgct 00000150
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432612 tcacaaacctattaaatacatatgaacgaataactacttacagttacact 52432661

00000151 gttaacattctgaaacttaacataacgaactggaacaatgccatcttctt 00000200
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432662 gttaacattctgaaacttaacataacgaagtggaacaatgccatcttctt 52432711

00000201 taatatcatcctctgtcagttccagagctcgagttgggttcacttcttctt 00000250
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432712 taatatcatcctctgtcagttccagagcttgagttgggttcacttcttctt 52432761

00000251 gcctcttcaaaatccatagatcggggtaggttgataaaaaatttttacata 00000300
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432762 gcctcttcaaaatccatagatcggggtaggttgataaaaaatttttacata 52432811

00000301 tttagggccctgacctataacaatggtagaataaaaataaaatgcttaaaaa 00000350
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432812 tttagggccctgacctataacaatggtagaataaaaataaaatgcttaaaaa 52432861

00000351 cctcaaatatactatactccctttaccactacactcacactatacacaga 00000400
>>>>>>> ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| >>>>>>>
52432862 cctcaaatatactatactccctttaccactacactcacactatacacaga 52432911
```

00000401 caca 00000404
>>>>>>> |||| >>>>>>>
52432912 caca 52432915

Alignment of YourSeq and chr6:30573215-30573572

Clone 31 YourSeq

```
GAGAAAGAAA GAAAGAGAGA GAGAAAGAAA GAAAGGAAAG AAGGAAAGAA 50
GGAAAGAAAG GAAGAAAGGA AGAAAGAAAG AAAGGCAAAT GATCACTTAG 100
AGGATTTTGT TTGGTAGTTA AAACCATTTT GAAACAGAGG GAGGGAAGAA 150
ATCACCTATG CTTCTCAGT GGTAAAGAGA CTGGGAACCA CCACGCCAGA 200
GTTAGAAAT ATGAGGCAAC AGAAGGGCTG TTATATGTAG TGAATTTTC 250
CAAAACCGGT CCCCTGGAGG GAATACTTGG TGAAGGGCC TTAGAGGAAA 300
GAGATGCTTG TCCAGCCCAT TGCCTGTGTG TCCAGGAGAG ACTGTGCCCA 350
CCTTGAGA
```

Genomic chr6 :

```
gatcacacca ttgactcca gcctgagcaa gaagagtga actgcgcttc 30573164
gaaaagaaag aaagagagag agggaggagg ggaggaagga aggaaggaga 30573214
GAGAAAGAAA GAAAGAGAGA GAGAAAGAAA GAAAGGAAAG AAGGAAAGAA 30573264
GGAAAGAAAG GAAGAAAGGA AGAAAGAAAG AAAGGCAAAT GATCACTTAG 30573314
AGGATTTTGT TTGGTAGTTA AAACCATTTT GAAACAGAGG GAGGGAAGAA 30573364
ATCACCTATG CTTCTCAGT GGTAAAGAGA CTGGGAACCA CCACGCCAGA 30573414
GTTAGAAAT ATGAGGCAAC AGAAGGGCTG TTATATGTAG TGAATTTTC 30573464
CAAAACCGGT CCCCTGGAGG GAATACTTGG TGAAGGGCC TTAGAGGAAA 30573514
GAGATGCTTG TCCAGCCCAT TGCCTGTGTG TCCAGGAGAG ACTGTGCCCA 30573564
CCTTGAGA ctgagagaag accctagtga ggagaagccc ccaggccagc 30573614
cgtcagcaca gggcattgga ggtccccaac cagctccaag tcctgaacag 30573664
agcacagc
```

Side by Side Alignment

```
00000001 gagaagaaagaaagagagagagaaagaaagaaagaaagaaagaa 00000050
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573215 gagaagaaagaaagagagagagaaagaaagaaagaaagaaagaa 30573264

00000051 ggaaagaaaggaagaaaggaagaaagaaagaaaggcaaatgatcacttag 00000100
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573265 ggaaagaaaggaagaaaggaagaaagaaagaaaggcaaatgatcacttag 30573314

00000101 aggatTTTgtttgtagTTaaaccatTTTgaacagagggagggaagaa 00000150
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573315 aggatTTTgtttgtagTTaaaccatTTTgaacagagggagggaagaa 30573364

00000151 atcacctatgcttcctcagtggtaagagactgggaaccaccacgccaga 00000200
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573365 atcacctatgcttcctcagtggtaagagactgggaaccaccacgccaga 30573414

00000201 gttagaaaatatgaggcaacagaagggctgttatatgtagtgaatTTTc 00000250
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573415 gttagaaaatatgaggcaacagaagggctgttatatgtagtgaatTTTc 30573464

00000251 caaacccggtcccctggagggaatacttggtagtgggccttagaggaaa 00000300
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573465 caaacccggtcccctggagggaatacttggtagtgggccttagaggaaa 30573514

00000301 gagatgcttTccagcccattgcctgtgtgtccaggagagactgtgccca 00000350
>>>>>>> |||||>>>>>>> |||||>>>>>>>
30573515 gagatgcttTccagcccattgcctgtgtgtccaggagagactgtgccca 30573564

00000351 ccttgaga 00000358
>>>>>>> |||||>>>>>>>
30573565 ccttgaga 30573572
```

Alignment of YourSeq and chr18:52432382-52432890

Clone 32 YourSeq

```
TATAAAGTTG TAGAAcAAAC TTCCAGCAAA ACTTACCATA TACcTATAAA 50
ATAACTGACA AAACCCACACA AATATTCAAA AATCAATCTG TCCTTCCTCT 100
TTAGGGTACA TAGATTAAAA AGAAGAAAAT TTATCCCAT TAAACATTTTA 150
CTCATTTCAA ACTGAGTGAA TAAATACCAC TTTAAAGAAT CACTTAGACT 200
TACCTAGGAT ACTGAAAATA GgATTGTTAC TCACAAACCT ATTAATATACA 250
TATGAACGAA ATACTACTTA CAGTTACACT GTTAACATTC TGAACCTTAA 300
CATAACGAAG gCcAAaAATG CCATCTTCTT TAATATCATC CTCTGTCAaT 350
TcaCAGAGCT TGAGTTGGTT CACTTCTTTC TGCCTCTTCA AAATCCATAG 400
ATCGGGGTAG GTTGATAAAat ATTTTACAT ATTaAGGGCC CTGACCTATA 450
CAATGGTAGA ATAAAAATAA ATGtaTAAAA ACCTCaTATA TACTATACTC 500
CCTTTACCAC
```

Genomic chr18 :

```
acttaaaaac tccatattca agaaaagtaa ataagatttt acaaacacat 52432331
cactactata ccagggtataa agaataaagc acaaatactc tcagttttag 52432381
TATAAAGTTG TAGAAtAAAC TTCCAGCAAA ACTTACCATA TAcATATAAA 52432431
ATAACTGACA AAACCCACACA AATATTCAAA AATCAATCTG TCCTTCCTCT 52432481
TTAGGGTACA TAaATTAAAA AGAAGAAAAT TTATCCCAT TAAACATTTTA 52432531
CTCATTTCAA ACTGAGTGAA TAAATACCAC TTTAAAGAAT CACTTAGACT 52432581
TACCTAGGAT ACTGAAAATA GtATTGTTAC TCACAAACCT ATTAATATACA 52432631
TATGAACGAA ATACTACTTA CAGTTACACT GTTAACATTC TGAACCTTAA 52432681
CATAACGAAG tGgAAcAATG CCATCTTCTT TAATATCATC CTCTGTCAgT 52432731
TCcAGAGCTT GAGTTGGTTC ACTTCTTCTT GCCTCTTCAA AATCCATAGA 52432781
TCGGGGTAGG TTGATAAAa TTTTACATA TTTAGGGCCC TGACCTATAC 52432831
AATGGTAGAA TAAAAATAAA TGttAAAAA CCTCAaATAT ACTATACTCC 52432881
CTTTACCACt acactcacac tatacacaga cacacacaaa tcaatacaca 52432931
tatacttcaa ataactccat tattagaact tgtacaaaag tctgagtatt 52432981
caggtagcc
```

Side by Side Alignment

```
00000001 tataaagttgtagaacaaacttccagcaaaacttaccatatacctataaa 00000050
>>>>>>> ||||||||||||| ||||||||||||||||||||||||| ||||||| >>>>>>>
52432382 tataaagttgtagaataaaacttccagcaaaacttaccatatacctataaa 52432431

00000051 ataactgacaaaacccacacaaatattcaaaaatcaatctgtccttcctct 00000100
>>>>>>> ||||||||||||| ||||||||||||||||||||||||| ||||||| >>>>>>>
52432432 ataactgacaaaacccacacaaatattcaaaaatcaatctgtccttcctct 52432481

00000101 ttagggtacatagattaaaaagaagaaaatttatccattaaacatttta 00000150
>>>>>>> ||||||||||||| ||||||||||||||||||||||||| ||||||| >>>>>>>
52432482 ttagggtacataaattaaaaagaagaaaatttatccattaaacatttta 52432531

00000151 ctcatittcaaactgagtgataaataaccacttttaagaatcacttagact 00000200
>>>>>>> ||||||||||||| ||||||||||||||||||||||||| ||||||| >>>>>>>
52432532 ctcatittcaaactgagtgataaataaccacttttaagaatcacttagact 52432581

00000201 tacctaggatactgaaaataggattgttactcacaaacctattaaatata 00000250
>>>>>>> ||||||||||||| ||||||||||||||||||||||||| ||||||| >>>>>>>
52432582 tacctaggatactgaaaatagattgttactcacaaacctattaaatata 52432631

00000251 tatgaacgaataactacttacagttacactgttaacattctgaaacttaa 00000300
>>>>>>> ||||||||||||| ||||||||||||||||||||||||| ||||||| >>>>>>>
52432632 tatgaacgaataactacttacagttacactgttaacattctgaaacttaa 52432681

00000301 cataacgaagggcaaaaatgccatcttctttaatatcatcctctgtcaat 00000350
>>>>>>> ||||||||| | || ||||||||||||||||||||||||| || >>>>>>>
52432682 cataacgaagtgaacaatgccatcttctttaatatcatcctctgtcagt 52432731
```

```
00000351 tcacagagcttgagttggttcacttctttctgcctcttcaaaatccatag 00000400
>>>>>>> || |||||  >>>>>>>
52432732 tc.cagagcttgagttggttcacttctttctgcctcttcaaaatccatag 52432780

00000401 atcggggtaggttgataaatatttttacatattaagggcctgacctata 00000450
>>>>>>> |||||  >>>>>>>
52432781 atcggggtaggttgataaaaatttttacatatttagggcctgacctata 52432830

00000451 caatggtagaataaaaataaaatgtataaaaacctcatatatactatactc 00000500
>>>>>>> |||||  >>>>>>>
52432831 caatggtagaataaaaataaaatgttataaaaacctcaaatactatactc 52432880

00000501 cctttaccac 00000510
>>>>>>> |||||  >>>>>>>
52432881 cctttaccac 52432890
```

Alignment of YourSeq and chr12:112829446-112829770

Clone 33 YourSeq

```
TTGTTTCATTT GTTTACTGCC CCTACTGCCA ACCACCATTA GAACATAAGA 50
GCCACGAGGG CAGGAAC TTT GCCTTGTTCA CAGCCACCTT CCCAGTGCCG 100
AGCAATGCAC CTGGTACAGA GAGAGGCTCC ATCAACGCCA GAGGAATGCC 150
AGGGGAATAA ATCTGCATCT CCCGTGGTGC AGAGGAGACA GGAGGCACCC 200
CATGCACACT GAAGGAATGA AAGCACGCAT TCATTCCGTC CTTTCAAACC 250
ACAGCgAAGT AGGAAGAGTG GGAATATCCT GATAGGAAAA CAGGGCAGAG 300
TGGGGAAATG ACCCGGTCCT CGCG
```

Genomic chr12 :

```
atggcgacca cagaaactgg tactggtctt attctcatcc ctcctaactc 112829395
ttgctttaac tgtcttcaga acgctcatgc caccatgtca cggaatttat 112829445
TTGTTTCATTT GTTTACTGCC CCTACTGCCA ACCACCATTA GAACATAAGA 112829495
GCCACGAGGG CAGGAAC TTT GCCTTGTTCA CAGCCACCTT CCCAGTGCCG 112829545
AGCAATGCAC CTGGTACAGA GAGAGGCTCC ATCAACGCCA GAGGAATGCC 112829595
AGGGGAATAA ATCTGCATCT CCCGTGGTGC AGAGGAGACA GGAGGCACCC 112829645
CATGCACACT GAAGGAATGA AAGCACGCAT TCATTCCGTC CTTTCAAACC 112829695
ACAGCaAAGT AGGAAGAGTG GGAATATCCT GATAGGAAAA CAGGGCAGAG 112829745
TGGGGAAATG ACCCGGTCCT CGCGccagc cctccgaggg ggtcaacagg 112829795
acttagcttt atttgaacc cctgtatggt ttataagggg aggaaaaaaa 112829845
taccttatct gtgtaactga aacta
```

Side by Side Alignment

```
000000001 ttgttcatttgtttactgcccctactgcccaaccaccattagaacataaga 000000050
>>>>>>>> |||||>>>>>>>> |||||>>>>>>>>
112829446 ttgttcatttgtttactgcccctactgcccaaccaccattagaacataaga 112829495

000000051 gccacgagggcaggaactttgccttggtcacagccaccttcccagtgccg 000000100
>>>>>>>> |||||>>>>>>>> |||||>>>>>>>>
112829496 gccacgagggcaggaactttgccttggtcacagccaccttcccagtgccg 112829545

000000101 agcaatgcacctggtacagagagaggctccatcaacgccagaggaatgcc 000000150
>>>>>>>> |||||>>>>>>>> |||||>>>>>>>>
112829546 agcaatgcacctggtacagagagaggctccatcaacgccagaggaatgcc 112829595

000000151 aggggaataaatctgcatctccgtggtgcagaggagacaggaggcacc 000000200
>>>>>>>> |||||>>>>>>>> |||||>>>>>>>>
112829596 aggggaataaatctgcatctccgtggtgcagaggagacaggaggcacc 112829645

000000201 catgcacactgaaggaatgaaagcacgcattcattccgtcctttcaaacc 000000250
>>>>>>>> |||||>>>>>>>> |||||>>>>>>>>
112829646 catgcacactgaaggaatgaaagcacgcattcattccgtcctttcaaacc 112829695

000000251 acagcgaagtaggaagagtgggaatatcctgatagggaaacagggcagag 000000300
>>>>>>>> |||||>>>>>>>> |||||>>>>>>>>
112829696 acagcaaaagtaggaagagtgggaatatcctgatagggaaacagggcagag 112829745

000000301 tggggaaatgacccggtcctcgcg 000000325
>>>>>>>> |||||>>>>>>>> >>>>>>>>
112829746 tggggaaatgacccggtcctcgcg 112829770
```

Alignment of YourSeq and chr3:123217290-123217355

Clone 34 YourSeq

GGACTAATAC ACAGTCTACA ATCAGATTGG GCTTATTTAT CGCCGAAATA 50
TTTCCAGAAT CTCTCT

Genomic chr3 :

tcctgaggcc tccccagccc tgcagaactg taagtgaatt aaacctcttt 123217239
cctttataaa ttatgcaatc tcaggcagtt ctttatagca gcatgagaac 123217289
GGACTAATAC ACAGTCTACA ATCAGATTGG GCTTATTTAT CGCCGAAATA 123217339
TTTCCAGAAT CTCTCTctct ctccaatttc actactatcc tagcacaagc 123217389
tactattatg tccagcctcc atatcacctg tgcttaccta gtactgtact 123217439
catgcatgct ctggtt

Side by Side Alignment

000000001 ggactaatacacagtctacaatcagattgggcttatttatcgccgaaata 000000050
>>>>>>>> || >>>>>>>>
123217290 ggactaatacacagtctacaatcagattgggcttatttatcgccgaaata 123217339

000000051 tttccagaatctctct 000000066
>>>>>>>> |||||||||||||||| >>>>>>>>
123217340 tttccagaatctctct 123217355

Alignment of YourSeq and chr4:34957924-34958031

Clone 35 YourSeq

