From VF2: trustworthy up to ~1000th bp

From VF: trustworthy after bp 1,000 ish

So I can trust complete coverage!

>pLac\_SH3-FLS-c9-42-lacI-seq-insert\_B04.ab1  
GNNNNNNCGNCNNNNNCGGGCAGTGATACTAGAGAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATAACAAGATACTGAGCACATACTAGAGAAAGAGGAGAAATACTAGAGATGCCGCCGCCGGCGCTGCCGCCGAAAAGAAGGAGAGGTAGCGGCGCGATGATCACGGGCGGCGAGCTGGTAGTGCGCACCTTAATCAAGGCGGGTGTTGAGCACCTGTTTGGTCTGCACGGTATCCATATTGACACGATCTTCCAGGCTTGTCTGGACCACGACGTGCCGATTATCGACACTCGTCACGAGGCGGCTGCCGGCCACGCTGCGGAGGGCTACGCTCGTGCCGGTGCGAAACTGGGTGTGGCTTTGGTCACCGCGGGTGGCGGCTTCACTAATGCGGTGACCCCTATTGCGAATGCGTGGCTGGACCGTACGCCGGTCCTGTTTCTGACCGGCAGCGGTGCGCTGCGTGACGACGAAACTAACACCCTGCAAGCGGGTATTGACCAAGTTGCGATGGCAGCGCCGATTACGAAGTGGGCACACCGCGTTATGGCCACCGAGCACATCCCGCGCCTGGTTATGCAGGCAATCCGTGCGGCGCTGAGCGCTCCGCGTGGCCCGGTTTTGTTGGACCTGCCGTGGGATATCCTGATGAACCAAATCGACGAGGACTCTGTCATTATCCCTGACCTGGTGCTGTCCGCACACGGTGCACGCCCGGACCCAGCTGATTTAGATCAGGCCTTGGCTCTGTTGCGCAAAGCAGAACGCCCGGTCATTGTCTTGGGCAGCGAAGCATCGCGCACCGCGCGTAAGACTGCCCTGAGCGCCTTCGTGGCGGCGACGGGTGTTCCGGTTTTCGCAGATTACGAGGGTCTGAGCATGCTGTCTGGTCTGCCTGACGCGATGCGTGGTGGCCTGGNGCAGAACCTGTACAGCTTCGCAAAGGCAGATGCGGCGCCGGACCTGGNTTCTGATGTTGGGTGCGCGCTTCGGCCTGAATACTGGNCACGGCAGCGGNCAGCTGATCCCGCATAGCGCACAGGTCATTCNNNTGATCCNNATGCGTGTGANTGGGNNTTTGCAGGGNATTGCTCTGGNATCNTCNCNGNNNNNGGGNGGNNCNTCNAAGCNNNTNNNNAGNCTACCNNNNANAATGCNNCNNNNNNNNGAATCN

>SH3-FLS-c9-VR\_A10.ab1  
NNNNNNNNNNNNNNNNCNNANNACCGANCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCGAAGTAATCTTTTCGGTTTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGACTGCAGCGGCCGCTACTAGTACTCGAGTCATTACTCCAGGGCGCCAGATTGAAAGTACAGATTTTCGGTGCTACCCGCGAACGGGTCCATACCGATCAGAATCAGTTCTTCAGGTGGAATCGGGTCCAGTGCAACTGCAACGTTGATACAGGCTGGACGGTTGTGGGCCAACGCTTGAGCCAGTGCGGCGGAGAAGCTCTCGACGCTGTCGACGTGGTAGCCATCTGCACCAAATGCCGCTGCAACACCATGATAAGAGCCATTTTCCAGGCGCGTACCCGTAACACGATTCGGACCAACGGCCAGTTGTTGGAAGTGCAGGGTCCAGCCCCAGCTCTGATTATTCATAATGATCACGATCAGCGGCAGCTGCTTGCGAACCAGGGTATCAAACTCGCCGATGCTGTAACCGACGCTACCATCACCGGTGACCAGGATCGTGCGACGACCCGCTTCCAGATCCGCAACTTGTGCACCCAGCGCGGTGCCGAAACCCACACCCATGCTGTTCAGGTAACCGTGGCACAGAAAGCCACCCGGCTTAACGCGAGACATGACTTCCGACAGCCACAGGTAGGTCAGACCACCGTCCGCCACCACGGTCACACCCGCGTCGACGTGTTTAGCGATGACTTGAGATGCGTGGAACGGATGCAACGCGTGTTCCGAGCTGCTCTTTGCCGCAATGCTGGCATAGCGCTCCTGGGCCAGATCAGTCACTTTTGCGCACCAATCACCACGATCTGGCCAGGCAGCATCTTGCGCGGTAGCCTGGGCCAGTGCTTCGATGGTACCACCCACGTCCGCGACGATGCCCAGAGCAATACCCTGCAAACGGCCCAGTTCACACGCATCCGGATCAACCTGAATGACCTGTGCGCTATGCGGGATCAGCTGANCGCTGCCGNGACCAGTATTCNNNCGAAGCGNGCACCCANATCAGAACCAGGTCCGGCGCCGCATCTGCNTTTGCGAAGCTGNNNNGGTNN

