

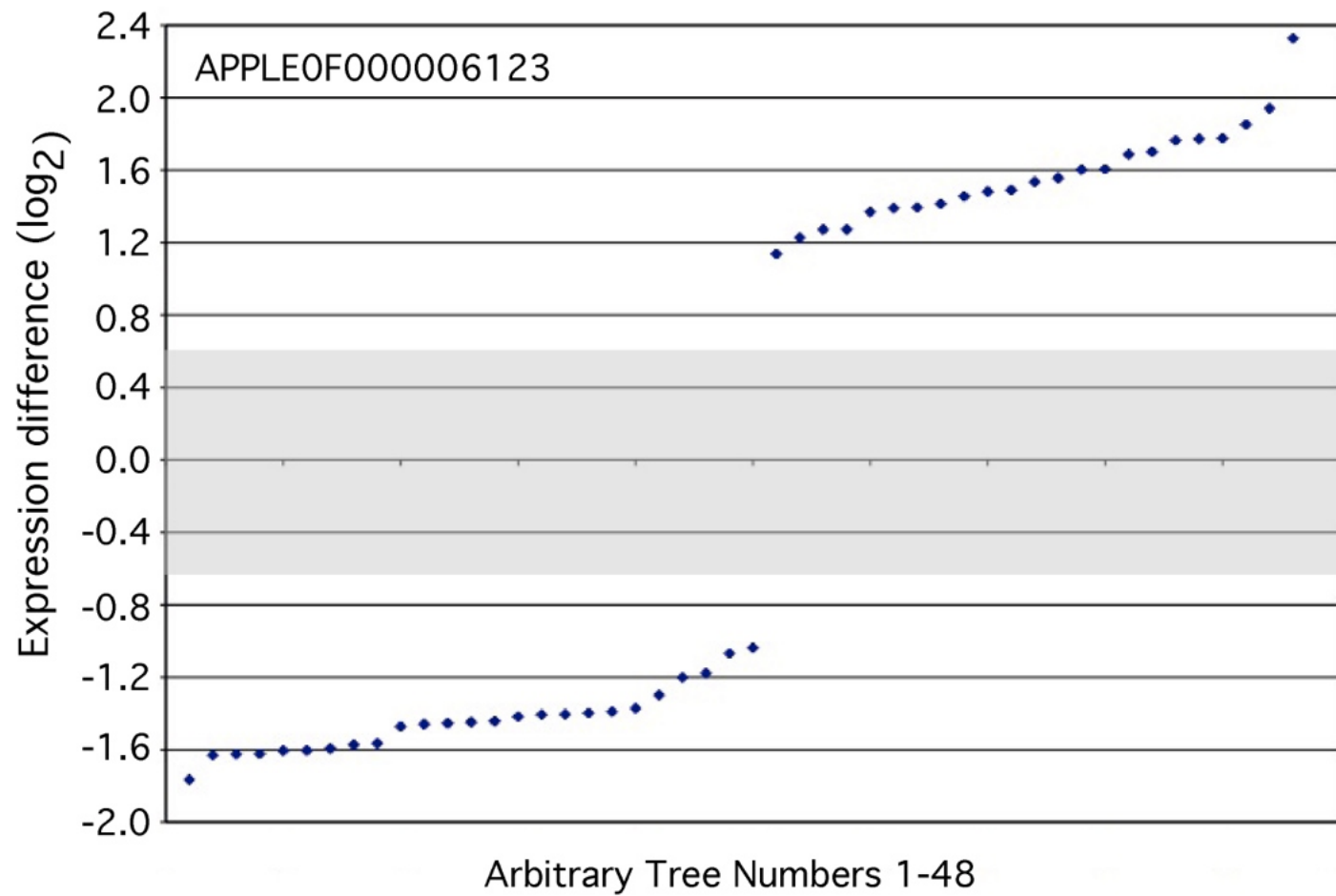


Figure S1
Jensen et al.
BMC Genomics

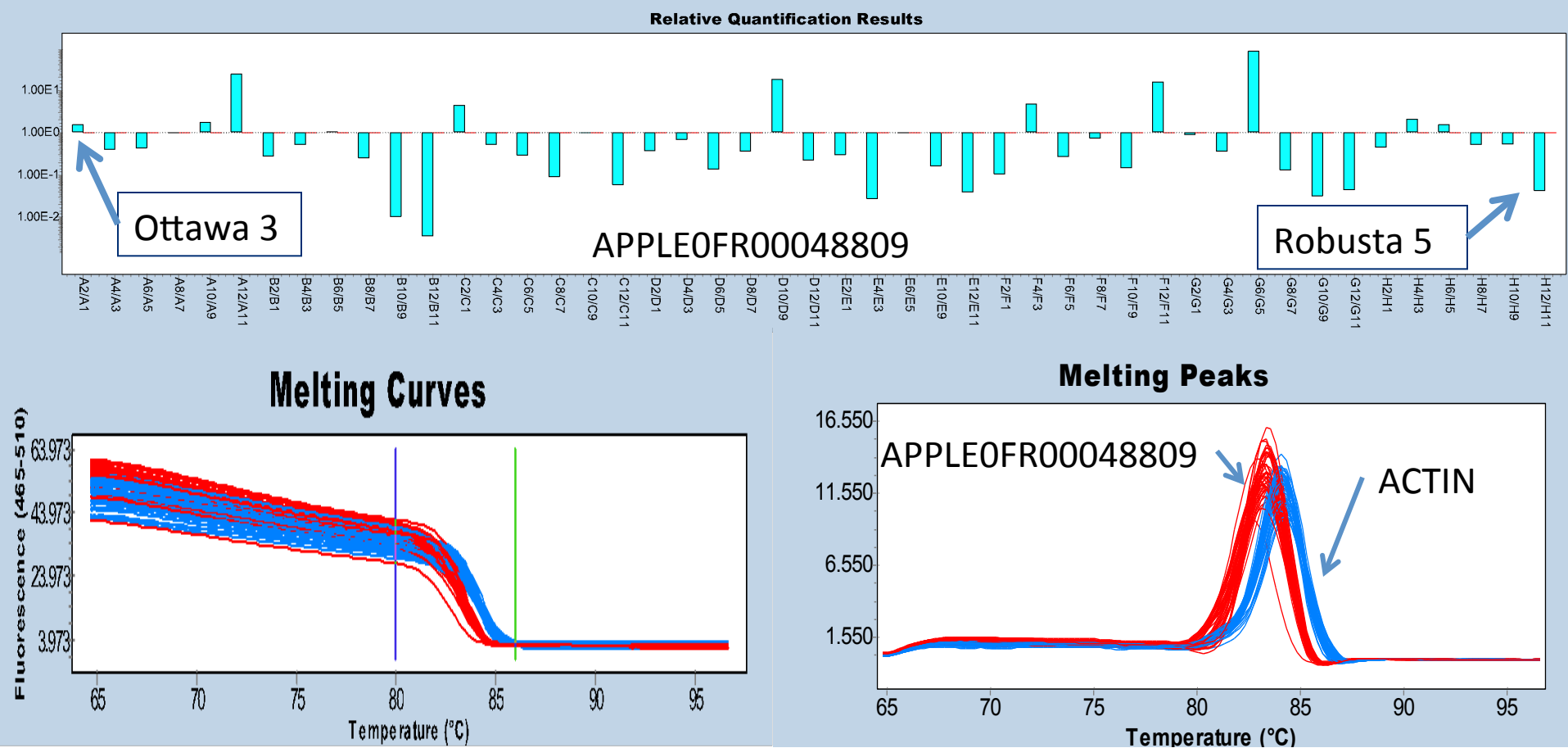


Figure S2.
Jensen et al.
BMC Genomics