```
tcgcccgcg tgacccggga gatctgaatt cagtcattgt gggccaaagt 50
ggcctgcacg gcttcagcac ctgtaggtag gaaggatagg tggtagagata 100
tagacaaaga ttatggtgga accattagaa cccgtagcga caggcggcaa 150
agatthttatg ggaatgtggtg tccagaaaga tctagttagg agaagaagga 200
catcgagtgg gtgatccaga aaatatgatg gttgaggact ttcaccaaatt 250
cgcttcggtt attcccgtaa atcaagtccg gaagaggagg tagAATAAA 300
AAGATAATAG CCGATGG
```

Genomic chr4 :

```
gctctggggc aacaaagaag aatacaacct taaatctttt ttttatttta 34957873
tttaattatt ttttacaaca gagctctcaa tctactagag tgaagatgcc 34957923
AATAAAAG ATAATAGCaa tacagggtat ttagcgttat aatgatagag 34957973
agagggtgcat gtaatatata gaagaggata gcttaattta aactggcttg 34958023
ggCGATGaa aactcctaag agaagagaat gcatgtatta aatcttaaag 34958073
aattcaaaac tttagggtgaa aaacaaggta aaaaatgagg tattgaatgt 34958123
caagagcc
```

Side by Side Alignment

```
00000294 aaataaaaagataatagc 00000311
>>>>>>> |||||>>>>>>>
34957924 aaataaaaagataatagc 34957941
```

```
00000312 ccatgg 00000317
>>>>>>> |||||>>>>>>>
34958026 ccatgg 34958031
```

Alignment of YourSeq and chr14:30621914-30622069

Clone 36 YourSeq

```
CCATGACTTT AGGTAAGTGA GCTGAGTTAC CTTACATCTA AAACAGGAAG 50
AGAGTCTTAC AAGACTAGAT ATTGAGAGAG TTAACGTGAA TCAGAGGTGA 100
AGGGATATGT ATTATAGTTG GATGAGTTGT GTTGATGTGT CGTATATTTA 150
CTAGAT
```

Genomic chr14 :

```
ctgcactcca gcctgggcga cagagcgaga ctccgtctca aaaaaaaaaa 30621863
aaaagactag aagagcttta acacctgac agccttaata gttgatgttg 30621913
CCATGACTTT AGGTAAGTGA GCTGAGTTAC CTTACATCTA AAACAGGAAG 30621963
AGAGTCTTAC AAGACTAGAT ATTGAGAGAG TTAACGTGAA TCAGAGGTGA 30622013
AGGGATATGT ATTATAGTTG GATGAGTTGT GTTGATGTGT CGTATATTTA 30622063
CTAGATgttt agtagaaata aagatgggta tacttgtctt ttagccttc 30622113
tgggtgtgtag tataggtctg tgtgatgagc tccagcattc ttgtttgaat 30622163
taaaat
```

Side by Side Alignment

```
00000001 ccatgacttttaggtaactgagctgagttaccttacatctaaaacaggaag 00000050
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
30621914 ccatgacttttaggtaactgagctgagttaccttacatctaaaacaggaag 30621963

00000051 agagtcttacaagactagatattgagagagttaacgtgaatcagaggtga 00000100
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
30621964 agagtcttacaagactagatattgagagagttaacgtgaatcagaggtga 30622013

00000101 agggatatgtattatagttggatgagttgtgttgatgtgtcgtatattta 00000150
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
30622014 agggatatgtattatagttggatgagttgtgttgatgtgtcgtatattta 30622063

00000151 ctagat 00000156
>>>>>>> ||||| >>>>>>>
30622064 ctagat 30622069
```

[illegible]

Alignment of YourSeq and chr3:111497276-111497704

Clone 38 YourSeq

```
GTTTAATTGG CTCACAGTTC CACATGGCTG GGGAGGTTTC AGGAACTTA 50
TAATCATGGT GGAAGGGGAA GCAGGCACAT CTTACCAGGC AAGATAGAGA 100
GAGCGTGTGA GTGAAGAAGT AAGATGCCAA AACTTAAAA AACCATCAGA 150
CCTCATGAGA ACTCACTCAC TATGATGAGA ACAGAATGGG AAAAACCACC 200
CCCGTGATGT AGTCACCTCC CACgAGGTTT CTCCCCAAC ACCTGAGGAT 250
TACAATTTAA GATGAGATTT GAGTGGGGAC ATCAAGCCTA ACCATATCAT 300
AGGTCCTCTA AAAATAAATT CAGGAATCAA TCAGTCCACA TGGAGAGAAA 350
AGCCTAAGCT TAAAGACAAA ATGAAAGAAC ACGATGTAAT TAAAGGGAT 400
GCTAGCCTAA ATAAGAAACA ATATCACCg
```

Genomic chr3 :

```
agtgccctac tacctcagta ctaaattatt gtattgtatt agtcgttttc 111497225
acacttctat aaagatctgc ctaggactgg gtactttata aaggaaagag 111497275
GTTTAATTGG CTCACAGTTC CACATGGCTG GGGAGGTTTC AGGAACTTA 111497325
TAATCATGGT GGAAGGGGAA GCAGGCACAT CTTACCAGGC AAGATAGAGA 111497375
GAGCGTGTGA GTGAAGAAGT AAGATGCCAA AACTTAAAA AACCATCAGA 111497425
CCTCATGAGA ACTCACTCAC TATGATGAGA ACAGAATGGG AAAAACCACC 111497475
CCCaTGATGT AGTCACCTCC CACcAGGTTT CTCCCCAAC ACCTGAGGAT 111497525
TACAATTTAA GATGAGATTT GAGTGGGGAC ATCAAGCCTA ACCATATCAT 111497575
AGGTCCTCTA AAAATAAATT CAGGAATCAA TCAGTCCACA TGGAGAGAAA 111497625
AGCCTAAGCT TAAAGACAAA ATGAAAGAAC ACGATGTAAT TAAAGGGAT 111497675
GCTAGCCTAA ATAAGAAACA ATATCACCg tggcatctac cttctactta 111497725
agatgtagaa atcggaaaat aatattcttt ccatgtaaca gcatgaataa 111497775
tgtgtataat ctacaaaacc acacatttc
```

Side by Side Alignment

```
000000001 gtttaattggctcacagttccacatggctggggagggtttcaggaaactta 000000050
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497276 gtttaattggctcacagttccacatggctggggagggtttcaggaaactta 111497325

000000051 taatcatggtggaaaggaagcaggcacatcttaccaggcaagatagaga 000000100
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497326 taatcatggtggaaaggaagcaggcacatcttaccaggcaagatagaga 111497375

000000101 gagcgtgtgagtgaagaagtaagatgccaaacacttaaaaaaccatcaga 000000150
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497376 gagcgtgtgagtgaagaagtaagatgccaaacacttaaaaaaccatcaga 111497425

000000151 cctcatgagaactcactcactatgatgagaacagaatgggaaaaaccacc 000000200
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497426 cctcatgagaactcactcactatgatgagaacagaatgggaaaaaccacc 111497475

000000201 cccgtgatgtagtcacctcccacagggttcctccccaacacctgaggat 000000250
>>>>>>> |||>>>>>>> |||||>>>>>>>
111497476 cccatgatgtagtcacctcccaccagggttcctccccaacacctgaggat 111497525

000000251 tacaatttaagatgagatttgagtggggacatcaagcctaaccatcat 000000300
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497526 tacaatttaagatgagatttgagtggggacatcaagcctaaccatcat 111497575

000000301 aggtcctctaaaaataaattcaggaatcaatcagtcacatggagagaaa 000000350
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497576 aggtcctctaaaaataaattcaggaatcaatcagtcacatggagagaaa 111497625

000000351 agcctaagctttaagacaaaatgaaagaacacgatgtaattaaaaggat 000000400
>>>>>>> |||||>>>>>>> |||||>>>>>>>
111497626 agcctaagctttaagacaaaatgaaagaacacgatgtaattaaaaggat 111497675
```

000000401 gctagcctaaataagaaacaatatcaccg 000000429
>>>>>>> |||||>>>>>>>
111497676 gctagcctaaataagaaacaatatcaccg 111497704

Alignment of YourSeq and chr7:63778799-63779130

Clone 39 YourSeq

```
CACAACAGTC ATGGAGGCTA GGGAGACAGG TCCCTGAAAG GAGGGCAGGG 50
TGGAGTGAGT GGCCCCCATA TCGATCAAAA AGGGGATGGA CTTACCCTCC 100
ACCTTAAGAG TTACCCGAGG TCCATGATGG TCCATGGGGC CTCCGAGGTG 150
TTCGGGCAGT GTCATTCTCT AGCCGCCAAG CCGAGGAGAT CAGAGAAGGA 200
GTCAGCCAGG GGGCTGTGGG GTTAAGCTCC AGGAGCTCTA GGGATGGCAG 250
CTTGAGTTGG ACAGTCTGAC TTCCAGTGAG GGCCTGCACA AACAGGGCAT 300
GGCTTAGGAG GAACCCAGG CTGCAGGCAT TC
```

Genomic chr7 (reverse strand):

```
ggacaagtgg ggatgactaa aaggagtga aaaaggagtg ctgatctagt 63779181
tgacacacaa gtggagtctg gagaggtctg gaggtttgc cgtcaattcc 63779131
CACAACAGTC ATGGAGGCTA GGGAGACAGG TCCCTGAAAG GAGGGCAGGG 63779081
TGGAGTGAGT GGCCCCCATA TCGATCAAAA AGGGGATGGA CTTACCCTCC 63779031
ACCTTAAGAG TTACCCGAGG TCCATGATGG TCCATGGGGC CTCCGAGGTG 63778981
TTCGGGCAGT GTCATTCTCT AGCCGCCAAG CCGAGGAGAT CAGAGAAGGA 63778931
GTCAGCCAGG GGGCTGTGGG GTTAAGCTCC AGGAGCTCTA GGGATGGCAG 63778881
CTTGAGTTGG ACAGTCTGAC TTCCAGTGAG GGCCTGCACA AACAGGGCAT 63778831
GGCTTAGGAG GAACCCAGG CTGCAGGCAT Tccttgccc agtgactatt 63778781
tttatggcac ttgaagcatg gccctggagg ggctgctggg cgctgcggtc 63778731
tggatgcctt gaaatcccta caggccattg gt
```

Side by Side Alignment

```
00000001 cacaacagtcattggaggctaggagacaggtccctgaaaggagggcaggg 00000050
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63779130 cacaacagtcattggaggctaggagacaggtccctgaaaggagggcaggg 63779081

00000051 tggagtgaagggtggccccatattgatcaaaaaggggatggacttacctcc 00000100
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63779080 tggagtgaagggtggccccatattgatcaaaaaggggatggacttacctcc 63779031

00000101 accttaagagttaccgaggtccatgatggtccatggggcctccgaggtg 00000150
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63779030 accttaagagttaccgaggtccatgatggtccatggggcctccgaggtg 63778981

00000151 ttcgggcagtgctattcctcagccgccaagccgaggagatcagagaagga 00000200
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63778980 ttcgggcagtgctattcctcagccgccaagccgaggagatcagagaagga 63778931

00000201 gtcagccagggggctgtggggttaagctccaggagctctagggatggcag 00000250
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63778930 gtcagccagggggctgtggggttaagctccaggagctctagggatggcag 63778881

00000251 cttgagttggacagtctgacttccagtgaaggcctgcacaaacagggcat 00000300
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63778880 cttgagttggacagtctgacttccagtgaaggcctgcacaaacagggcat 63778831

00000301 ggcttaggaggaacccaggtgcaggcattc 00000332
<<<<<<<< |||||<<<<<<<< |||||<<<<<<<<
63778830 ggcttaggaggaacccaggtgcaggcattc 63778799
```

Alignment of YourSeq and chr12:60895257-60895391

Clone 40 YourSeq

ATTTTGGGTT ATTGGTAAGT CAATTTTCA CAAATTGTTT ATTAATTGAA 50
TGCAGATGTG CAGTCACCAA AAGCAGCCCT GTGTGTCTTA TCTCTAAATC 100
ATTTGAGTTT TCCCTTCTCA GTAGTTGCTC CAACA

Genomic chr12 :

gctatctctg tatatcctca taagagacca aaactttcca agacaatcat 60895206
acctccaggT tttggaattg aagaacaaaa gtcaatgtct acttggtcac 60895256
ATTTTGGGTT ATTGGTAAGT CAATTTTCA CAAATTGTTT ATTAATTGAA 60895306
TGCAGATGTG CAGTCACCAA AAGCAGCCCT GTGTGTCTTA TCTCTAAATC 60895356
ATTTGAGTTT TCCCTTCTCA GTAGTTGCTC CAACAgtagg aataacctga 60895406
aatgggaaaa ggcaaggtaa taggatacaa gaataacaaa tttccagaa 60895456
catctcatag cctggggaag tactgacatt ttcac

Side by Side Alignment

00000001 attttgggttatttggttaagtcaatttttcacaaattgtttattaattgaa 00000050
>>>>>>> |||||>>>>>>> >>>>>>>
60895257 attttgggttatttggttaagtcaatttttcacaaattgtttattaattgaa 60895306

00000051 tgcagatgtgcagtcaccaaagcagccctgtgtgtcttatctctaaatc 00000100
>>>>>>> |||||>>>>>>> >>>>>>>
60895307 tgcagatgtgcagtcaccaaagcagccctgtgtgtcttatctctaaatc 60895356

00000101 atttgagttttcccttctcagtagttgctccaaca 00000135
>>>>>>> |||||>>>>>>> >>>>>>>
60895357 atttgagttttcccttctcagtagttgctccaaca 60895391

Genomic chr14 :

Side by Side Alignment

Alignment of YourSeq and chr1:167637003-167637200

Clone 42 YourSeq

```
TCCTTTCTCA GATCTCAAAC TCCGTGCTGG GAAAAGCACT ACTCTCTTCA 50
AAGCTGTCAG ACTGGGACGT TTAAGTCTGC AGAAGTTTCT GCTGCCTTTT 100
GTTCAAGCTGT GTCTTGCCCC CAGAGGTAGA GTCTACAGAG GCAGGCAGGC 150
CTCCTTGAGC TGTGGTCAGC TCCACCCAGT TGGAGCTTCC CAGCTGCT
```

Genomic chr1 (reverse strand):

```
aggggcaccc ggctgtatga ggtgtcagtt ggccccctact gggaggtgtc 167637251
tcccagttag cctacttggg cgtcagggac ccacttgagg aggcagtctg 167637201
TCCTTTCTCA GATCTCAAAC TCCGTGCTGG GAAAAGCACT ACTCTCTTCA 167637151
AAGCTGTCAG ACTGGGACGT TTAAGTCTGC AGAAGTTTCT GCTGCCTTTT 167637101
GTTCAAGCTGT GTCTTGCCCC CAGAGGTAGA GTCTACAGAG GCAGGCAGGC 167637051
CTCCTTGAGC TGTGGTCAGC TCCACCCAGT TGGAGCTTCC CAGCTGCTtt 167637001
gtttacctac ttaagcctca gcaatggcag acatctctcc cctagccttg 167636951
ctgtggcatt gcagtttgat ctcagactgc tgtgttagca gtgagtga
```

Side by Side Alignment

```
000000001 tcctttctcagatctcaaactccgtgctgggaaaagcactactctcttca 000000050
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
167637200 tcctttctcagatctcaaactccgtgctgggaaaagcactactctcttca 167637151

000000051 aagctgtcagactgggacgtttaagtctgcagaagtttctgctgcctttt 000000100
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
167637150 aagctgtcagactgggacgtttaagtctgcagaagtttctgctgcctttt 167637101

000000101 gttcagctgtgtcttgccccagaggtagagtctacagaggcaggcaggc 000000150
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
167637100 gttcagctgtgtcttgccccagaggtagagtctacagaggcaggcaggc 167637051

000000151 ctcccttgagctgtggtcagctccacccagttggagcttcccagctgct 000000198
<<<<<<<<< ||||||||||||||||||||||||||||||||||||||||||| <<<<<<<<<
167637050 ctcccttgagctgtggtcagctccacccagttggagcttcccagctgct 167637003
```

Alignment of YourSeq and chrX:36370495-36370707

Clone 43 YourSeq