-----------VF2------------------

BLASTN 2.2.26+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and

Webb Miller (2000), "A greedy algorithm for aligning DNA

sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: S71CD46S112

Query= pLac\_SH3-FLS-c9-42-lacI-seq-insert\_B04.ab1

Length=1183

Score E

Sequences producing significant alignments: (Bits) Value

lcl|46275 1943 0.0

ALIGNMENTS

>lcl|46275

Length=5586

Score = 1943 bits (1052), Expect = 0.0

Identities = 1076/1093 (98%), Gaps = 4/1093 (0%)

Strand=Plus/Plus

Query 17 CGGGCAGTGATACTAGAGAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATAACAA 76

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1686 CGGGCAGTGATACTAGAGAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATAACAA 1745

Query 77 GATACTGAGCACATACTAGAGAAAGAGGAGAAATACTAGAGATGCCGCCGCCGGCGCTGC 136

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1746 GATACTGAGCACATACTAGAGAAAGAGGAGAAATACTAGAGATGCCGCCGCCGGCGCTGC 1805

Query 137 CGCCGAAAAGAAGGAGAGGTAGCGGCGCGATGATCACGGGCGGCGAGCTGGTAGTGCGCA 196

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1806 CGCCGAAAAGAAGGAGAGGTAGCGGCGCGATGATCACGGGCGGCGAGCTGGTAGTGCGCA 1865

Query 197 CCTTAATCAAGGCGGGTGTTGAGCACCTGTTTGGTCTGCACGGTATCCATATTGACACGA 256

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1866 CCTTAATCAAGGCGGGTGTTGAGCACCTGTTTGGTCTGCACGGTATCCATATTGACACGA 1925

Query 257 TCTTCCAGGCTTGTCTGGACCACGACGTGCCGATTATCGACACTCGTCACGAGGCGGCTG 316

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1926 TCTTCCAGGCTTGTCTGGACCACGACGTGCCGATTATCGACACTCGTCACGAGGCGGCTG 1985

Query 317 CCGGCCACGCTGCGGAGGGCTACGCTCGTGCCGGTGCGAAACTGGGTGTGGCTTTGGTCA 376

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1986 CCGGCCACGCTGCGGAGGGCTACGCTCGTGCCGGTGCGAAACTGGGTGTGGCTTTGGTCA 2045

Query 377 CCGCGGGTGGCGGCTTCACTAATGCGGTGACCCCTATTGCGAATGCGTGGCTGGACCGTA 436

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2046 CCGCGGGTGGCGGCTTCACTAATGCGGTGACCCCTATTGCGAATGCGTGGCTGGACCGTA 2105

Query 437 CGCCGGTCCTGTTTCTGACCGGCAGCGGTGCGCTGCGTGACGACGAAACTAACACCCTGC 496

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2106 CGCCGGTCCTGTTTCTGACCGGCAGCGGTGCGCTGCGTGACGACGAAACTAACACCCTGC 2165

Query 497 AAGCGGGTATTGACCAAGTTGCGATGGCAGCGCCGATTACGAAGTGGGCACACCGCGTTA 556

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2166 AAGCGGGTATTGACCAAGTTGCGATGGCAGCGCCGATTACGAAGTGGGCACACCGCGTTA 2225

Query 557 TGGCCACCGAGCACATCCCGCGCCTGGTTATGCAGGCAATCCGTGCGGCGCTGAGCGCTC 616

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2226 TGGCCACCGAGCACATCCCGCGCCTGGTTATGCAGGCAATCCGTGCGGCGCTGAGCGCTC 2285