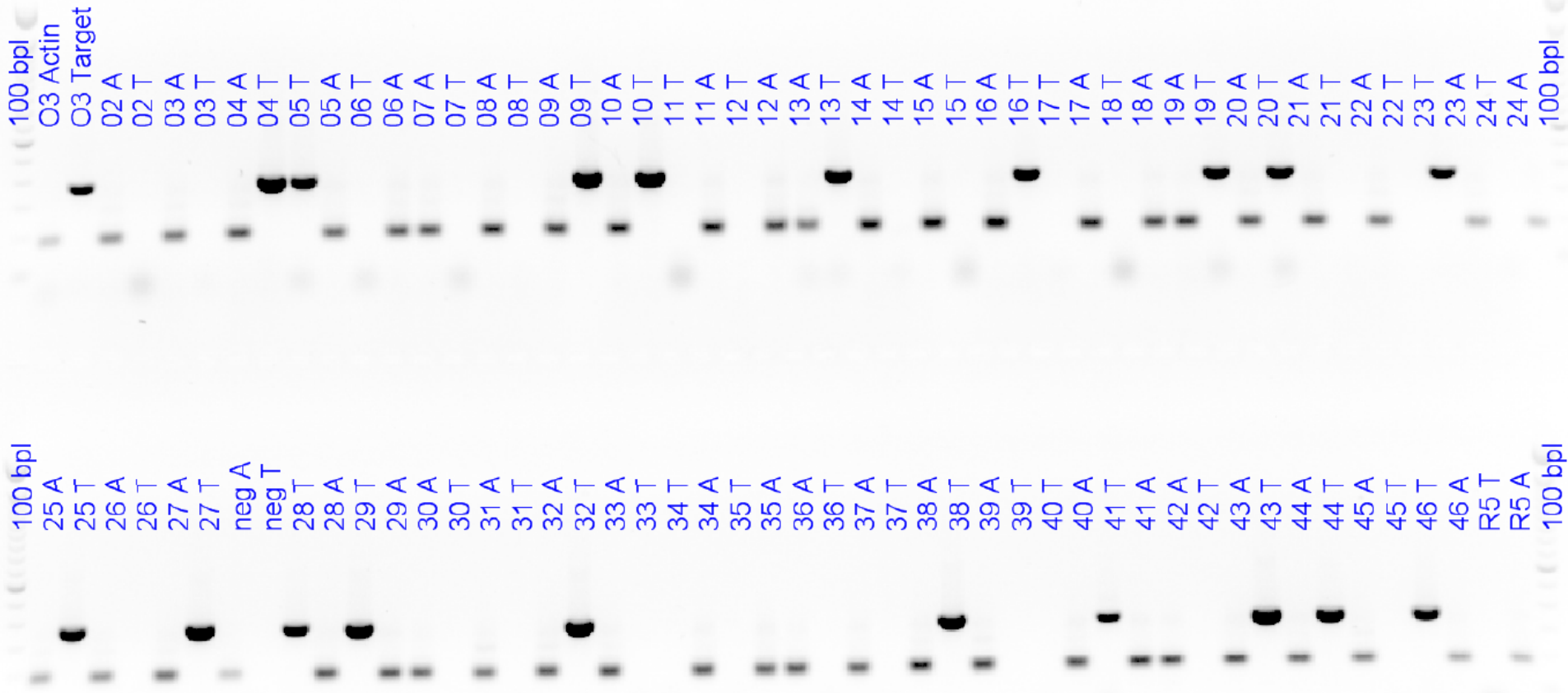


Figure S3.
Jensen et al.
BMC Genomics

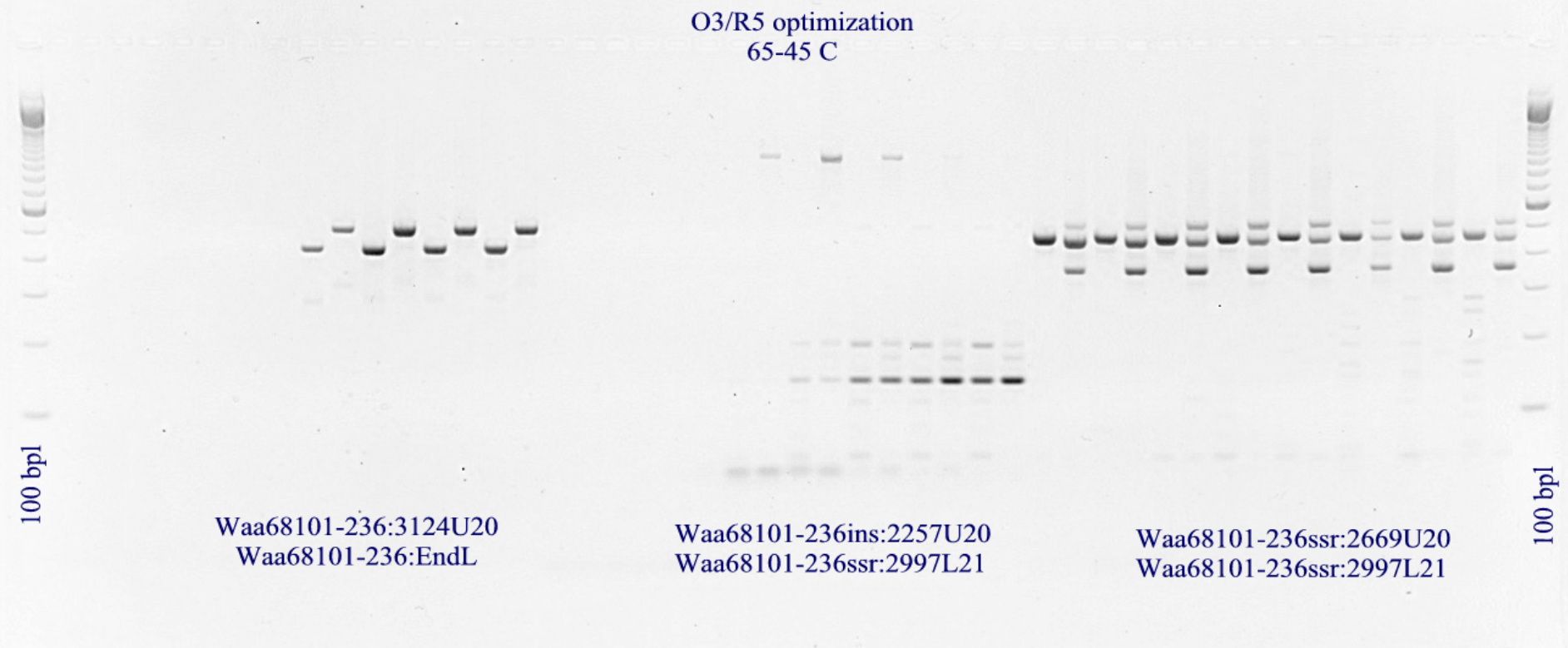
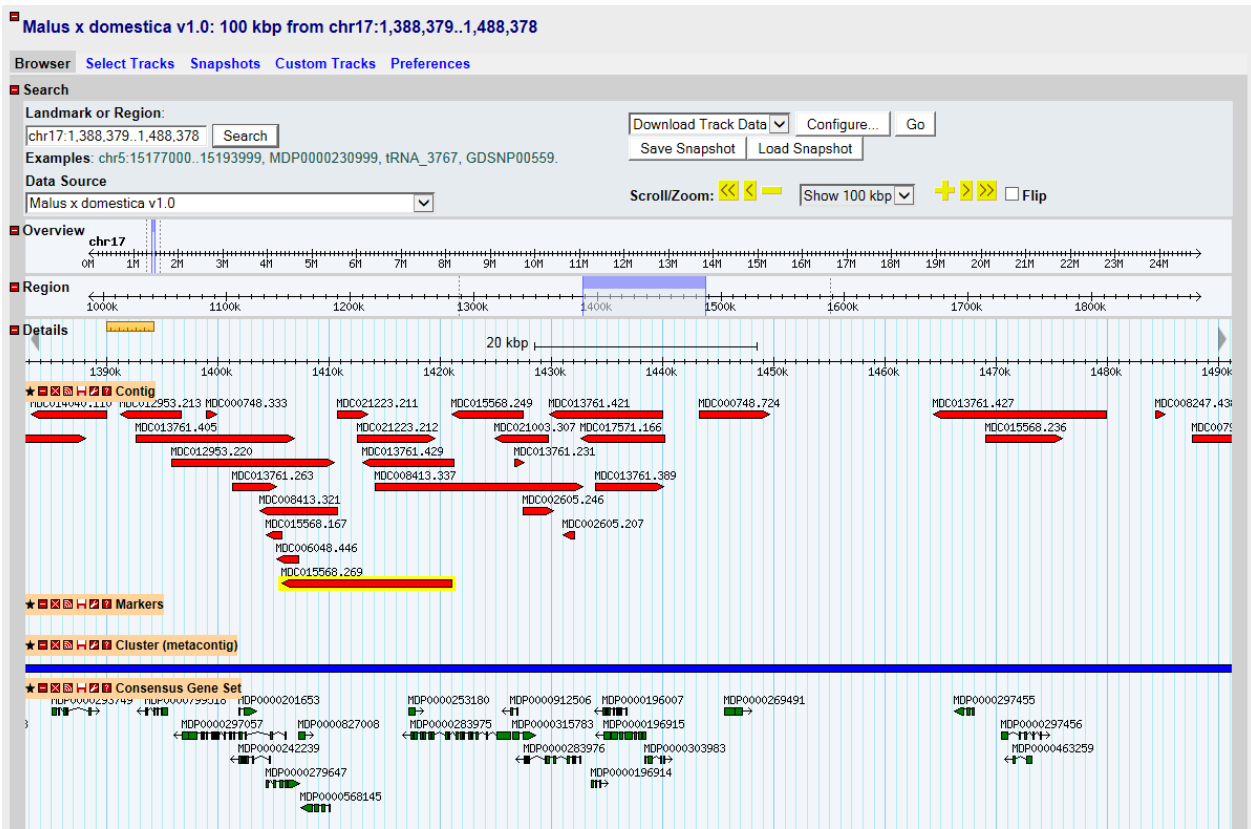


Figure S4.
Jensen et al.
BMC Genomics

Figure S5 Alignment of microarray feature APPLE0FR00068101 to Chromosome 17 of the apple genome displayed in Genome Browser at the Genome Database for Rosaceae (www.rosaceae.org) and the BLAST alignments to the four contigs (MDC015568.269, MDC000748.724, MDC015568.236, MDC013761.427) that matched the best with it.