```
ATTTAGCCAC AGGAAGTTTT CAGGTTCAAC CTACTTTCCT TAGCACTCCA 50
TGCATCACAG ACACTGGTTT TCTATTAGC AAACCCATTT CCTTTTCTTT 100
TATTTCTTTT TGAGACAGAG TCTCACTCTT ATATGAGGCT GGCATGAGGT 150
GGCACAGTCA CAGATCACTG TAACGTTGAC CACCTGGGCT CAAGTGATTC 200
TCCCACCTCA GCT
```

Genomic chrX :

```
tcaaaataag taaataaata aatgaataaa tggaaccatt acaagctggg 36370444
gtttgtctgt atagccatta atccctaaac catagcctgg tacttgagtt 36370494
ATTTAGCCAC AGGAAGTTTT CAGGTTCAAC CTACTTTCCT TAGCACTCCA 36370544
TGCATCACAG ACACTGGTTT TCTATTAGC AAACCCATTT CCTTTTCTTT 36370594
TATTTCTTTT TGAGACAGAG TCTCACTCTT ATATGAGGCT GGCATGAGGT 36370644
GGCACAGTCA CAGATCACTG TAACGTTGAC CACCTGGGCT CAAGTGATTC 36370694
TCCCACCTCA GCTtcccaag tagctgctac aacagacaca caccaccatg 36370744
cttgggctaatttggttatta ttgtagaga caagatcttg ctctgctgcc 36370794
caaaatggtc cca
```

Side by Side Alignment

```
00000001 atttagccacaggaagttttcaggttcaacctactttccttagcactcca 00000050
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
36370495 atttagccacaggaagttttcaggttcaacctactttccttagcactcca 36370544

00000051 tgcatacacagacactggttttctatttagcaaaccatttccttttcttt 00000100
>>>>>>> |||||||||||||||||||||||||||||||||||||||| >>>>>>>
36370545 tgcatacacagacactggttttctatttagcaaaccatttccttttcttt 36370594

00000101 tatttctttttgagacagagtctcactcttatatgaggctggcatgaggt 00000150
>>>>>>> |||||||||||||||||| >>>>>>>
36370595 tatttctttttgagacagagtctcactcttatatgaggctggcatgaggt 36370644

00000151 ggcacagtcacagatcactgtaacgttgaccacctgggctcaagtgattc 00000200
>>>>>>> |||||||||||||||| >>>>>>>
36370645 ggcacagtcacagatcactgtaacgttgaccacctgggctcaagtgattc 36370694

00000201 tcccacctcagct 00000213
>>>>>>> |||||||||||| >>>>>>>
36370695 tcccacctcagct 36370707
```

```

000000001 ttgtgatgtgttcgttcaactcacagagttaaacctttctgttcatagag 000000050
>>>>>>> |||||>>>>>>>
121186462 ttgtgatgtgtttgttcaactcacagagttaaacctttctgttcatagag 121186511

000000051 cagttaggaaacactctgtttgtaaagctctgtaagtggaattctgacat 000000100
>>>>>>> |||||>>>>>>>
121186512 cagttaggaaacgctctgtttgtaaagctctgtaagtggaattctgacat 121186561

000000101 tttgtggccttcgttggaacgggatttcttcattctgctagacagaa 000000150
>>>>>>> |||||>>>>>>>
121186562 cttgtggccttcgttggaacgggatttcttcctattctgctagacagat 121186611

000000151 gaattctcagtaacttccttgtgttgtgtgtattcaactcacagagtga 000000200
>>>>>>> |||||>>>>>>>
121186612 gaattctcagtaacttccttgtgttgtgtgtattcaactcacagagtga 121186661

000000201 acgatcctttacacagagcagacttg 000000226
>>>>>>> |||||>>>>>>>
121186662 acgatcctttacacagagcagacttg 121186687

```

Alignment of YourSeq and chr14:60618889-60619062

Clone 45 YourSeq

```
CTCTGTTTTA GTCAAGTGAA GGGCACACTC CTTTTCATTG GCCACCTCTT 50
ACTTTTCCTC CAAGAGGAGT ACTCACTCCC AGAACCCCTT GCTGGGCTCT 100
CATGCCGAGC TTAGGTGCCC CTTCACTGTG CTTCTGCAGC ACTCATTACC 150
CCGTAGTAGC ATTGTAGTTT AATT
```

Genomic chr14 :

```
gtcttttagtc ctgttgactg ctttgatttt gttttttaac ttgtaccaag 60618838
acctgttgcc atgatgggtc tctgcaaatg ggctttcttg ttccatgagt 60618888
CTCTGTTTTA GTCAAGTGAA GGGCACACTC CTTTTCATTG GCCACCTCTT 60618938
ACTTTTCCTC CAAGAGGAGT ACTCACTCCC AGAACCCCTT GCTGGGCTCT 60618988
CATGCCGAGC TTAGGTGCCC CTTCACTGTG CTTCTGCAGC ACTCATTACC 60619038
CCGTAGTAGC ATTGTAGTTT AATcctgtt tgcttgactg aagcagagac 60619088
tcacctgcag acgcctgtag gtgccttcca cgttgctcag atgaacagta 60619138
gagaagggtc aggcctgccc tagg
```

Side by Side Alignment

```
00000001 ctctgttttagtcaagtgaagggcacactccttttcattggccacctctt 00000050
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
60618889 ctctgttttagtcaagtgaagggcacactccttttcattggccacctctt 60618938

00000051 acttttcctccaagaggagtactcactcccagaaccctttgctgggctct 00000100
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
60618939 acttttcctccaagaggagtactcactcccagaaccctttgctgggctct 60618988

00000101 catgccgagccttaggtgccccttcagtgtgcttctgcagcactcattacc 00000150
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
60618989 catgccgagccttaggtgccccttcagtgtgcttctgcagcactcattacc 60619038

00000151 ccgtagtagcattgtagtttaatt 00000174
>>>>>>> |||||||||||||||||||| >>>>>>>
60619039 ccgtagtagcattgtagtttaatt 60619062
```

Alignment of YourSeq and chr5:2179167-2179189

Clone 46 YourSeq

```
cggtgacccg ggagatctga attccagcgg acaacaacag cgacagcacg 50
atcaagcgca tggggcggCC CATCCTGGGA AAGTGCCgAG CAtaacgcca 100
aggccaaggc gtcggccgat tcggcatacc tgcacgtacg ctacggcgct 150
gcgcgatgct tgaactgtat cgggaaatga ctgcaatcgc gtctgctaac 200
attcatcggt tcctacaagg agttgggata tgggggcttc gaattcagat 250
ctcccgggtc accg
```

Genomic chr5 (reverse strand):

```
cacagtctcc agccatgtcc catcccacag cctcacactg ggcttggagt 2179240
ccatggtcca tccctgcgag caccttcaca cagcctcca tgcctttccc 2179190
CCCATCCTGG GAAAGTGCCA GCAgggcagg ccgtcttctt cctcttctga 2179140
gcctgtgcct taagcagcaa agctctgaag atagaaaggt ccccgccca 2179090
gtctcccccac ctgtatccat cac
```

Side by Side Alignment

```
0000069 cccatcctgggaaagtgccgagca 0000092
<<<<<<< |||||  <<<<<<<
2179189 cccatcctgggaaagtgcc.agca 2179167
```

```
000000209 atgtattgtatagcattgtttcatacgtt 000000237  
>>>>>>> ||||| ||||||| ||||||| ||||||| >>>>>>>  
132035447 atgtcttgtataccattgtttcatacgtt 132035475
```

```
00000256 atttta....tgagaagaatatctgtcaggaacgaagatcaattaagt 00000300  
>>>>>>> ||||| | |||||||||||||||| | ||| | ||||||>>>>>>  
50551009 attttattatctgaaaagaatatctgtcaggaatgaagctaaattaagt 50551058  
  
00000301 atagtcatatgaaggcaaaaaaacaccctaatag 00000334  
>>>>>>> ||| ||| ||||| |||||||||||||||| >>>>>>  
50551059 atactcagatgaaggaaaaaaaacaccctaatag 50551092
```

Alignment of YourSeq and chr2:236765821-236765847

Clone 49 YourSeq

```
ccttccaata tggtcagcat acagtcacgc tggaaactgg agaaattgca 50
cgccaggctt ctggtgctgt actggtgtcg attgacgata ccgttgtatt 100
ggcaaccgtT GTTGCTAAGA AagatGCTAA GCCTGGTcag gatttcttcc 150
ccctgactgt tgattacatg gaaaaaagct atgcggctgg ccgtattcct 200
ggcgggtttt tcaagcgcgga aggacgtcct tcggagaaaag aaacgctgac 250
gtcagccctg atcgatcgtc cgatccgccc gttatttcct gagggatadc 300
tgaacgaagt acaggtgata gtgcatgttt tgtcggtgaa tcc
```

Genomic chr2 :

```
tgagaaagag tgggatataa gaggtggttg aggtgtgggc tctgggctcc 236765770
agattgggtg gctaacattg gaaaagcatg ctttgtgtgg aattgtttac 236765820
TGTGCTAAG AACcaGCTAA GCCTGGTggg tggggggcag tcagttcctc 236765870
ctgggtcagc aaggcccccag atgtcaaagc atctgaatag agaaagtaag 236765920
ctgggggagg gggctcactc ctgcaat
```

Side by Side Alignment

```
000000110 tgttgctaagaa 000000121
>>>>>>> |||||>>>>>>>
236765821 tgttgctaagaa 236765832
```

```
000000126 gctaagcctggt 000000137
>>>>>>> |||||>>>>>>>
236765836 gctaagcctggt 236765847
```

Alignment of YourSeq and chr6:78817330-78817484

Clone 50 YourSeq

```
ggaaccaggc agatgttcca ataattgaag ataagcaaga gcactcagtg 50
ggaaggggag taaccccggt ggtagccga atcatgaata gagataacag 100
gacaggatcc tgaTGGGAA GGGGAAGTA gggctaaaca atgaaagtgg 150
gataagcaat caaatgctc AACTTAGCA ACcaattagc cattccggat 200
ggttgccatg gggaatgtag aaccgagaac gatttcactc ttgtaaccgt 250
tgggaccggg aataggactt gcctgcaatt tttcctcaac aacgggaacg 300
aaagccggag atctaccgga acggaggacg gtttcgcccc cgatcacccg 350
tgagatctga attagaaatt cccagggga aataaggtaa tgagacatac 400
agtgcagcta gaagaccagc aatccatagg actggtattt aaccgagatg 450
tatagattga tagaattacg gaacaccgtc aattacattc ctccagggat 500
aaagaccggt gcgcacagcc tcgtatccga ggtccaacc acgatctaac 550
agggcgcgca acttaatcct ctcgttcgag tgcagacagg gatttggggt 600
gcgaccggcc cgtat
```

Genomic chr6 :

```
tctagcaaca atgcttcaag atacatgaag cattgttttt tattgaagta 78817279
tcattcatac atattaaatt aatctatttt aagaggagag cctgggggct 78817329
TGGAAGGG GGAAGTA agt agttataatc aatgggcaga tttcctataa 78817379
tcaatagggtg gttataatca agtttcagtt aagcaagatg aataaaactct 78817429
agacatttgc tgaataacac tgcattatag tcaacaataa tgtAACTTA 78817479
GCAACatgtt aagaggtaga tctcatgttt gtttttatca caataaaatg 78817529
agatttttaa aagaacatag ttgaatttta ataattatat ataaccgtgt 78817579
acca
```

Side by Side Alignment

```
00000114 gtgggaagggggaagta 00000130
>>>>>>> |||||>>>>>>>
78817330 gtgggaagggggaagta 78817346
```

```
00000171 acacttagcaac 00000182
>>>>>>> |||||>>>>>>>
78817473 acacttagcaac 78817484
```

Alignment of YourSeq and chr6:55345780-55345966

Clone 51 YourSeq

```
CAAACACTAA CACACCCAAA CgCCCACTAT AAACCTACAT ATAGTATCAG 50
GGACAGCAAA ACCTCAAAAA AAAAAAAAC TTCTATTCAA AATCAGGAAA 100
AATGGGAGAA CAATAACACA CAGTGAGATC CTATACTATA GGCATTGTGC 150
AGCCTCTCTG GCAGTGTGGA TTTCAGTAAG GAGAAC
```

Genomic chr6 :

```
cgcgaaactca aagccctgaa tgttaaaaga tgtgcaagct aaatgtttgtg 55345729
gcaccttgta atagacagga aaccactgc catcttccg acacagacac 55345779
CAAACACTAA CACACCCAAA CcCCCACTAT AAACCTACAT ATAGTATCAG 55345829
GGACAGCAAA ACCTCAAAAA AAAAAAAa CTTCTATTCA AAATCAGGAA 55345879
AAATGGGAGA ACAATAACAC ACAGTGAGAT CCTATACTAT AGGCATTGTG 55345929
CAGCCTCTCT GGCAGTGTGG ATTTAGTAA GGAGAActg aatcagatat 55345979
ctgtgaagaa ccaccttctg tggctcctat tttatcctct gaaaggttct 55346029
tccttgaccg tatttttcca cggccatattc tgaaata
```

Side by Side Alignment

```
00000001 caaacactaacacaccccaaacgcccactataaacctacatatagtatcag 00000050
>>>>>>> ||||||||||||||||||||||| ||||||||||||||||||||||| >>>>>>>
55345780 caaacactaacacaccccaaaccccccactataaacctacatatagtatcag 55345829

00000051 ggacagcaaaacctcaaaaaaaaaaaaaa.cttctattcaaaatcaggaa 00000099
>>>>>>> ||||||||||||||||||||||| ||||||||||||||||||||||| >>>>>>>
55345830 ggacagcaaaacctcaaaaaaaaaaaaaaacttctattcaaaatcaggaa 55345879

00000100 aaatgggagaacaataacacacagtgagatcctatactataggcattgtg 00000149
>>>>>>> ||||||||||||||||||||||| ||||||||||||||||||||||| >>>>>>>
55345880 aaatgggagaacaataacacacagtgagatcctatactataggcattgtg 55345929

00000150 cagcctctctggcagtggtgatttcagtaaggagaac 00000186
>>>>>>> ||||||||||||||||||||||| >>>>>>>
55345930 cagcctctctggcagtggtgatttcagtaaggagaac 55345966
```

Alignment of YourSeq and chr17:40282696-40283217

Clone 52 YourSeq

```
GAGAAAAGAA ATAATGCCCC TTGGCATCAA ACCCTTCACC CGTCCTCTGG 50
CTaTCAGGCG TCCcAGGGGT TCACCTCTAG CTGCTCCCTT GAGAGTCCAG 100
CTTCCCGCTC ATCTTTCTGC CCCAGGTCCC AACAGCTGtT TCAAGCATCT 150
GACCACACAA CCTGGGGAAA CCACTTATCT GACAGTTCAC GAAACACTTT 200
CACATGTATT GTGTATCTGA GAAACCTCAC AGCAGCCTGC AAGGTAGGCA 250
GGCCAGGGGT GGTATTGTGTC ATGTTACACA TCAGGAAACT GAGGCTCAGT 300
GAGAAAGATT TGTCCACTGT CACACAGTTA GCAAGTGGCT GTCTGCTTTT 350
TAATCTCAAG AGGAAGAGAA ATTCAACATC TGTCTGTTG CATGATTTTT 400
aTCACCCgTA GGGCAAAC TG CATGAGACA CTGTCCCAC AGGCCTGGGA 450
CAGGAGCtTA AACAGGGAAG ATGGCTCAGT ATAGGGGaTT CACCAAGCAT 500
GTGATGTGGA GCCCAGAACA aG
```

Genomic chr17 (reverse strand):