Query 617 CGCGTGGCCCGGTTTTGTTGGACCTGCCGTGGGATATCCTGATGAACCAAATCGACGAGG 676

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2286 CGCGTGGCCCGGTTTTGTTGGACCTGCCGTGGGATATCCTGATGAACCAAATCGACGAGG 2345

Query 677 ACTCTGTCATTATCCCTGACCTGGTGCTGTCCGCACACGGTGCACGCCCGGACCCAGCTG 736

|||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||

Sbjct 2346 ACTCTGTCATTATCCCTGACCTGGTGCTGTCCGCACACGGTGCACGCCCGGATCCAGCTG 2405

Query 737 ATTTAGATCAGGCCTTGGCTCTGTTGCGCAAAGCAGAACGCCCGGTCATTGTCTTGGGCA 796

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2406 ATTTAGATCAGGCCTTGGCTCTGTTGCGCAAAGCAGAACGCCCGGTCATTGTCTTGGGCA 2465

Query 797 GCGAAGCATCGCGCACCGCGCGTAAGACTGCCCTGAGCGCCTTCGTGGCGGCGACGGGTG 856

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2466 GCGAAGCATCGCGCACCGCGCGTAAGACTGCCCTGAGCGCCTTCGTGGCGGCGACGGGTG 2525

Query 857 TTCCGGTTTTCGCAGATTACGAGGGTCTGAGCATGCTGTCTGGTCTGCCTGACGCGATGC 916

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2526 TTCCGGTTTTCGCAGATTACGAGGGTCTGAGCATGCTGTCTGGTCTGCCTGACGCGATGC 2585

Query 917 GTGGTGGCCTGGNGCAGAACCTGTACAGCTTCGCAAAGGCAGATGCGGCGCCGGACCTGG 976

|||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2586 GTGGTGGCCTGGTGCAGAACCTGTACAGCTTCGCAAAGGCAGATGCGGCGCCGGACCTGG 2645

Query 977 NTTCTGATGTTGGGTGCGCGCTTCGGCCTGAATACTGGNCACGGCAGCGGNCAGCTGATC 1036

||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||

Sbjct 2646 -TTCTGATGTTGGGTGCGCGCTTCGGCCTGAATACTGGTCACGGCAGCGGTCAGCTGATC 2704

Query 1037 CCGCATAGCGCACAGGTCATTCNNNT-GATCCNNATGCGTGTGAN-TGGGNN-TTTGCAG 1093

|||||||||||||||||||||| | ||||| |||||||||| |||| |||||||

Sbjct 2705 CCGCATAGCGCACAGGTCATTCAGGTTGATCCGGATGCGTGTGAACTGGGCCGTTTGCAG 2764

Query 1094 GGNATTGCTCTGG 1106

|| ||||||||||

Sbjct 2765 GGTATTGCTCTGG 2777

------------VR------------------

BLASTN 2.2.26+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and

Webb Miller (2000), "A greedy algorithm for aligning DNA

sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: S71DY6J6112

Query= SH3-FLS-c9-VR\_A10.ab1

Length=1119

Score E

Sequences producing significant alignments: (Bits) Value

lcl|9443 1962 0.0

ALIGNMENTS

>lcl|9443

Length=5586

Score = 1962 bits (1062), Expect = 0.0

Identities = 1078/1090 (99%), Gaps = 2/1090 (0%)

Strand=Plus/Minus

Query 23 ACCGANCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCGAAGTAATCTTTTCGGT 82

||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3700 ACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCGAAGTAATCTTTTCGGT 3641

Query 83 TTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGACTGCAGCGGCCG 142

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3640 TTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGACTGCAGCGGCCG 3581

Query 143 CTACTAGTACTCGAGTCATTACTCCAGGGCGCCAGATTGAAAGTACAGATTTTCGGTGCT 202

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3580 CTACTAGTACTCGAGTCATTACTCCAGGGCGCCAGATTGAAAGTACAGATTTTCGGTGCT 3521

Query 203 ACCCGCGAACGGGTCCATACCGATCAGAATCAGTTCTTCAGGTGGAATCGGGTCCAGTGC 262

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3520 ACCCGCGAACGGGTCCATACCGATCAGAATCAGTTCTTCAGGTGGAATCGGGTCCAGTGC 3461

Query 263 AACTGCAACGTTGATACAGGCTGGACGGTTGTGGGCCAACGCTTGAGCCAGTGCGGCGGA 322

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3460 AACTGCAACGTTGATACAGGCTGGACGGTTGTGGGCCAACGCTTGAGCCAGTGCGGCGGA 3401