Sequences producing significant alignments:		(bits)	Value
MDC015568.269	chr17:1405743..1421014	<u>682</u>	0.0
MDC000748.724	chr17:1443321..1449646	<u>682</u>	0.0
MDC015568.236	chr17:1469063..1475893	<u>379</u>	e-103
MDC013761.427	chr17:1464328..1479871	<u>379</u>	e-103

```
>MDC015568.269 chr17:1405743..1421014
      Length = 15272
```

```
Score = 682 bits (344), Expect = 0.0
Identities = 353/356 (99%)
Strand = Plus / Minus
```

```
Query: 1      aaccaaactgtagcacacaattcatcactgctatgacagctaagacattccaaatcacac 60
             |||
Sbjct: 3311  aaccaaactgtagcacacaattcatcactgctatgacagctaagacattccaaatcacac 3252
```

Query: 61 aagtttacatacattgggataaaacccacagttattcattgttaaataataattacaataa 120
|||||
Sbjct: 3251 aagtttacatacattgggataaaacccacagttattcattgttaaataataattacaataa 3192

Query: 121 gttgatttttgttggatgcaaccatccaactactatgatccttcagcgcccaatgttgga 180
|||||
Sbjct: 3191 gttgatttttgttggatgcaaccatccaactactatgatccttcagcgcccaatgttgga 3132

Query: 181 ttttcaaaggcgaagaaactccataactcaaaatcgtgggcatcggctggagagagattgt 240
|||||
Sbjct: 3131 ttttctaaggcgaagaaactccataactcaaaatcgtgggcatcggctggagagagattgt 3072

Query: 241 cttcgcgctcttgggttgaagtgcgagaccttgaagaatatgagaactggatcatctgggt 300
|||||
Sbjct: 3071 cttcgcgctcttgggttgaagtgcgagaccttgaagaatatgagaactggatcatctgggt 3012

Query: 301 cctcttcttcttattattcttcttcaaaagtttgaactcttatgggttagagaga 356
|||||
Sbjct: 3011 cctcttcttcttattattcttcttcaaatgcttgaactcttatgggttagagaga 2956

>MDC000748.724 chr17:1443321..1449646
Length = 6326

Score = 682 bits (344), Expect = 0.0
Identities = 353/356 (99%)
Strand = Plus / Minus

Query: 1 aaccaaactgtagcacacaattcatcactgctatgacagctaagacattccaaatcacac 60
|||||
Sbjct: 4944 aaccaaactgtagcacacaattcatcactgctatgacagctaagacattccaaatcacac 4885

Query: 61 aagtttacatacattgggataaaacccacagttattcattgttaaataataattacaataa 120
|||||
Sbjct: 4884 aagtttacatacattgggataaaacccacagttattcattgttaaataataattacaataa 4825

Query: 121 gttgatttttgttggatgcaaccatccaactactatgatccttcagcgcccaatgttgga 180
|||||
Sbjct: 4824 gttgatttttgttggatgcaaccatccaactactatgatccttcagcgcccaatgttgga 4765

Query: 181 ttttcaaaggcgaagaaactccataactcaaaatcgtgggcatcggctggagagagattgt 240
|||||
Sbjct: 4764 ttttctaaggcgaagaaactccataactcaaaatcgtgggcatcggctggagagagattgt 4705

Query: 241 cttcgcgctcttgggttgaagtgcgagaccttgaagaatatgagaactggatcatctgggt 300
|||||
Sbjct: 4704 cttcgcgctcttgggttgaagtgcgagaccttgaagaatatgagaactggatcatctgggt 4645

Query: 301 cctcttcttcttattattctttcttcaaaagtttgtaactcttatgggttagagaga 356
|||||
Sbjct: 4644 cctcttcttcttattattctttcttcaaagcttgtaactcttatgggttagagaga 4589