```
tggacagccc cggtctctat aggagtccta cttctctcca gcatcctgtg 40283268
ccatcctctt gacgtaatcg ctgtacattg tgtacacagc acctgtgtga 40283218
GAGAAAAGAA ATAATGCCCC TTGGCATCAA ACCCTTCACC CGTCCTCTGG 40283168
CTcTCAGGCG TCCTAGGGGT TCACCTCTAG CTGCTCCCTT GAGAGTCCAG 40283118
CTTCCCGCTC ATCTTTCTGC CCCAGGTCCC AACAGCTGcT TCAAGCATCT 40283068
GACCACACAA CCTGGGGAAA CCACTTATCT GACAGTTCAC GAAACACTTT 40283018
CACATGTATT GTGTATCTGA GAAACCTCAC AGCAGCCTGC AAGGTAGGCA 40282968
GGCCAGGGGT GGTATTGTGTC ATGTTACACA TCAGGAAACT GAGGCTCAGT 40282918
GAGAAAGATT TGTCCACTGT CACACAGTTA GCAAGTGGCT GTCTGCTTTT 40282868
TAATCTCAAG AGGAAGAGAA ATTCAACATC TGTCTGTTG CATGATTTTT 40282818
cTCACCCcTA GGGCAAAC TG CATGAGACA CTGTCCCAC AGGCCTGGGA 40282768
CAGGAGCcTA AACAGGGAAG ATGGCTCAGT ATAGGGGcTT CACCAAGCAT 40282718
GTGATGTGGA GCCCAGAACA gGagaactta attcacagtc cttttttttt 40282668
tttttttttt tttttgagac agagtctcac tctgtcacc gggctggagt 40282618
gcagtggcgg atctcagccc ac
```

Side by Side Alignment

```
00000001 gaaaaaagaataatgcccttggcatcaaacccttcaccgctcctctgg 00000050
<<<<<<<< ||||| <<<<<<<<
40283217 gaaaaaagaataatgcccttggcatcaaacccttcaccgctcctctgg 40283168

00000051 ctatcaggcgctccagggttcacctctagctgctcccttgagagtccag 00000100
<<<<<<<< || <<<<<<<<
40283167 ctctcaggcgctcctagggttcacctctagctgctcccttgagagtccag 40283118

00000101 cttcccgctcatctttctgccccagggtcccaacagctgtttcaagcatct 00000150
<<<<<<<< ||||| <<<<<<<<
40283117 cttcccgctcatctttctgccccagggtcccaacagctgtttcaagcatct 40283068

00000151 gaccacacaacctggggaaccacttatctgacagttcacgaaacacttt 00000200
<<<<<<<< ||||| <<<<<<<<
40283067 gaccacacaacctggggaaccacttatctgacagttcacgaaacacttt 40283018

00000201 cacatgtatttgttatctgagaaacctcacagcagcctgcaaggtaggca 00000250
<<<<<<<< ||||| <<<<<<<<
40283017 cacatgtatttgttatctgagaaacctcacagcagcctgcaaggtaggca 40282968

00000251 ggccaggggtggttattgtcatgttacacatcaggaaactgaggctcagt 00000300
<<<<<<<< ||||| <<<<<<<<
40282967 ggccaggggtggttattgtcatgttacacatcaggaaactgaggctcagt 40282918

00000301 gagaagatttgtccactgtcacacagtttagcaagtggctgtctgctttt 00000350
<<<<<<<< ||||| <<<<<<<<
40282917 gagaagatttgtccactgtcacacagtttagcaagtggctgtctgctttt 40282868
```

00000351 taatctcaagaggaagagaaattcaacatctgttctgttgcattttt 00000400
<<<<<<< ||||||||||||||||||||||||||||||||||||||| <<<<<<<
40282867 taatctcaagaggaagagaaattcaacatctgttctgttgcattttt 40282818

00000401 atcacccgtagggcaaaactgtcatgagacactgtccccacaggcctggga 00000450
<<<<<<< |||||| ||||||||||||||||||||||||||||||| <<<<<<<
40282817 ctcaccctagggcaaaactgtcatgagacactgtccccacaggcctggga 40282768

00000451 caggagcttaaacagggaagatggctcagtataggggattcaccaagcat 00000500
<<<<<<< |||||| ||||||||||||||||||||||||||| ||||||| <<<<<<<
40282767 caggagcctaaacagggaagatggctcagtataggggcttcaccaagcat 40282718

00000501 gtgatgtggagcccagaacaag 00000522
<<<<<<< ||||||||||||||||| | <<<<<<<
40282717 gtgatgtggagcccagaacagg 40282696

Alignment of YourSeq and chr15:53425196-53425231

Clone 53 YourSeq

```
cancagggcc ggatctcgct cgccaagacc ggtgatgtcg atcaccccg 50
agacccggcc gtcgagatcg tgcagtggct cgctcaggca gaacaccggc 100
gcgaaccgct gcaggtagtg ttcgttgccg cgcaccagtg ccggcacgtc 150
GTCAgCCAGG CTGaccgccg gcgcgGTGGT GCCGATCTCG Gtctcgccca 200
gctgtcgccc gacct
```

Genomic chr15 (reverse strand):

```
ctgggaaaga gagactttga actactaacc ataatgaggg tactgggcac 53425282
agatgaaggt atcaagaaga attttttttt tttagacaga atctcgctct 53425232
GTCAcCCAGG CTGgagtga GTGGTGCCGA TCTCGctca atgcaacctc 53425182
cacctccagg gttcaagtga ttctcctgtc tcagcctccc aagtagctgg 53425132
cattacaggt gcgtgccacc acaccagct aatttt
```

Side by Side Alignment

```
00000151 gtcagccaggctg 00000163
<<<<<<<< |||| |||||<<<<<<<<
53425231 gtcacccaggctg 53425219
```

```
00000176 gtggtgccgatctcg 00000191
<<<<<<<< |||||<<<<<<<<
53425211 gtggtgccgatctcg 53425196
```

Alignment of YourSeq and chr5:2179167-2179189

Clone 54 YourSeq

```
gaagcccca tatccaact cttttagga aacgatgaat gtagcagac 50
gcgattgcag tcatttcccg atacagttca agcatcgcg agcgccgtag 100
cgtacgtgca ggtatgccga atcggccgac gccttggcct tggcgttaTG 150
CTcGGCACTT TCCCAGGATG Gccgccccca tgcgcttgat cgtgctgtcg 200
ctgttgttgt ccgctg
```

Genomic chr5 :

```
gtgatggata caggtgggga gactgggagg gggacctttc tatcttcaga 2179116
gctttgctgc ttaaggcaca ggctcagaag aggaagaaga cggcctgccc 2179166
TGCTGGCACT TCCCAGGAT Ggggggaaag gcatggaggc gtgtgtgaag 2179216
gtgctcgag ggatggacca tggactccaa gccagtggtg aggcgtgtggg 2179266
atgggacatg gctggagact gtg
```

Side by Side Alignment

```
0000149 tgctcggcactttccaggatggg 0000172
>>>>>> |||| ||||| ||||| ||||| ||||| >>>>>>
2179167 tgct.ggcactttccaggatggg 2179189
```

Alignment of YourSeq and chr12:121363540-121363770

Clone 55 YourSeq

```
CCACCAGTCA TCAGGGGCAG GGGCTTTTTC AACCTACTCC CCATACCTCC 50
TGTGCCAGCT TCCATGGAAC GCTACCAGCG TGTCTCCCAC TGTCCTCCC 100
TCCCGTTAAC AGTCCCAGCC ATATTGTGCC AAGTCACTGA CAGGAAGATG 150
TGATTCCCTC AGGTCTGTTG GGGCAGAAAA ATAGTAGAAA ATCCAAAGCA 200
GCCCAGGCTC TTTCTGCCCT GGGATCCGGT C
```

Genomic chr12 :

```
aagactaagg aatagcaaag tgactgcttt gttttgagaa gcaactgttcc 121363489
cattacacag tcctcttacc gcagaaggcc ctggaaatct gaccacaaag 121363539
CCACCAGTCA TCAGGGGCAG GGGCTTTTTC AACCTACTCC CCATACCTCC 121363589
TGTGCCAGCT TCCATGGAAC GCTACCAGCG TGTCTCCCAC TGTCCTCCC 121363639
TCCCGTTAAC AGTCCCAGCC ATATTGTGCC AAGTCACTGA CAGGAAGATG 121363689
TGATTCCCTC AGGTCTGTTG GGGCAGAAAA ATAGTAGAAA ATCCAAAGCA 121363739
GCCCAGGCTC TTTCTGCCCT GGGATCCGGT Ccctccccac ctgaatgtgt 121363789
tcaggggatca gaggtctggg gagtacagca ccaggaacag ctcagcacag 121363839
gctgggggta gcgtgacagc agctggagcc a
```

Side by Side Alignment

```
000000001 ccaccagtcacaggggcaggggctttttcaacctactccccatacctcc 000000050
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
121363540 ccaccagtcacaggggcaggggctttttcaacctactccccatacctcc 121363589

000000051 tgtgccagcttccatggaacgctaccagcgtgtctccactgttcctccc 000000100
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
121363590 tgtgccagcttccatggaacgctaccagcgtgtctccactgttcctccc 121363639

000000101 tcccggttaacagtcacagccatattgtgccaagtcactgacaggaagatg 000000150
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
121363640 tcccggttaacagtcacagccatattgtgccaagtcactgacaggaagatg 121363689

000000151 tgattccctcaggtctgttggggcagaaaaatagtagaaaatccaaagca 000000200
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
121363690 tgattccctcaggtctgttggggcagaaaaatagtagaaaatccaaagca 121363739

000000201 gcccaggctctttctgccctgggatccggtc 000000231
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
121363740 gcccaggctctttctgccctgggatccggtc 121363770
```

Alignment of YourSeq and chr12:49427254-49427530

Clone 56 YourSeq

```
GCCAAATGTG ACTAGTGGCT ACCATATTAG ACAGTGCAGA TCTATACTCA 50
TTCCTTCAAA TACATTACTC TGTTAATCTC AAAGTGTGGC CAACTCCCAT 100
TTACTTAGAG GCTGATTATC TAGTTTTGTA GTTCCTCAGG CCTCTAATTT 150
ATTTTTTGCT TTA TGCTTTA TTGATCTTTT GCATGTCCCC CAAAGCCAGA 200
ATCTGCTCAT GGAGGAAGGA AGGCTAAGAA CTGTCCTTGA GGAAC TTCAT 250
CAGTA ACTCT GGTAAAGCAT CCTGTG
```

Genomic chr12 :

```
ttaatgagtt attttacttt ttttcatatt aggcctttga aattcagtgt 49427203
gtattaaaca catctcaatt caaacatca ccatatttca agtctttgta 49427253
GCCAAATGTG ACTAGTGGCT ACCATATTAG ACAGTGCAGA TCTATACTCA 49427303
TTCCTTCAAA TACATTACTC TGTTAATCTC AAAGTGTGGC CAACTCCCAT 49427353
TTACTTAGAG GCTGATTATC TAGTTTTGTA GTTCCTCAGG CCTCTAATTT 49427403
ATTTTTTGCT TTA TGCTTTA TTGATCTTTT GCATGTCCCC CAAAGCCAGA 49427453
ATCTGCTCAT GGAGGAAGGA AGGCTAAGAA CTGTCCTTGA GGAAC TTCAT 49427503
CAGTA ACTCT GGTAAAGCAT CCTGTGagg gagaggagag cccagtcatt 49427553
tgcttagatg gtgtttgtgg gatcacctgc agatttaaag cctactctgc 49427603
cacagactcg agtaagaaaa tgttctc
```

Side by Side Alignment

```
00000001 gccaaatgtgactagtggctaccatattagacagtgcagatctataactca 00000050
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
49427254 gccaaatgtgactagtggctaccatattagacagtgcagatctataactca 49427303

00000051 ttccttcaaatacattactctgttaatctcaaagtgtggccaactcccat 00000100
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
49427304 ttccttcaaatacattactctgttaatctcaaagtgtggccaactcccat 49427353

00000101 ttacttagaggctgattatctagttttgtagttcctcaggcctctaattt 00000150
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
49427354 ttacttagaggctgattatctagttttgtagttcctcaggcctctaattt 49427403

00000151 attttttgctttatgctttattgatcttttgcatgtcccccaggccaga 00000200
>>>>>>> |||||||||||| |||||||||||||||||||||||||||||||| >>>>>>>
49427404 attttttgcttttgctttattgatcttttgcatgtcccccaggccaga 49427453

00000201 atctgctcatggaggaaggaaggctaagaactgtccttgaggaacttcat 00000250
>>>>>>> |||||||||||||||||||||||||||||||||||||||||||| >>>>>>>
49427454 atctgctcatggaggaaggaaggctaagaactgtccttgaggaacttcat 49427503

00000251 cagtaactctggtaaagcatcctgtgg 00000277
>>>>>>> |||||||||||||||||||||||| >>>>>>>
49427504 cagtaactctggtaaagcatcctgtgg 49427530
```

Alignment of YourSeq and chr16:44962360-44962766

Clone 57 YourSeq

```
ATTGATTCT AtTCGAAAT GATTCCATT GAATCCATT GATGATGATT 50
CCATTAGATT CCATTGATG ATTCCATTG ATTCCATTG ACGATGATTC 100
CATTGATTC CaTTTGATGA TTCCATTCTA TTCTATTCTGA TGATGATTC 150
ATTGATTCC ATTTGATGAT GATTGGATTC GATTCCATT GATGATTCA 200
TTTGATTCCA TTCGTTAATG ATTTGATCA AcTCCATTTCG ATGATTCCAT 250
TtGATTCCAT TCGATAATGA TTACATCCGA GTCCATTCTGA TGATTCCATT 300
TGAGCCcGTT CGATAATTCC ATTTGAGTCC AATCAATGAT TCCATTTCATT 350
TCCATTCAAT GATTCCATT GAGTCCATT GATCATTctG GTAGGGTCCg 400
TTCGATG
```

Genomic chr16 :

```
ttccatgcga tgattctatt cgattccatt caatgataat tccattcaat 44962309
tcagtcattc ctctggactc catttgatga tgattccatt caatgattcc 44962359
ATTGATTCT AcTCGAAAT GATTCCATT GAATCCATT GATGATGATT 44962409
CCATTAGATT CCATTGATG ATTCCATTca ATTCCATTcG ACGATGATTC 44962459
CATTGATTC CgTTTGATGA TTCCATTCTA TTCTATTCTGA TGATGATTC 44962509
ATTGATTCC ATTTGATGAT GATTGGATTC GATTCCATT GATGATTCA 44962559
TTTGATTCCA TTCGTTAATG ATTTGATCA AtTCCATTTCG ATGATTCCAT 44962609
TcGATTCCAT TCGATAATGA TTACATCCGA GTCCATTCTGA TGATTCCATT 44962659
TGAGCctGTT CGATAATTCC ATTTGAGTCC AATCAATGAT TCCATTTCATT 44962709
TCCATTCAAT GATTCCATT GAGTCCATT GATCATTCCG GTAGGGTCCa 44962759
TTCGATGttg attccattgg agtgcattcg atgattccat tcgagtccat 44962809
tttaggattt gattcgagtc ctttcgatga ttccattcga ttccactcga 44962859
tgatgat
```

Side by Side Alignment

```
00000001 attcgattctattcgaaaatgattccatttgaatccatttgatgatgatt 00000050
>>>>>>> |||||>>>>>>> |||||>>>>>>>
44962360 attcgattctactcgaaaatgattccatttgaatccatttgatgatgatt 44962409

00000051 ccattagattccatttgatgattccattcgattccatttgacgatgattc 00000100
>>>>>>> |||||>>>>>>> |||||>>>>>>>
44962410 ccattagattccatttgatgattccattcaattccattcgacgatgattc 44962459

00000101 cattcgattccatttgatgattccattctattctattcgatgatgattcc 00000150
>>>>>>> |||||>>>>>>> |||||>>>>>>>
44962460 cattcgattccgtttgatgattccattctattctattcgatgatgattcc 44962509

00000151 attcgattccatttgatgatgattggattcgattccatttgatgatttca 00000200
>>>>>>> |||||>>>>>>> |||||>>>>>>>
44962510 attcgattccatttgatgatgattggattcgattccatttgatgatttca 44962559

00000201 tttgattccattcgtaaatgatttcgatcaactccattcgatgattccat 00000250
>>>>>>> |||||>>>>>>> |||||>>>>>>>
44962560 tttgattccattcgtaaatgatttcgatcaattccattcgatgattccat 44962609

00000251 ttgattccattcgataatgattacatccgagtcattcgatgattccatt 00000300
>>>>>>> | |||||>>>>>>> |||||>>>>>>>
44962610 tcgattccattcgataatgattacatccgagtcattcgatgattccatt 44962659