Query 323 GAAGCTCTCGACGCTGTCGACGTGGTAGCCATCTGCACCAAATGCCGCTGCAACACCATG 382

|||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||

Sbjct 3400 GAAGCTCTCGACGCTGTCGACGTGGTAGCCATCTGCACCAAACGCCGCTGCAACACCATG 3341

Query 383 ATAAGAGCCATTTTCCAGGCGCGTACCCGTAACACGATTCGGACCAACGGCCAGTTGTTG 442

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3340 ATAAGAGCCATTTTCCAGGCGCGTACCCGTAACACGATTCGGACCAACGGCCAGTTGTTG 3281

Query 443 GAAGTGCAGGGTCCAGCCCCAGCTCTGATTATTCATAATGATCACGATCAGCGGCAGCTG 502

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3280 GAAGTGCAGGGTCCAGCCCCAGCTCTGATTATTCATAATGATCACGATCAGCGGCAGCTG 3221

Query 503 CTTGCGAACCAGGGTATCAAACTCGCCGATGCTGTAACCGACGCTACCATCACCGGTGAC 562

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3220 CTTGCGAACCAGGGTATCAAACTCGCCGATGCTGTAACCGACGCTACCATCACCGGTGAC 3161

Query 563 CAGGATCGTGCGACGACCCGCTTCCAGATCCGCAACTTGTGCACCCAGCGCGGTGCCGAA 622

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3160 CAGGATCGTGCGACGACCCGCTTCCAGATCCGCAACTTGTGCACCCAGCGCGGTGCCGAA 3101

Query 623 ACCCACACCCATGCTGTTCAGGTAACCGTGGCACAGAAAGCCACCCGGCTTAACGCGAGA 682

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3100 ACCCACACCCATGCTGTTCAGGTAACCGTGGCACAGAAAGCCACCCGGCTTAACGCGAGA 3041

Query 683 CATGACTTCCGACAGCCACAGGTAGGTCAGACCACCGTCCGCCACCACGGTCACACCCGC 742

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 3040 CATGACTTCCGACAGCCACAGGTAGGTCAGACCACCGTCCGCCACCACGGTCACACCCGC 2981

Query 743 GTCGACGTGTTTAGCGATGACTTGAGATGCGTGGAACGGATGCAACGCGTGTTCCGAGCT 802

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2980 GTCGACGTGTTTAGCGATGACTTGAGATGCGTGGAACGGATGCAACGCGTGTTCCGAGCT 2921

Query 803 GCTCTTTGCCGCAATGCTGGCATAGCGCTCCTGGGCCAGATCAGTCACTTTTGCGCACCA 862

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2920 GCTCTTTGCCGCAATGCTGGCATAGCGCTCCTGGGCCAGATCAGTCACTTTTGCGCACCA 2861

Query 863 ATCACCACGATCTGGCCAGGCAGCATCTTGCGCGGTAGCCTGGGCCAGTGCTTCGATGGT 922

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2860 ATCACCACGATCTGGCCAGGCAGCATCTTGCGCGGTAGCCTGGGCCAGTGCTTCGATGGT 2801

Query 923 ACCACCCACGTCCGCGACGATGCCCAGAGCAATACCCTGCAAACGGCCCAGTTCACACGC 982

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2800 ACCACCCACGTCCGCGACGATGCCCAGAGCAATACCCTGCAAACGGCCCAGTTCACACGC 2741

Query 983 ATCCGGATCAACCTGAATGACCTGTGCGCTATGCGGGATCAGCTGANCGCTGCCGNGACC 1042

|||||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||

Sbjct 2740 ATCCGGATCAACCTGAATGACCTGTGCGCTATGCGGGATCAGCTGACCGCTGCCGTGACC 2681

Query 1043 AGTATTCNNNC-GAAGCGNGCACCCAN-ATCAGAACCAGGTCCGGCGCCGCATCTGCNTT 1100

||||||| | |||||| ||||||| ||||||||||||||||||||||||||||| ||

Sbjct 2680 AGTATTCAGGCCGAAGCGCGCACCCAACATCAGAACCAGGTCCGGCGCCGCATCTGCCTT 2621

Query 1101 TGCGAAGCTG 1110

||||||||||

Sbjct 2620 TGCGAAGCTG 2611