Score = 111 bits (56), Expect = 8e-23
Identities = 107/124 (86%), Gaps = 10/124 (8%)
Strand = Plus / Plus

Query: 198 actccatactcaaaatcgtgggcatcggctggagagagattgtcttcgcg-----t 248
|||||
Sbjct: 3347 actccatactcaaaatcgtgggaatcgtctggagagagattgccttcccgcgctcagggt 3406

Query: 249 cttggggtgaagtgcgagaccttgaagaatatgagaactggatcatctgggtcctcttct 308
|||||
Sbjct: 3407 cttggggtgaagagcaagac-ttgaagaatatgagaactggatcatctgggtcctcttcc 3465

Query: 309 tctt 312
||||
Sbjct: 3466 tctt 3469

>MDC015568.236 chr17:1469063..1475893
Length = 6831

Score = 379 bits (191), Expect = e-103
Identities = 200/203 (98%)
Strand = Plus / Minus

Query: 1 aaccaaactgtagcacacaattcatcactgctatgacagctaagacattccaaatcacac 60
|||||
Sbjct: 1419 aaccaaactgtagcacacaattcatcactgggtatgacagctaagacattccaaatcacac 1360

Query: 61 aagtttacatacattgggataaaacccacagttattcattgttaaataataattacaataa 120
|||||
Sbjct: 1359 aagtttacatacattgggataaaacccacagttattcattgttaaataatcattacaataa 1300

Query: 121 gttgatttttgttgatgcaaccatccaactactatgatccttcagcgcccaatggttga 180
|||||
Sbjct: 1299 gttgatttttgttgatgctaccatccaactactatgatccttcagcgcccaatggttga 1240

Query: 181 ttttcaaaggcgaagaaactcca 203
|||||
Sbjct: 1239 ttttcaaaggcgaagaaactcca 1217

Score = 123 bits (62), Expect = 2e-26
Identities = 103/116 (88%), Gaps = 8/116 (6%)
Strand = Plus / Plus

```
Query: 201 ccataactcaaaatcgtgggcatcggtggagagagattgtcttcgcg-----tcttgg 253
          ||||||| ||||||| ||||||| |||||||||||||||| ||||||| |||||||
Sbjct: 2478 ccataacttaaaatcgcgggcat-ggctggagagagatagtcttcgcgctcaggatcttgg 2536
```

```
Query: 254 gttgaagtgcgagaccttgaagaatatgagaactggatcatctgggtcctcttctt 309
          |||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Sbjct: 2537 gttgaagtgcgagactttgaagaatatgagaaatggatcatctgggtcctcttctt 2592
```

>MDC013761.427 chr17:1464328..1479871
Length = 15544

Score = 379 bits (191), Expect = e-103
Identities = 200/203 (98%)
Strand = Plus / Plus

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Query: 1 aaccaaactgtagcacacaattcatcactgctatgacagctaagacattccaaatcacac 60
          |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Sbjct: 9417 aaccaaactgtagcacacaattcatcactgggtatgacagctaagacattccaaatcacac 9476
```

```
Query: 61 aagtttacatacattgggataaaaaccacagttattcattgttaaataataattacaataa 120
          |||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Sbjct: 9477 aagtttacatacattgggataaaaaccacagttattcattgttaaataatcattacaataa 9536
```

```
Query: 121 gttgatttttgttggtatgcaaccatccaactactatgatccttcagcgcccaatgttgga 180
          |||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Sbjct: 9537 gttgatttttgttggtatgctaccatccaactactatgatccttcagcgcccaatgttgga 9596
```

```
Query: 181 ttttcaaaggcgaagaaactcca 203
          ||||||||||||||||
Sbjct: 9597 ttttcaaaggcgaagaaactcca 9619
```

Score = 123 bits (62), Expect = 2e-26
Identities = 103/116 (88%), Gaps = 8/116 (6%)
Strand = Plus / Minus

```
Query: 201 ccataactcaaaatcgtgggcatcggtggagagagattgtcttcgcg-----tcttgg 253
          ||||||| ||||||| ||||||| |||||||||||||||| ||||||| |||||||
Sbjct: 8358 ccataacttaaaatcgcgggcat-ggctggagagagatagtcttcgcgctcaggatcttgg 8300
```

Query: 254 gttgaagtgcgagaccttgaagaatatgagaactggatcatctgggtcctcttctt 309
|||||
Sbjct: 8299 gttgaagtgcgagactttgaagaatatgagaaatggatcatctgggtcctcttctt 8244