00000301 tgagcccgttcgataattccatttgagtccaatcaatgattccattcatt 00000350
>>>>>>> ||||| |||||>>>>>>> |||||>>>>>>>
44962660 tgagcctgttcgataattccatttgagtccaatcaatgattccattcatt 44962709

00000351 tccattcaatgattccattcgagtcatttgatcattctggtaggggtccg 00000400
>>>>>>> |||||>>>>>>> |||||>>>>>>>
44962710 tccattcaatgattccattcgagtcatttgatcattccggtaggggtcca 44962759
```

00000401 ttcgatg 00000407
>>>>>>> ||||| >>>>>>>
44962760 ttcgatg 44962766

Alignment of YourSeq and chrX:135058016-135058039

Clone 58 YourSeq

```
aggacgtatg gtcagcgttc taccatcact tgactccact aggggtgtgac 50
accgccggta ggtcatcagg gctgaagact tggatttcag ggggttaggt 100
caggccgtgc ggttAGGTCT CCCATCTCCC CCCggcTCCA Ccaaattcaa 150
aaaagaagac gccctagggc gtc
```

Genomic chrX (reverse strand):

```
caaccacccc acaagcatcc cagtcaagaa aaccgaggcg ggccccctca 135058090
cgtctactcc tcgtcgccac ccccgccatc ctcgttgagc gaagcaaggc 135058040
AGGTCTCCCA TCTCCCCCT CCACgatccc cgccatcctt gatgggaaaa 135057990
ccaaggaggt cgaccaccg cttcatcctc acccgctccc cacagcccct 135057940
gctagctatc ctggctgaaa gaac
```

Side by Side Alignment

```
000000115 aggtctccatctcccccggtccac 000000141
<<<<<<<< ||||| ||||| <<<<<<<<
135058039 aggtctccatctcccccc...tccac 135058016
```

Alignment of YourSeq and chr20:30059491-30059513

Clone 59 YourSeq

```
ggcagcaCCG GCAGGATGCA GGGctgAGC AGGgtcaatg cgccccccag 50
gtaagcaagc agcaacagca gcatggtcag gctccggaag caggagaaga 100
accgaccggc acccgccagc cgtcggcggt gccatccgtg gcgccgggaa 150
cgaacaccat cgccgcaccg ttcatgcagt agcgcagccc ggtcgggagc 200
gggccgtcgt tgaacacatg gccgaggtgg ccaccgcagc ggcggcagtg 250
cacctctacc cgcagcatcc cgaaggtgac gtcgag
```

Genomic chr20 :

```
acatccagag cagagtcagg aattggctag cacaccctgg cctcttcctg 30059440
ttcgctggc aggtgagtg gagatctcac ttcctgagct ggggggtgac 30059490
CCGGCAGGAT GCAGGGGAGC AGGagggagt ggctgtgaga gccagcacta 30059540
agcaacctgg gccatttccc ctccaaggga ggggaaggaa gaggaagggc 30059590
tagtggctag gagtctcctg tag
```

Side by Side Alignment

```
00000008 ccggcaggatgcaggggctgagcagg 00000033
>>>>>>> ||||| ||||| >>>>>>>
30059491 ccggcaggatgcagggg...agcagg 30059513
```

Alignment of YourSeq and chr11:85215148-85215513

Clone 60 YourSeq

```
TGTGAGCAAA GGTGAATTT CAGACCAGGA GCCTGGTCTT GAGGCAATGT 50
CCAGAGGTCA AGGAGGCAAG AAATCAAGTC CAGGGGAGTC AGGTGAGAGA 100
GAAGCTAAAA CAGGCTGTGC TGGTCTAGGG AGCCAGCGTC TGGAGGACAA 150
GGGGCTGGGG AGAAACAGAA AGCAAACAAT TCTGCTGATA CTTGCTGAGC 200
CTCTAACGGT ATGTCAGAGA GAGAGCTCTC ACTTTAGGAG AAGTTGCTAC 250
CCATGCTCGT TTAACCTCCT TCAGCCTGGA GGTGGATGTG CTATAAAGCT 300
CTAGTTCACA GTCGGCAGGG ACTCAGCATC ACAACATATT CACTCCTCGT 350
GAAGGCAGGT ATGAAT
```

Genomic chr11 :

```
ctgtctgtga gggtttgggc agatggccag gctgctctgc atcagaggag 85215097
ccaggccctc aatccatctg tgcagagaca gtctgcagat tccatgtgta 85215147
TGTGAGCAAA GGTGAATTT CAGACCAGGA GCCTGGTCTT GAGGCAATGT 85215197
CCAGAGGTCA AGGAGGCAAG AAATCAAGTC CAGGGGAGTC AGGTGAGAGA 85215247
GAAGCTAAAA CAGGCTGTGC TGGTCTAGGG AGCCAGCGTC TGGAGGACAA 85215297
GGGGCTGGGG AGAAACAGAA AGCAAACAAT TCTGCTGATA CTTGCTGAGC 85215347
CTCTAACGGT ATGTCAGAGA GAGAGCTCTC ACTTTAGGAG AAGTTGCTAC 85215397
CCATGCTCGT TTAACCTCCT TCAGCCTGGA GGTGGATGTG CTATAAAGCT 85215447
CTAGTTCACA GTCGGCAGGG ACTCAGCATC ACAACATATT CACTCCTCGT 85215497
GAAGGCAGGT ATGAATcctg ccgaaaggtc ttctctcctg ctgacatgaa 85215547
gagatgaaca gtgaaagtgg gaaagtgaat tttcagggtg catttctgaa 85215597
agttctgtga aaaaca
```

Side by Side Alignment

```
00000001 tgtgagcaaaaggttgaatttcagaccaggagcctgggtcttgaggcaatgt 00000050
>>>>>>> |||||  >>>>>>>
85215148 tgtgagcaaaaggttgaatttcagaccaggagcctgggtcttgaggcaatgt 85215197

00000051 ccagaggtcaaggaggcaagaaatcaagtcaggaggagtcagggtgagaga 00000100
>>>>>>> |||||  >>>>>>>
85215198 ccagaggtcaaggaggcaagaaatcaagtcaggaggagtcagggtgagaga 85215247

00000101 gaagctaaaacaggtgtgctggtctagggagccagcgtctggaggacaa 00000150
>>>>>>> |||||  >>>>>>>
85215248 gaagctaaaacaggtgtgctggtctagggagccagcgtctggaggacaa 85215297

00000151 ggggctgggggagaaacagaaagcaacaattctgctgatacttgctgagc 00000200
>>>>>>> |||||  >>>>>>>
85215298 ggggctgggggagaaacagaaagcaacaattctgctgatacttgctgagc 85215347

00000201 ctctaacggtatgtcagagagagagctctcactttaggagaagttgctac 00000250
>>>>>>> |||||  >>>>>>>
85215348 ctctaacggtatgtcagagagagagctctcactttaggagaagttgctac 85215397

00000251 ccatgctcggttaactcccttcagcctggaggtggatgtgctataaagct 00000300
>>>>>>> |||||  >>>>>>>
85215398 ccatgctcggttaactcccttcagcctggaggtggatgtgctataaagct 85215447

00000301 ctagttcacagtcggcagggactcagcatcacacaacatattcactcctcgt 00000350
>>>>>>> |||||  >>>>>>>
85215448 ctagttcacagtcggcagggactcagcatcacacaacatattcactcctcgt 85215497

00000351 gaaggcaggtatgaat 00000366
>>>>>>> |||||  >>>>>>>
85215498 gaaggcaggtatgaat 85215513
```

Alignment of YourSeq and chr6:17281926-17281947

Clone 61 YourSeq

```
tgctctccca agcgggtggtc gtcattggccg accgttcggg ttcgagggct 50
cccaaagctt cgaagtcgtc gtcggcagcc aggatcacct tgcggaacat 100
cgcattgctc accatgacgg tgaAGGCTCg tTGGTTGGAC GTGAACGtcc 150
gcgccgggctg gacctcctcg gggttcctcgt cgaggggatg ggtgaggtcc 200
tcccattcgt cgatgagga ggaatcgggtg gag
```

Genomic chr6 (reverse strand):

```
tcattagatt tacagcctac cctaaatcca ggataattta atctcgaggt 17281998
tctagcaaat gcatctgcaa agaccctatt tccaaacaag ggcacttctg 17281948
AGGCTCTGGT TGGACGTGAA CGgggggtgg gacatgattc aaccactat 17281898
caggaggacc tgggaagtgg tgctgaatgg gggatggaac atgccatcaa 17281848
gttaaagggtt ttctctagaa ct
```

Side by Side Alignment

```
00000124 aggctcgttggttgacgtgaacg 00000147
<<<<<<< ||||| ||||| <<<<<<<
17281947 aggctc..tggttgacgtgaacg 17281926
```

Clone 62 YourSeq

Genomic chr18 :

Side by Side Alignment

```
00000210  tgttaacattctgaaacttaacataacgaagtggaacagtgccattctt 00000259
>>>>>>> ||||||||||| ||||||||||| ||||||||||| >>>>>>>
52432661  tgttaacattctgaaacttaacataacgaagtggaacaatgccattctt 52432710

00000260  ttaatatcatcctctgtcgaattccagaggttgagttggttcactctcttt 00000309
>>>>>>> ||||||||||| ||||||||||| ||||||||||| >>>>>>>
52432711  ttaatatcatcctctgtcagttccagagcttgagttggttcact.tcttt 52432759

00000310  ctgcctcttcaaaatccatagatcggggggtgttgataaaaatttttaca 00000359
>>>>>>> ||||||||||| ||||||||||| >>>>>>>
```

```
00000360 tatttagggcctgacctatacaatggtagaataaaaataaaatgtttaaa 00000409
>>>>>> |||||  >>>>>>
52432810 tatttagggcctgacctatacaatggtagaataaaaataaaatgtttaaa 52432859
```

```
00000410 aaccacatatatactattctccctt 00000434
>>>>>> |||| | | ||||| ||||| >>>>>>
52432860 aacctcaaatactatactccctt 52432884
```

Alignment of YourSeq and chr6:36919097-36919116

Clone 63 YourSeq

```
cggtgaccg ggagatctga attccagctc ggcgtggcgc caagttccac 50
caaTGAGCCA ATGACTGGCA GAAcgcttta gggctaggat tgcctcaggg 100
gcgtagtagg agttggtgtc agtctgcgtc cgaattcaga tctcccgggt 150
caccgcgggc ggatgcgg
```

Genomic chr6 (reverse strand):

```
aaggctttct ctggcttctg gaacctgcat tggcctctct gtgctggtta 36919167
ggccagaagt gccaggaaat taataccctc caaaagcagc cctcagccac 36919117
TGAGCCAATG ACTGGCAGAA gttggtataa acatatccca gcttcctcac 36919067
ccctctggca gcctaagttt gaaatgcggt ctacagtctc ccagagttct 36919017
gcagcaggac tataccctag
```

Side by Side Alignment

```
00000054 tgagccaatgactggcagaa 00000073
<<<<<<<< ||||||||||||||||||| <<<<<<<<
36919116 tgagccaatgactggcagaa 36919097
```

cgggtgacccg	ggagatctga	attcgaatcg	ctctattcgc	cgaccaacat	50
tatgctgatg	catcacgtca	ccgcggctct	gcgcgcccat	gcgctgttta	100
cgcgcgacgt	agattacatt	gtgaaggacg	gcgaagtggg	tatcgtcgac	150
gagcacaccg	gccgtaccat	gcagggccgc	cgctggtcgg	atggtctgca	200
ccagcgcatg	gaagccaaag	aggggtgtgga	gatccagaac	gagaaccaga	250
cgcTGGCTTC	TATCACCTTC	CAGaactact	tccgtctcta	cgataagctg	300
gccggtatga	ccggtacggc	ggacaccgag	gccttcgagt	tcagctctat	350
ttgaattcag	atctcccggg	tcaccg			

gttcttcatt	cctcccttat	ctcagagagg	tgcacctaca	tttagctcac	106065233
tctgaataaa	atgtctgcc	ggtcagagga	gtaaatcatt	gcaagctcaa	106065183
TGGCTTATAT	CACCTTGCA	cctatggcagc	agctagaaac	aaataatatt	106065133
accatagaag	gcagtaattc	tgcttctcag	ccagtcaggt	catctaagct	106065083
taaggtccta	ggttcaagcc				

```
000000254 tggcttctatcaccttcag 000000273  
<<<<<<< ||||| <<<<<<<  
106065182 tggcttctatcaccttcag 106065163
```

Alignment of YourSeq and chr11:121068026-121068045

Clone 65 YourSeq

```
gcggccgctc tagcccgcgg tgacCCGGGA GATCTGAATT CAGCgtagag 50
aactcgcgct gacgaatata gtaatctgtg atgccaatcc cgagcggcgt 100
taaacggtaa atggcggtgc cttcagcctg ctcgctggta aagcggttca 150
gcagacgttg acgcaccatg tcgttgatcg cgttgttggc gcggacgccg 200
atggtttcgc tggtttgctc aaacgcatca ctcacatggc ggaacgcac 250
gaattcagat ctcccgggtc accg
```

Genomic chr11 (reverse strand):

```
tttggagcca aacagaggaa actaaggaaa cttgtctctg tggggttggc 121068096
ttccctagag aaaggtgata ttgtggcaa agaatacta gggtagggag 121068046
CCGGGAGATC TGAATTCAGC tcttggttgg accacagtct ctatgataat 121067996
gtccctgaag cacagtttcc tcattctataa aactaaagag tagaaaagag 121067946
tctctagggt ctcttctctg
```

Side by Side Alignment

```
000000025 ccgggagatctgaattcagc 000000044
<<<<<<<< |||||< <<<<<<<<
121068045 ccgggagatctgaattcagc 121068026
```

Alignment of YourSeq and chr6_random:936738-936766

Clone 66 YourSeq

```
cggtgaccg ggagatctga attccTGCAG CAGGCTTCCT GTCTCACTTC 50
gtagagaact accatgaagg ctggctgcac attgactgct ccgcaacgta 100
ccgtaaagcg gcggttgagc agtgggtctgc gggcgcgacc ggtctgggcg 150
tacgtaccgt tgcgaacctg ctgacggctg agtaatcgtc attgccctcg 200
aattcagatc tcccgggtca ccg
```

Genomic chr6_random (reverse strand):

```
aaaattaatt gaggggctgt gattctctgt ttttataatt caaattagtc 936817
ttttgtccat tcgacctaga agttttctcc ttatataaat taagtaggaa 936767
TGCAGCAGGC TTCCTGTcaa ttCACTTCt aggaacacca ttattaatta 936717
gccaatgcca gagctctaca tgagtcagac tattctgatt gcagctttcc 936667
ctctgctggc cattacagta gtagctgtg
```

Side by Side Alignment

```
000026 tgcagcaggcttcctgtc...tcacttc 000050
<<<<<< ||||| ||||| ||||| ||||| <<<<<<
936766 tgcagcaggcttcctgtcaatttcacttc 936738
```

Alignment of YourSeq and chr7:10534236-10534257

Clone 67 YourSeq

```
cggTACCcG GGAGATCTGA ATTCTGatcg tgacccgcaa cggccatcac 50
cgcacctgta ccgtattcca tcagcacgaa gtttgccacc cagacaggga 100
tcgtttcgcc tgtcagcggg tgtttgcat agaagcctgt tgcaacgcct 150
tttttctcca tcgttgccat atcggcttcg gccactttgg tgctgcggca 200
ttcgtcgatg aaggaggcca gttccggatt gttctcggct gctttctgcg 250
ccagcgggtg acctgcggcc acggccagggt agggaattca gatctcccgg 300
gtcaccg
```

Genomic chr7 (reverse strand):

```
cactcatctg ggctacctgg attccccata actaccagga ggagaggcca 10534308
agtctgctgg tccacagaga ctgcagccac cttccccct aggggctcag 10534258
GACCAggGAG ATCTGAATTC TGtccctgag cctctggctg tcgttagcct 10534208
cttccctgta gagatcctgc agggaagccc caccactga tgggtgatgg 10534158
acaagggtta gacctgaaga gg
```

Side by Side Alignment

```
00000005 gacccgggagatctgaattctg 00000026
<<<<<<< |||| |||||<
10534257 gaccagggagatctgaattctg 10534236
```


gcggccgcgtc	tagcccgcg	tgacccgga	gatctgAATT	CCTTTAGGAC	50
ATgaaatatg	gcgaggacaa	cggaaaaag	tggaaaaTTT	AGAAATGTC	100
ACTgtaggac	atggaatatg	gtaagaaaac	tgaaaatcac	ggaaaatgag	150
aaatatccaa	tgtatgactt	gaaaaatgac	gaaatcactg	cgaattcaga	200
tctccgggt	caccg				

aaagatcct	gtgaattagt	gagaatatat	acacatgaaa	atttttagta	162080095
ataatttggg	tgacatatgg	ttaaaagcca	gaataaattg	gcagataaca	162080145
AATTCCTTTA	GGACATtggt	caatcaaatc	agaatcccag	ggcatgcctg	162080195
ttaaaacaca	gattttctatg	tcccacacct	agagttttctg	attttgtaag	162080245
tctagggtgt	gtgcagcttg	ataattttgga	tttctataata	gttttcagct	162080295
gggtgcttatg	ctgctgatatc	gtccttttct	ccagttctctc	acagtgtatac	162080345
aaattgagaa	ctgctcctgt	aggagaccag	agactagaga	ggtctgcagt	162080395
atgattgccg	tgtgttgaga	tgatgcttcc	tttcatcatt	cacctgctgc	162080445
agttaccact	gttttctctt	tctggccctc	attttatgac	aacagctggg	162080495
agcactcTTT	AAATGTCCA	CTctgtgaaa	aagtgtctacc	tggtagcact	162080545
cttgatgtca	taagcagaga	gcatgccctt	ttctataatt	aggtaattct	162080595
ctacagagag	aggaatttat	ac			

```
000000037 aattcctttaggacat 000000052
>>>>>>> |||||>>>>>>>
162080146 aattcctttaggacat 162080161
```

```
000000088 tttagaaatgtccact 000000103
>>>>>>> |||| ||||| ||||| >>>>>>>
162080503 ttta.aaatgtccact 162080517
```

cgggtgacccg	ggagatctga	attccgagcc	gatgatgcgg	cccagcaccg	50
acgacaacag	gatgattggc	aggatgcctt	tcagtcgcga	ccaggcgccc	100
aggcgctgcca	gcagcttgaa	atcgccGTGG	CCCATGCCTT	CCTTGCCggt	150
cagctgccttg	aacagccacc	agaccgtcca	cagcgacagg	tagcccaccg	200
ccgcgcctac	gaattcagat	ctcccggttc	acag		

atggtatttta	ttaacttgca	catcgttatg	ctttagcacc	tctcactactg	100335612
gtgctccagt	gaggggaggg	tttagtgttt	tattaatgcc	tcattcattt	100335562
TGGCCCATG	CTTCCCTTG	Cctcactgct	gttacgttat	attttgtcac	100335512
tgaatattca	tttgcccttag	cctgcaggtt	tatagaatct	gctattttaaa	100335462
aggcctcttt	cgtcatcaaa	a			

```
000000127 gtggcccatgccttccttgcc 000000147
<<<<<<<< |||||< <<<<<<<<
100335561 gtggcccatgccttccttgcc 100335541
```

Alignment of YourSeq and chr17:71582696-71582719

Clone 71 YourSeq

```
cggtgaccgc ggagatctga attcgtggc gaaggcatac agcatccact 50
gcacgtactc ggattcactc acccggccgt cgccatcgct gtcgatccgc 100
tgcaggtagc tgggtgtatc ggtgacctgg gccagCGCCG CaccgGCAG 150
CAGCACCGCC AGCAgaactc cgtaccctgg cctcacgcgc ccaccaggct 200
gtagcccttc agccgtgcgg cgtaggcctg caacgccgcg ataccgcttt 250
cctcggaat tcagatctcc cgggtcaccg
```

Genomic chr17 (reverse strand):

```
gtgtagatgg tggcctggaa gggcacgcag cacaggatga aacacaggtc 71582770
ggccacgccc aggttaagga tgaacagggt ggtagtgtg accgcctggc 71582720
CGCCGCGCAG CAGCACCGCC AGCAccagcg tggtgcccac ggtgcccacg 71582670
aggaagatga gcgcgaagag caggggcacg atgaccgcct cggggtgcca 71582620
gcctccccgc ccgccgcct ggct
```

Side by Side Alignment

```
00000136 cgccgcacccggcagcagcaccgccagca 00000164
<<<<<<<< ||||| ||||| <<<<<<<<
71582719 cgccgc.....gcagcagcaccgccagca 71582696
```

Alignment of YourSeq and chr6:163940565-163940587

Clone 72 YourSeq

```
gcggccgctc tagcccgcgg tgacccggga gatctgaatt ctccagcatt 50
tcttgccctcg ccgcgctaag cgccACAGAA GCAGTGGCCG TagttccTCC 100
ATCggatacc attaatctcg ccgcatcaat accttctttc tcatagacac 150
ttttcatgtc cattactttt actttatagt cttcaaaggc gcggatgggt 200
tttttaatta attcaccatc atgttgggtc gaaatcagat ttgactggta 250
ttcatttaat gaattcagat ctcccgggtc accg
```

Genomic chr6 (reverse strand):

```
tttctacaag gatggattcc cctccttttt tttcttagca agacgtcatt 163940638
tggaaggtt ttgagcaatg ggcacgtct tatcacctgc tgtttgggt 163940588
ACAGAAGCAG TGGCCGTTC ATCtgggtcg gccccaaat ctctatactc 163940538
cctttgtcc actccacctc ttcctactca ccaggccatt cttttctgag 163940488
ctccctcttt cttttaatat ctt
```

Side by Side Alignment

```
000000075 acagaagcagtggccgtagttcctccatc 000000103
<<<<<<<< ||||| ||||| ||||| <<<<<<<<
163940587 acagaagcagtggccgt.....tccatc 163940565
```

Alignment of YourSeq and chr9:86226366-86226670

Clone 73 YourSeq

cggtgacccg ggagatctga attcggatcg gcaggatgta gtACGGGTCC 50
TGTGagaca ggtcatggat ccacagtgcg aacggcgcgt ggcgcagctc 100
aacgGAACCC ATCAGATGAT ctgcccgaag gaagccat

Genomic chr9 (reverse strand):

ccagttgctc ctatagataa catcactatt gtagaaccta cgattggtct 86226721
tttgagatat tttcagactg acccaacctg gattcatgat tcatgactca 86226671
ACGGGTCCTG Tcgtacccac ccccaacca cccaaggca acctcagtgc 86226621
acaagggcca ttttccacac ccctatgatt gcattcccca gccaatcagc 86226571
agcaccatt ccctagtccc atgccacca aatcatccct gaaaaatcct 86226521
aactttcaat ccttcaggga gactgatttg agtgataatg ccagttttcc 86226471
acatggtaaa cttcaatgta aattaatctc tttttactt cactaccaca 86226421
gtctcagtga attggttttg tctgtgcacc tgtcaggacG AACCCTCAG 86226371
ATGATtataa gagttgagca catctgggaa attcaaatca acttcctcag 86226321
tccaaagaac agtgggaaca cacagtcagg catggggatc acttcccaca 86226271
agaat

Side by Side Alignment

00000043 acgggtcctgtg 00000054
<<<<<<< |||||<<<<<<< <<<<<<<
86226670 acgggtcctgtg 86226659

00000105 gaaccatcagatgat 00000120
<<<<<<< |||||<<<<<<< <<<<<<<
86226381 gaaccatcagatgat 86226366

Alignment of YourSeq and chr9:22969261-22969299

Clone 74 YourSeq

```
cggtgaccgc ggagatctga attctcttga ggtaaacgta tgtcttacc 50
gttcctgtct ccatttcgat agtaaaatcg gggaaatcta atttttcgga 100
cacatctaac ccttgctcca ttggaacagt acgcaaatta tcaaggattt 150
tgctttccga tatagttagc ctattgcctt cgccaatgat thtagcactg 200
tcatcATGTT GAAAGAATTC AGATCTCCg ggtcaccg
```

Genomic chr9 :

```
gaaaatgact gatttcaggg atgggcaggg aaagtgtgag atgtacctgg 22969210
aaattatttt ggtgccagaa agagaggaga tgctcaaac tgattaaaat 22969260
ATGTTGAAAG AATTCAgag acaataggaa aaATCTCCa ggtgacacat 22969310
atgggacaac ttgagcacia tttaaaaaat gagggcaacg gattaaaccc 22969360
atagactaag ataaacatct atgtcttcct aataataaa
```

Side by Side Alignment

```
00000206 atgttgaaagaattcag 00000222
>>>>>>> |||||>>>>>>>
22969261 atgttgaaagaattcag 22969277
```

```
00000223 atctccc 00000229
>>>>>>> |||||>>>>>>>
22969293 atctccc 22969299
```

Alignment of YourSeq and chr1:243752902-243752933

Clone 75 YourSeq

```
cggtgaccg ggagatctga attcgggtct gttcattgca gcgcacccgg 50
atccagccca tgctaaatgc gacggtccat ccgcgctgcc gctggcgaaa 100
ctgGAACAGT TCCTGACGCA GATTAAGcc attgatgACC TGGTgaaaag 150
cttcgacgag ctggatactg aaaactaaga gcgttcaaca ggccggggga 200
tattcctccg gaattcagat ctcccgggtc accg
```

Genomic chr1 (reverse strand):

```
ttccttaact ttcctgtgcc acagtttccc cagctgtaaa acaggatggt 243752984
aagagtagct agcctcatgg aattgttgca aagttcaaat aagattatca 243752934
GAACAGTTCC TGACGCAGAg TAAACACCTG GTaggtgttt gctccatta 243752884
ttgttaaaat aaaacattaa tatgaaaact atacctaag tgtctccgtt 243752834
tagacatttt ttcttagcag ctcttagaa ta
```

Side by Side Alignment

```
000000104 gaacagttcctgacgcagattaaa 000000127
<<<<<<<< ||||| <<<<<<<<
243752933 gaacagttcctgacgcagagtaaa 243752910
```

```
000000138 acctggt 000000144
<<<<<<<< ||||| <<<<<<<<
243752908 acctggt 243752902
```

Alignment of YourSeq and chr3:72579076-72579098

Clone 76 YourSeq

```
gcggccgctc tagcccgcg tgacccggga gatctgaatt cggacatgtg 50
ccggaggatg aggggatgat cgaggcggcg atcgccaaag atccggcgcg 100
cttcccgtg atggcgattt gcgcccgaag cggcaagccc gcgcgatctc 150
gctatcgtgt cgttgagcgc ttttatcag CGGGGGAAG CGGGGTGGCG 200
atgccgttaa cgcgcgtcgc gctgacgcca gagaccgggc gcacccatca 250
gctgcgcatt cactgccagc tgatggggca tgctatgaat tcagatctcc 300
cgggtcaccg
```

Genomic chr3 :

```
cgccgagtga ctgacgaggg gcggggcctg gcgccgcgcg tcacgcgccg 72579025
tgccggccaat gggagggcgg cggccggcgc cgcgagggcg gaggcggggc 72579075
CGGGGGAAG GCGGGGcgTG GCGgacgtgg gccgggcggt cggtgtgcgt 72579125
gcccgggagt gtgtgcgcgc tgggggcgcg cgtgcctgtc ggtggccccg 72579175
cggcccgcg cgccggaagc tgc
```

Side by Side Alignment

```
00000180 gcgggggaaggcgggg..tggcg 00000200
>>>>>>> |||||||||||||||| |||| >>>>>>>
72579076 gcgggggaaggcggggcgtggcg 72579098
```


Alignment of YourSeq and chr15:23784105-23784506

Clone 78 YourSeq

```
gcggccgctc tagcccgcg tgacccggga gatctgaatt cagtttcaat 50
gacgatgagt tgaattctt aaagcgaaga cattcttcaa aaagagcgct 100
cgatgttggtg aatacatgta aatcgtagg ttataataat atcagtatcg 150
acctgatgta tgGTCTTCCC AACCAGACTA TGGATATTTG gcaacgtaat 200
ttAGATAAG CCATTTCTct agatagaatt cagatctccc gggtcaccg
```

Genomic chr15 :

```
ctgcaggga attcagcttc cagagtttct gtcactgaag tgcagcatgg 23784054
ccactcagc catcgaactc ctacctgttt gtttcatttg cattcgcttt 23784104
GTCTTCCCA CCAGACTgaa aggtcagcca cacacacca gtcctccca 23784154
ccaaccctc ctggggccca cccaaagct gagtgtgctt cagttcagta 23784204
catgcagttt ggcataagcA TGGATATTTG cagaatggta tgctcaaacg 23784254
tccttgaac atcccagtg gaaagggtgtg tgctcccttc actcattaaa 23784304
gtgatacgta atgcttgagg acctagctta gacatgggtcc tgtttgtgaa 23784354
agaaatagac attttgtgat ataattatca aaacacaaca ttcgggggcta 23784404
gaagtggctt tcaaaatcat ttaaacgaat tttgtaattt cacagataag 23784454
ttcacagtta gctcatggta tttggatata ttacAGATAA tgtGCCATT 23784504
CTaacagctg ggcattctggg cagccaaacc tgacaacttt ttgcagtgac 23784554
cacataaacc agtctgctgg ccagtggcct acccatgtcc atggagccca 23784604
gg
```

Side by Side Alignment

```
00000163 gtcttcccaaccagact 00000179
>>>>>>> |||||>>>>>>>
23784105 gtcttcccaaccagact 23784121
```

```
00000180 atggatatttg 00000190
>>>>>>> |||||>>>>>>>
23784224 atggatatttg 23784234
```

```
00000203 agataa 00000208
>>>>>>> |||||>>>>>>>
23784489 agataa 23784494
```

```
00000210 gccatttct 00000218
>>>>>>> |||||>>>>>>>
23784498 gccatttct 23784506
```

Alignment of YourSeq and chr6_random:936738-936766

Clone 79 YourSeq

```
cggtgaccg ggagatctga attccTGCAG CAGGCTTCCT GTCTCACTTC 50
gtagagaact accatgaagg ctggctgcac attgactgct ccgcaacgta 100
ccgtaaagcg gcggttgagc agtggctctgc gggcgcgacc ggtctgggcg 150
tacgtaccgt tgcgaacctg ctgacggctg agtaatcgtc attgccctcg 200
aattcagatc tcccgggtca ccg
```

Genomic chr6_random (reverse strand):

```
aaaattaatt gaggggctgt gattctctgt ttttataatt caaattagtc 936817
ttttgtccat tcgacctaga agttttctcc ttatataaat taagtaggaa 936767
TGCAGCAGGC TTCCTGTcaa ttCACTTCt aggaacacca ttattaatta 936717
gccaatgcca gagctctaca tgagtcagac tattctgatt gcagctttcc 936667
ctctgctggc cattacagta gtagctgtg
```

Side by Side Alignment

```
000026 tgcagcaggcttcctgtc...tcacttc 000050
<<<<<< |||||  |||||  <<<<<<
936766 tgcagcaggcttcctgtcaatttcacttc 936738
```

Alignment of YourSeq and chr13:83330613-83330637

Clone 80 YourSeq

```
cggtgaccgc ggagatctga attcaccgtc tttgggtgcac gttcaaacgc 50
cgcggaatc gcctgatgca attcattctg ggcgataggt ttatgcaggt 100
agttctggat cccgatccgC TTCAGcaTaT TGATATCAAA ATGTCGgctc 150
atggagctca gcatgatgat gtggctctca gcaacctgcg gcagaattca 200
gatctcccg gtcaccg
```

Genomic chr13 :

```
gcttctgtgt catctggatg atttcttcta taacaataat tttattcaaa 83330562
atattctgta attcctaaat ctatatTTTT aattcaagcc tctcccctgc 83330612
CTTCAGTcTT GATATCAAAA TGTCGatagt attccaagaa gatttatcac 83330662
ttagcatgca taaaaaatgga ctcatcttca cccacaaacc agtgatecat 83330712
ttggtatttt ttgtccaaat tggtg
```

Side by Side Alignment

```
00000120 cttcagcatattgatatcaaaatgtcg 00000146
>>>>>>> ||||| | |||||>>>>>>>
83330613 cttcag..tcttgatatcaaaatgtcg 83330637
```

Alignment of YourSeq and chr1:243752902-243752933

Clone 81 YourSeq

```
cggccgctct agcccgcggt gaccggggag atctgaattc gggctctgttc 50
attgaagcgc acccggatcc agcccatgct aaatgcgacg gtccatccgc 100
gctgccgctg gcgaaactgG AACAGTTCCT GACGCAGAT AAAgccattg 150
atgACCTGGT gaaaagcttc gacgagctgg atactgaaaa ctaagagcgt 200
tcaacaggcc gggggatatt cctccggaat tcagatctcc cgggtcaccg 250
```

Genomic chr1 (reverse strand):

```
ttccttaact ttcctgtgcc acagtttccc cagctgtaaa acaggatggt 243752984
aagagtagct agcctcatgg aattgttgca aagttcaaat aagattatca 243752934
GAACAGTTCC TGACGCAGAG TAAACACCTG GTaggtgttt gctccatta 243752884
ttgttaaaat aaaacattaa tatgaaaact atatcctaag tgtctccgtt 243752834
tagacatttt ttcttagcag cttcttagaa ta
```

Side by Side Alignment

```
000000120 gaacagttcctgacgcagattaaa 000000143
<<<<<<<< ||||| <<<<<<<<
243752933 gaacagttcctgacgcagagtaaa 243752910
```

```
000000154 acctggt 000000160
<<<<<<<< ||||| <<<<<<<<
243752908 acctggt 243752902
```

Alignment of YourSeq and chr22:19678441-19678482

Clone 82 YourSeq

```
cggtgaccgc ggagatctga attctggaag gcggcctggc cgcGCTGCTG 50
GccgaaccGG GCCCGGCaCT GCTGCACGTG GCCATCgatg cacgcgccaa 100
cgtgtggccg ctggtgccgc cgaacaccgc caacagcacg atgctggaaa 150
gcaaccccg ccatgccgc caggagacc ccaatgcaat accggcttga 200
cctggtgctg gaattcagat ctcccgggtc accg
```

Genomic chr22 :

```
cagccatgcc tgggtgtccac tgggggtgtcc ttgagctccc ttctccccac 19678390
agaagctgga gcaggaggcc gccccagttc ccaggaggc ccccggcgtg 19678440
GCTGCTGStg GGGCCCGGCc gcccTGCTG CACGTGGCCA TCcgggaggc 19678490
cgaggcccg cccttcgagg tgctcatgca gttcctctac accgacaaga 19678540
tcaaatacc acggaagggt ccgcctgggt gggggtggag ca
```

Side by Side Alignment

```
00000044 gctgctgg 00000051
>>>>>>> ||||| >>>>>>>
19678441 gctgctgg 19678448
```

```
00000059 gggcccggc 00000067
>>>>>>> ||||| >>>>>>>
19678451 gggcccggc 19678459
```

```
00000069 ctgctgcacgtggccatc 00000086
>>>>>>> ||||| >>>>>>>
19678465 ctgctgcacgtggccatc 19678482
```

Alignment of YourSeq and chr1:112991110-112991132

Clone 83 YourSeq

```
cggtgaccg ggagATCTGA ATTCGTCTTT CACAAAtcc aggttgtcca 50
gatcaaaacg gtgcatcacg tagaagtagc cgtttttcgc catccactcg 100
cagatccgct catccaccac cgtcttcacg ttggcgggca cgaccggcag 150
gcgaaaacgc cgtccgcca gctccacgcc ggcacgcac tccgatcgga 200
attcagatct cccgggtcac cg
```

Genomic chr1 (reverse strand):

```
actgtttagg agtcttcaaa ttttcttttc ataaagcacc ccaaagctgt 112991183
tactatcaat ataggtacat tctgatttgg gaatatacgt gttttgataa 112991133
ATCTGAATTC GTCTTTCAAA AACaggataa tagtttttga ccaatacat 112991083
tacattcaca aaaagagaaa gctatgatct tgattatgaa catttaagca 112991033
aaactaaata aaatattagc aaa
```

Side by Side Alignment

```
000000015 atctgaattcgtctttcaciaaac 000000037
<<<<<<<< |||||  <<<<<<<<
112991132 atctgaattcgtctttcaaaaac 112991110
```

gcggccgcctc	tagccgcgcg	tgacccgga	gatctgaaTT	CTTCCTGAAC	50
CCTGccgact	gccatgacgc	cgctaccga	tccGCTGATC	TCCCTttcgc	100
actattacct	gccggtctac	aagcccccgc	agtggtgact	ggagcgaggc	150
cagggcgccc	gcgtgtggga	cagccagggc	cgtgagttca	tcgacctggc	200
cgccggcatc	gccgaattc	agatctccc	ggtcacgcg	ggc	

cgggtgccc	gagcaaggcc	atagtgcctc	tggctctgg	ggacctagg	1185287
cacatccctac	caccagggtg	tggcctggtg	acctccctgc	ccccaggggc	1185237
TTCTTCTGA	ACCCTG tga	ctggagccag	cctgccaggg	cccctcccg	1185187
caggacgtgg	atctcagtt	tctactaaat	tctgaacat	cctttcgtgg	1185137
gagggtagaa	gcttgagagc	catcgaccgg	ggacatcagc	ttggggggccc	1185087
ttccctggga	ccctcgtgcc	agccccgcc	caggcatctg	aggcctccag	1185037
ggtgggtgtg	ggtcgcaggca	gcctgagccc	ccggggcctg	caggggtggt	1184987
gcatcagg GC	TGATCTCCCT	ctgggtggga	cagtcagagg	agcagccccc	1184937
caaccctgcc	cgggtgggaa	tgagcctctg	gctcagccca	gccagagagg	1184887
agcagtggga	cgctggcctg				

```
0000039 ttcttcctgaaccctg 0000054
<<<<<< |||||<<<<<<
1185236 ttcttcctgaaccctg 1185221

0000084 gctgatctccct 0000095
<<<<<< |||||<<<<<<
1184978 gctgatctccct 1184967
```

Alignment of YourSeq and chr2:23362288-23362514

Clone 85 YourSeq

```
cggtgaccgc ggagatctga attccctccg tattaccgcg gctgctggca 50
cggagttagc cggtgcttct tctgcgggta acgtcaattg ctgtgggtat 100
taaccacaac accttcctcc ccgctgaaag tactttacaa cccgaaggcc 150
ttcttcatac acgcggcatg gctgcatcag gcttgcgccc attgtgcaat 200
attccccact gctgcctccc gtaggagtct ggaccgtgtc tcagttCCAG 250
TGTGGCTGGT CATCctctca gaccaGCTAG GGATCctcgc ctaggtgagc 300
cgttacccca cctactagct aatcccatct gggcacatct gatggcaaga 350
ggcccgaagg tccccctctt tggctcttgcg acattatgcg gtattagcta 400
ccgtttccag tagttatcga attcagatct cccgggtcac cg
```

Genomic chr2 :

```
ttgaaaatcg aagttactta ggaagctaga aaatggaaat gaccagaacc 23362237
tggttttgag aaaggatgga aaggtacaat caccaaagct aaggtggttg 23362287
CCAGTGTGGC TGGTCATCC tgccagctgt ggctggaaat tgagactttc 23362337
tagaaccatc attaaactcc aggggccgat gagcggatga ctaggtccta 23362387
attggacagt gactgctggc cacacctcat aatctcagga ttatgcctct 23362437
ctctagacaa gaattcgag tgtactgcat gagcctcctc ctttattaga 23362487
ttgtcaattc cttagGCTA GGGATCgaga tggattcttc tctttgtctc 23362537
ctcagttccc tgcagaagcc tttaccaagg atcaaagctc aggaaatgtt 23362587
ataggtagat taccacgtct gcttcat
```

Side by Side Alignment

```
00000247 ccagtgtggctggatcatcc 00000265
>>>>>>> |||||>>>>>>>
23362288 ccagtgtggctggatcatcc 23362306
```

```
00000276 gctagggatcg 00000286
>>>>>>> |||||>>>>>>>
23362504 gctagggatcg 23362514
```

Alignment of YourSeq and chr7:10534236-10534257

Clone 86 YourSeq

```
cggtGACCcG GGAGATCTGA ATTCTGatcg tgacccgga cggccatcac 50
cgcacctgta ccgtattcca tcagcacgaa gtttgccacc cagacaggga 100
tcgtttcgcc tgtcagcggg tgtttgcat agaagcctgt tgcaacgcct 150
tttttctcca tcgttgccat atcggcttcg gccacttttg tgctgcggca 200
ttcgtcgatg aaggaggcca gttccggatt gttctcggct gctttctgcg 250
ccagcgggtg acctgcggcc acggccagggt agggaattca gatctcccgg 300
gtcaccg
```

Genomic chr7 (reverse strand):

```
cactcatctg ggctacctgg attccccata actaccagga ggagaggcca 10534308
agtctgctgg tccacagaga ctgcagccac ctttcccct aggggctcag 10534258
GACCAGGGAG ATCTGAATTC TGtccctgag cctctggctg tcgttagcct 10534208
cttccctgta gagatcctgc agggaagccc caccactga tgggtgatgg 10534158
acaagggtta gacctgaaga gg
```

Side by Side Alignment

```
00000005 gacccgggagatctgaattctg 00000026
<<<<<<< |||| |||||<
10534257 gaccagggagatctgaattctg 10534236
```

gcggccgctc	tagccccggt	gacccgggag	aTCTGAATTC	ACTTGCCCCT	50
Tgttgcgcac	agggatgtcg	gtcgtatctg	ctgcttgcaa	ctcagcccct	100
cgcgctcgaa	aacgcctgca	tccgagtgtt	gcggcctgag	cttcaatgag	150
attgtcctga	cgacgaattc	agatctccc	ggtcaccg		

tcgccccctc	cactccctcg	tacttttctt	cgttctcttt	gggtcaagct	218492490
gtttgattcag	tcagtcccag	tgcaagaacc	tgggtatctc	agttgaaggt	218492440
CTGTGAATCA	CTTGCCCCCT	ttcatttctc	tccataagct	ccacagacca	218492390
cagctgcttc	taatcggtcc	tttcagggtc	gagacttctt	tcagactttc	218492340
tgtgctcagt	caacacacac				

```
000000032 tctgaattcacttgcccctt 000000051  
<<<<<<<< |||||<<<<<<<<  
218492439 tctgaattcacttgcccctt 218492420
```

Alignment of YourSeq and chr12:39485907-39486021

Clone 88 YourSeq

```
cggtgaccgc GGAGATCTGA ATTctgggtg tagattatac agatcttatt 50
tctacataca aaactcttgc tatacaGTT GCTGTTGCTT GTgatccgct 100
ggctttgggt aaattaaaat ctccagctga aatgggtgca gatttgctg 150
ttggtacatc tcagcgtttt ggtgttccta tgggatacgg aggtcctcat 200
gcagctttct ttacttgtaa agaggattat aagagagata ttccgggaag 250
aattattggg gtttctcagg atatgtatgg taagcctgca ttaagaatgg 300
ctttacaac aagagagcag catattaagc gtgaaagagc gacatctaac 350
atttgtacag gaattcagat ctcccgggtc accg
```

Genomic chr12 :

```
gaatgctaaa catttgttat ggaacagtag aggctgaggt caatgggtatt 39485856
tataacctgaa aatgagcagt ccccttctat tgggttgta gtgtgtggaa 39485906
GGAGATCTGA ATTtttagtt ttttcttacc ctggctatct tcaatgggac 39485956
acaggcttca aatttctcta gcgtggcctg atgcttagag agaaggctgG 39486006
GTTGCTGTTG CTGTttggt ttctttccta ttttttaaata caatgttgta 39486056
atctgctccc agctctccgc tgactctatg tgccctttgc acagatgata 39486106
tctctctcca tgcttc
```

Side by Side Alignment

```
00000011 ggagatctgaatt 00000023
>>>>>>> |||||>>>>>>>
39485907 ggagatctgaatt 39485919
```

```
00000077 ggttgctgttgcttgt 00000092
>>>>>>> |||||>>>>>>>
39486006 ggttgctgttgcttgt 39486021
```

cggtgacccg	ggagatctga	attcaatgcg	gtttacctta	tcgtgtcGAA	50
CACGATGTCC	ACGTCGccc	cgccatgagc	acctacgacg	ccaccctgcc	100
ctaccgcgct	gacctgatgc	gctacggccg	caaccgcgcc	catgcgcaat	150
ggccccggcg	gcgccgcatic	gcggtgcatt	tcgtgtctta	ttacaaggag	200
aattaagatc	tcccggttca				

actgcaaattg	ttccaccacg	tgaaccttc	cgtggccaac	tacctcgag	20568793
gtttctctca	ccccacactc	catatttttg	gctcctcact	tgactttgct	20568743
GAACACGATG	TCCACGTCCTC	tggaaggtag	tgtcttgcca	tccatgatgc	20568693
cacagctctt	gcacagcttg	gagaagttct	tgttgttcat	ttcagtgcca	20568643
ctgcttgatg	attctccaaa				

```
00000048 gaacacgatgtccacgtccg 00000067
<<<<<<< |||||<
20568742 gaacacgatgtccacgtccg 20568723
```

Alignment of YourSeq and chr5:8830497-8830517

Clone 90 YourSeq

```
cggtgaccg ggagatctga attccagcgc accgtatctt gacgatgcg 50
aaattgactt cgtcaccgat cagctgggtt ctcagctgac cctgaaagca 100
cccaacgcaa aaatgcgtaa agtgtctgac gatgccccgc tgatggagcg 150
cgttgagtac ctgctgcaat ccagatcAA CCCACAGCTG GCAGGTCAc 200
gcggccgtgt ctcactgatg gaaatcactg aagatggcct ggcgatccga 250
attcagatct cccgggtcac cg
```

Genomic chr5 :

```
aactgtgcat atatggagga agagaagttc attggaagga atggcaagaa 8830446
caagaacatt taggcaggat ggagctgggc atgatttaag acagaaagga 8830496
AACCCACAGC TGGCAGGTCA Caacaggtag tgggatgctt tcaaacaatc 8830546
aggtagacag gtgaggttgc atggctcctt taagactatg caaatgcaaa 8830596
gagtgctggc ttctgtagaa g
```

Side by Side Alignment

```
0000179 aaccacagctggcaggtcac 0000199
>>>>>> |||||>>>>>>
8830497 aaccacagctggcaggtcac 8830517
```

Alignment of YourSeq and chr7:20343309-20343346

Clone 91 YourSeq

```
ccgggagatc tgaattcggc cacaagagAA ATATAAAAAG TAATCCagcc 50
actaaatggt tgacctataa tgtgtcattc ttataagata tgctagaaca 100
aacatggcac agaatttctg ggagtagcca atcaatatct gatttgactt 150
aacaccagt caacaagtag gaaacaaTAC CTTGGGTATg gtaaggaaga 200
accagaaaca agaccagaa ttcagatctc ccgggtcacc g
```

Genomic chr7 :

```
caaagattaa aagctgagac ttagtactct ttaatcttat tttc aaaagt 20343258
ctgtcttgtt ttcaaacttt ctgtgacaat gatttctatt gttgataata 20343308
AAATATAAAA AGTAATCCta attcttTACC CTTGGTATca actttaaaat 20343358
tgattttaca attttcaaaa attgtaatta gattacaaaa actggaattt 20343408
gtagtcattt tcaactaaat acttcaaaaa ttacaaaa
```

Side by Side Alignment

```
00000029 aaatataaaaagtaatcc 00000046
>>>>>>> |||||>>>>>>>
20343309 aaatataaaaagtaatcc 20343326
```

```
00000178 tacccttggtat 00000189
>>>>>>> |||||>>>>>>>
20343335 tacccttggtat 20343346
```

cgccgcgtct	agccccgcggt	gacccgggag	atctgaaTTC	TTCCTGAACC	50
CTGccgcagt	ccatgacccg	cgctaccgat	ccGCTGATCT	CCCTTctcgca	100
ctattacctg	ccggtctaca	agccccgcca	ggttggtactg	gagcgaggcc	150
agggcgcccc	cgtgtgggac	agccagggcc	gtgagttcat	cgacctggcc	200
gccggcatcg	ccggaattca	gatctcccgg	gtcaccgcgg	gc	

cgggtgccc	gagcaaggcc	atagtgcctc	tggctctgg	ggacctagg	1185287
cacatccctac	caccagggtg	tggcctggtg	acctccctgc	ccccaggggc	1185237
TTCTTCTGA	ACCCTG tga	ctggagccag	cctgccaggg	cccctcccg	1185187
caggacgtgg	atctctagtt	tctactaaat	tctgaacat	cctttcgtgg	1185137
gagggtagaa	gcttgagagc	catcgaccgg	ggacatcagc	ttggggggccc	1185087
ttccctggga	ccctcgtgcc	agccccgcc	caggcatctg	aggcctccag	1185037
ggtgggtgct	ggcgcaggca	gcctgagccc	ccggggcctg	caggggtggt	1184987
gcatcagg GC	TGATCTCCCT	ctgggtggga	cagtcagagg	agcagccccc	1184937
caaccctgcc	cgggtgggaa	tgagcctctg	gctcagccca	gccagagagg	1184887
agcagtggga	cgctggcctg				

```
0000038 ttctttcctgaaccctg 0000053
<<<<<<< |||||< <<<<<<<
1185236 ttctttcctgaaccctg 1185221
```

```
0000083 gctgatctccct 0000094
<<<<<<< |||||< <<<<<<<
1184978 gctgatctccct 1184967
```

Alignment of YourSeq and chr1:112991110-112991132

Clone 93 YourSeq

```
gcggccgctc tagcccgcg tgacccggga gATCTGAATT CGTCTTTCAc 50
AAACtgcagg ttgtccagat caaaacgggtg catcacgtag aagtagccgt 100
ttttcgccat ccactcgag atccgctcat ccaccaccgt cttcatgttg 150
gcgggcacga ccggcaggcg aaaacgccgt ccgcccagct ccacgccggc 200
atcgcatcc gatcggaatt cagatctccc gggtcaccg
```

Genomic chr1 (reverse strand):

```
actgtttagg agtcttcaaa ttttcttttc ataaagcacc ccaaagctgt 112991183
tactatcaat ataggtacat tctgatttgg gaatatacgt gttttgataa 112991133
ATCTGAATTC GTCTTTCAaa AACaggataa tagtttttga ccaatacat 112991083
tacattcaca aaaagagaaa gctatgatct tgattatgaa catttaagca 112991033
aaactaaata aaatattagc aaa
```

Side by Side Alignment

```
000000032 atctgaattcgtctttcaciaaac 000000054
<<<<<<<< ||||| ||||| <<<<<<<<
112991132 atctgaattcgtctttcaaaaac 112991110
```

Alignment of YourSeq and chr10:70924803-70924826

Clone 94 YourSeq

```
gcggccgctc tagcccgcg tgaccggga gatctgaatt cggaagcaaa 50
gccatagcat cgctggtggg gttggccccg atgaaccgcg aaagtggcac 100
ctggcagggc caacggcgga tcagtgggtg gcgcgcagta gtacgcgaag 150
ccctttacat ggcggccctg acggccatcc ggtacgaGCC AGGACTGGAA 200
TTCAGaTCTC Ccgggtcacc g
```

Genomic chr10 (reverse strand):

```
cctctccaca ctctccacc atccagcctc ttgttttaca gatgaggagc 70924877
tcgagacttg gggagggagt gaggtcacag agcaggctgg gtgggggtctt 70924827
GCCAGGACTG GAATTCAGgt CTCtgacct ccctcatggg ctgttctcct 70924777
catcactgca gactcggtc cccctcggct agggctggga caatccctgc 70924727
cgggaggaac atggcaggcc gccc
```

Side by Side Alignment

```
00000188 gccaggactggaattcagatctcc 00000211
<<<<<<< ||||| <<<<<<<
70924826 gccaggactggaattcaggtctcc 70924803
```

Alignment of YourSeq and chr14:50668000-50668127

Clone 95 YourSeq

```
gcggccgctc tagcccgcg tgacccGGGA GATCTGAATT CTGgccagtt 50
caacccACAG GGTTCgtta accagacgca cctcaatcaa ctccagcgcg 100
tcattctaccg acagcggcgc aaccatcacc ctttgcgcg gaataatctg 150
cagcagcccc tcggttgaaa ggcgatgaat cgctgattg accggcgctg 200
ggcccatggt taaatcctcc atgaattcag atctcccggt tcaccg
```

Genomic chr14 (reverse strand):

```
atctggtctg cccagattcc tcagaactac caggaggagt ggtaagtct 50668178
gctagtctgc agagactgtg gccacccttc cccctagagg ctcaggccca 50668128
GGGAGATCTG AATTCTGtcc ctgagcctct ggctgggatt attggagatc 50668078
ctgcagggaa gccccacca ctaaggaagg atgggtcagg gttacgcctg 50668028
aagaggcttg tagtagagAC AGGGTTTcac catgttgcc aggctggtgt 50667978
aatactccta acctcaagtg ctctgccac ctcggactct gaaagtgctg 50667928
gattgcaggc attagccgc actcccag
```

Side by Side Alignment

```
00000027 gggagatctgaattctg 00000043
<<<<<<< |||||<<<<<<<
50668127 gggagatctgaattctg 50668111
```

```
00000057 acagggtttc 00000066
<<<<<<< |||||<<<<<<
50668009 acagggtttc 50668000
```

Alignment of YourSeq and chr6_random:936738-936766

Clone 96 YourSeq

```
cggtgaccg ggagatctga attccTGCAG CAGGCTTCCT GTCTCACTTC 50
gtagagaact accatgaagg ctggctgcac attgactgct ccgcaacgta 100
ccgtaaagcg gcggttgagc agtgggtctgc gggcgcgacc ggtctgggcg 150
tacgtaccgt tgcgaacctg ctgacggctg agtaatcgtc attgccctcg 200
aattcagatc tcccgggtca ccg
```

Genomic chr6_random (reverse strand):

```
aaaattaatt gaggggctgt gattctctgt ttttataatt caaattagtc 936817
ttttgtccat tcgacctaga agttttctcc ttatataaat taagtaggaa 936767
TGCAGCAGGC TTCCTGTcaa ttCACTTct aggaacacca ttattaatta 936717
gccaatgcca gagctctaca tgagtcagac tattctgatt gcagctttcc 936667
ctctgctggc cattacagta gtagctgtg
```

Side by Side Alignment

```
000026 tgcagcaggcttcctgtc...tcacttc 000050
<<<<<< |||||  |||||  <<<<<<
936766 tgcagcaggcttcctgtcaatttcacttc 936738
```

Alignment of YourSeq and chr1:32245826-32245851

Clone 97 YourSeq

```
cggccgctct agcccgcggt gaccggggag atctgaattc taacttgttg 50
acatgggtga tcgttccggc gatctcttga ttagtagtaa tcggtttgat 100
cgtcacggcc gcactttgat gcacttgagg atagtcatat tcagaagcct 150
tcgcctcgac tgttacttcg ttgctgacaa ttTTACAGC gggaaCTGGA 200
ATTCAGATCT CCcggtcac cg
```

Genomic chr1 (reverse strand):

```
ctgagtattt gggaagtggc caggtggagg gagggccagg gcatttaaatt 32245902
gttgggagtt cagcaaagct tggtcctgtg ccggtactcc ttcctccatg 32245852
TTACAGCtC TGAATTCAG ATCTCcaact caaacttctg aattccaaat 32245802
ccagaaagcc aattgcatcc ctgacatcct catctggatg tctcagaggc 32245752
tcctcaaact caacatgtcc ccagta
```

Side by Side Alignment

```
00000183 ttacagc 00000190
<<<<<<< ||||| <<<<<<<
32245851 ttacagc 32245844
```

```
00000196 ctggaattcagatctcc 00000212
<<<<<<< ||||| <<<<<<<
32245842 ctggaattcagatctcc 32245826
```

Alignment of YourSeq and chr16:24411988-24412236

Clone 98 YourSeq

```
cggccgctct agcccgcggt gaccgggag atctgaattC CTTGGCATCC 50
gtcgcaatga acTGAAGGTG GAGGAGATcc cacgggatga catcatacgg 100
gcagcggcat atttcagaga cagtccggaa aaagcacgaa agcgatttgg 150
tgaagaggga tggtagctca ataagggtga tgacgcgccg caggccgtaa 200
tggcgctcct gtgccacgga aaaaacctcg gctgggacaa atcgctaagg 250
gagggtgctgc acgtgtttta gaattcagat ctcccgggtc accg
```

Genomic chr16 :

```
cgggcttgag ccaccatgcc cagctattta tttatttttg tggagacagg 24411937
gtctcaccat ttigcctagg ctcatcttaa acggctcaag caatctccca 24411987
CTTGGCATC Ccaaagtgt gagattacag gcatgtcca ccacgccggc 24412037
ctctctttac ctttctaatt tggctagcag aaagtttaaa attacatgtg 24412087
tgggtcagat gacatttctc ttgggcagca cttccctgga caggcagtgt 24412137
atcccagaaa ggcagacctg ggctagccac agaatcttca accccatccc 24412187
caagacttga ggctgacaag aagtaaaaca aagTGAAGGT GGAGGAGATg 24412237
aaaaatggga tgcaaagaaa cagatgtgat atagtccatc tttctctctc 24412287
ttttttaaaa tatagactgg gtctcactgt gttgcccagg ctggtctca
```

Side by Side Alignment

```
00000040 ccttggcatcc 00000050
>>>>>>> |||||>>>>>>>
24411988 ccttggcatcc 24411998
```

```
00000063 tgaagggtgaggagat 00000078
>>>>>>> |||||>>>>>>>
24412221 tgaagggtgaggagat 24412236
```

Alignment of YourSeq and chr6:8509799-8509821

Clone 99 YourSeq

```
cggtgacccg ggagatctga attcccagag accgacgcga gagtctcacc 50
agaaagcccg aggagcttgg caagtttcgg ctcaaccttt gcaccaacgt 100
tcgatgctgg aagaagcccg ggtagccaag GCTTGCCtgc ctgatctaga 150
ACATGGGAGA TGTTCtgc gctgcactcc cacgaattca ggatctcccg 200
ggtcacag
```

Genomic chr6 :

```
tacatttttt gtttaatttt ctgtcttctc aatgaagaat gaatatctat 8509748
gtcatagact tttctttatt catggctgtc tttataacac ctaggatggg 8509798
GCTTGCCACA TGGGAGATGT TCTagtagtt ttgaatgaat aaataaatga 8509848
atgagctact ttttatatct ttttgatgct ttagtctttt tatatctatt 8509898
tgtatgactt tttaatatta acc
```

Side by Side Alignment

```
0000131 gcttgcc 0000137
>>>>>> ||||| >>>>>>
8509799 gcttgcc 8509805
```

```
0000151 acatgggagatgttct 0000166
>>>>>> ||||| >>>>>>
8509806 acatgggagatgttct 8509821
```

ATATTgAAAA	ATAaATCTGT	CCTTCCTCTT	TAGGGTAcT	AAATTAaaaa	50
GAaCaaaaATT	TcTCCCATaa	AACATTtTAC	TCATTtCAgA	CTGAGTAAAT	100
aATTcCCAAT	TTAAAGAAcC	ACTTAGACTT	ACCTAGGATA	CTGAAAAATAG	150
aaTTTGTTACT	CACAAaCCTA	TcAAATACAT	ATaAACGAAA	TACTACTTgC	200
AGTTAcAtgt	GTTAACATTc	TGAAACTTAA	CATAACGAAG	TGGAACAgTG	250
CCATCTTCTT	TAATATCATc	CTCTGTCAaT	TCCAGAGgTT	GAGTTGGTTC	300
ACTcTCTTTC	TGGCTCTTCA	AAATCCAAT	ATCGGGgggt	GTTGATAAAA	350
ATTTTTCAT	ATGTTAGGCC	CTGACCATA	CAATGGTAGA	ATAAAAATAA	400
ATGTTTAAAA	ACCaCAtATA	TACTATtCTC	CCTT		

gaataaagca	caaatatcct	cagttttagt	ataaagttgt	agaataaaact	52432402
tccagcAAAA	cttaccatat	acataataaaa	taactgacaa	aacccccacaa	52432452
ATATTCAAAA	ATcAACTCTG	CCTTCTCTTT	TAGGGTACaT	AAATTAaaaa	52432502
GAGGAAAAAT	TaTCCCATtA	AACATTTTAC	TCATTTCaAA	CTGAGTGAAT	52432552
AAaTaCCACT	TTAAAGAAtC	ACTTAGACTT	ACCTAGGATA	CTGAAAAATAG	52432602
tATTGTACT	CACAAAACTA	TtAAATACAT	ATgAACGAAA	TACTACTtAc	52432652
AGTTaACtTG	TTAACATTCT	GAAACTTAAC	ATAAACGAAT	GGAAcATGc	52432702
CATCTTCTTT	AATATCATCC	TCTGTcagTT	CCAGAGcTTG	AGTTGGTTCA	52432752
CtTCTTTCTG	CCTCTTCAAA	ATCCATAGAT	CGGGGtagGT	TGATAAAAAAT	52432802
TTTTACATAT	TTAGGGCCCT	GACCTATACA	ATGGTAGAAT	AAAATAAAAT	52432852
GTTTAAAAAC	CtCAaATATA	CTATaCTCCC	TtTaccacta	cactcacact	52432902
atacacagac	acacacaaat	caatacacat	atacttcaaa	taactccatt	52432952
attagaactt	gtacaaaagt	ctgagtattc	ag		

```

00000001  atattgaaaaataaatctgtccttctctttagggtacttaataaaaa 00000050
>>>>>>> ||||| >>>>>>>
52432453  atattcaaaaatcaatctgtccttctctttagggtacataaataaaaa 52432502
>>>>>>>
00000051  gaacaaaatttctccataaaacattttactcatttcagactgagtgaat 00000100
>>>>>>> ||| ||||| >>>>>>>
52432503  gaagaaaatttatccattaaacattttactcatttcaaactgagtgaat 52432552
>>>>>>>
00000101  aattccactttaagaaccacttagacttacctaggatactgaaaatag 00000150
>>>>>>> || | ||||| >>>>>>>
52432553  aaataccactttaagaatcacttagacttacctaggatactgaaaatag 52432602
>>>>>>>
00000151  aattgttactcacaacctatcaatacatataaacgaaatactacttgc 00000200
>>>>>>> ||||| ||||| >>>>>>>
52432603  tattgttactcacaacctattaatacatatgaacgaaatactacttac 52432652
>>>>>>>
00000201  agttaca 00000207
>>>>>>> ||||| >>>>>>>
52432653  aqttaca 52432659

```

```
00000210  tgttaacattctgaaacttaacataacgaagtggaacagtgccattctt 00000259
>>>>>>> ||||||||||||||||||||||||||||||||||||||| >>>>>>>
52432661  tgttaacattctgaaacttaacataacgaagtggaacaatgccattctt 52432710

00000260  ttaatatcatcctctgtcgaattccagaggttgagttggttcactctctt 00000309
>>>>>>> ||||||||||||||||||| ||||||| ||||||||||||| |||| >>>>>>>
52432711  ttaatatcatcctctgtcagttccagagcttgagttggttcact.tcttt 52432759

00000310  ctgcctcttcaaaatccatagatcggggggtgttgataaaaatttttaca 00000359
```

```
>>>>>>> ||||| ||||| >>>>>>>
52432760 ctgcctcttcaaaatccatagatcgggtaggttgataaaaattttaca 52432809

00000360 tatttagggccctgacctataacaatggtagaataaaaataaaatgtttaaa 00000409
>>>>>>> ||||| ||||| >>>>>>>
52432810 tatttagggccctgacctataacaatggtagaataaaaataaaatgtttaaa 52432859

00000410 aaccacatatatactattctccctt 00000434
>>>>>>> |||| || ||||| ||||| >>>>>>>
52432860 aacctcaaatactatactccctt 52432884
```
