Sequence Report

Organism Name : HA Elk1 pShuttle A

Sequence length : 5410 bp

Base Count : 1357 A 1441 C 1320 G 1292 T

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   1  TAACTATAAC GGTCCTAAGG TAGCGAAAGC TCAGATCTGG ATCTCCCGAT
                SalI(60)
  51  CCCCTATGGT CGACTCTCAG TACAATCTGC TCTGATGCCG CATAGTTAAG
 101  CCAGTATCTG CTCCCTGCTT GTGTGTTGGA GGTCGCTGAG TAGTGCGCGA
 151  GCAAAATTTA AGCTACAACA AGGCAAGGCT TGACCGACAA TTGCATGAAG
 201  AATCTGCTTA GGGTTAGGCG TTTTGCGCTG CTTCGCGATG TACGGGCCAG
 251  ATATACGCGT TGACATTGAT TATTGACTAG TTATTAATAG TAATCAATTA
 301  CGGGGTCATT AGTTCATAGC CCATATATGG AGTTCCGCGT TACATAACTT
 351  ACGGTAAATG GCCCGCCTGG CTGACCGCCC AACGACCCCC GCCCATTGAC
 401  GTCAATAATG ACGTATGTTC CCATAGTAAC GCCAATAGGG ACTTTCCATT
 451  GACGTCAATG GGTGGACTAT TTACGGTAAA CTGCCCACTT GGCAGTACAT
 501  CAAGTGTATC ATATGCCAAG TACGCCCCCT ATTGACGTCA ATGACGGTAA
 551  ATGGCCCGCC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTTCCTA
 601  CTTGGCAGTA CATCTACGTA TTAGTCATCG CTATTACCAT GGTGATGCGG
 651  TTTTGGCAGT ACATCAATGG GCGTGGATAG CGGTTTGACT CACGGGGATT
 701  TCCAAGTCTC CACCCCATTG ACGTCAATGG GAGTTTGTTT TGGCACCAAA
 751  ATCAACGGGA CTTTCCAAAA TGTCGTAACA ACTCCGCCCC ATTGACGCAA
 801  ATGGGCGGTA GGCGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCTCTG
 851  GCTAACTAGA GAACCCACTG CTTACTGGCT TATCGAAATT AATACGACTC
                             NheI(923)
 901  ACTATAGGGA GACCCAAGCT GGCTAGCATG TACCCATACG ATGTTCCAGA
                    XbaI(965)
                  ApaI(963)
 951  TTACGCTGGG CCCTCTAGAA TGGACCCATC TGTGACGCTG TGGCAGTTTC
1001  TGCTGCAGCT TCTGAGAGAA CAAGGTAATG GCCACATCAT CTCCTGGACC
1051  TCACGGGATG GTGGTGAGTT CAAGTTGGTG GATGCAGAGG AGGTGGCCCG
1101  GCTATGGGGA CTGCGCAAGA ACAAGACCAA CATGAATTAC GACAAGCTTA
1151  GCCGGGCCTT GCGGTACTAC TATGATAAGA ATATCATCCG CAAGGTGAGC
1201  GGCCAGAAGT TTGTCTACAA GTTTGTGTCC TACCCAGAGG TTGCAGGGTG
1251  CTCCACTGAA GACTGCCCAC CCCAGCCTGA GGTGTCTGTA ACCTCGGCCA
1301  TAGCCATGGC CCCTGCTACT GTCCATGCAG GCCCAGGGGA CACTGCCACT
1351  GGAAAGCCAG GAACACCAAA GGGTGCAGGA ATGACAGGCC AAGGTGGCTT
1401  AGCACGAAGC AGCCGGAATG AATACATGCG CTCGGGCCTC TATTCTACCT
1451  TCACAATACA ATCCCTGCAG CCACAGCCAC AGCCACCCAT TCCTCCTCGG
1501  CCTGCCTCAG TGCTTCCCAA CACTACCCCT GCAGGAGTAC CAGCACCCGC
1551  CTCAGGGAGC AGGAGCACCA GTCCAAACCC CTTAGAAGCC TGTTTGGAAG
1601  CAGAAGAGGC TGGTCTGCCC CTGCAGGTTA TCCTAACCCC ACCAGAGGCC
1651  CCAAACCAGA AATCCGAAGA GTTGAGTCTG GACCCAAGTT TTGGCCATCC
1701  ACAGCCCCCA GAAGTCAAAG TGGAGGGGCC TAAGGAAGAA TTGGAAGCTG
1751  CAAGGGCTGG AGGCTTCAGT TCAGAAGCTG TCAAAGCTGA ACCAGAAGTC
1801  TCAGCCTCAG AAGGCCTGCT GGCTCGGCTC CCAGCCATCC TAACAGAGAA
1851  CACAGCCCAG GTGTGTGGCC TCTCCACTTC CACCACTGAG ATCACCCAAC
1901  CGCAGAAGGG CCGAAAGCCT CGGGACCTGG AACTTCCACT TAGCCCAAGC
1951  CTGCTGGGTG GCCAGGGACC TGAACGGACT CCAGGATCAG GAACAAGCTC
2001  TGGTCTTCAG GCACCGGGGC CAGCGCTAAC GCCATCCCTG CTCCCCACAC
2051  ATACCTTGAC CCCGGTGCTG CTGACACCCA GCTCGCTGCC CCCTAGCATC
2101  CATTTCTGGA GCACTCTGAG TCCAATTGCA CCCCGTAGTC CAGCCAAGCT
2151  CTCCTTCCAG TTTCCGTCCA GTGGCAGCGC ACAGGTGCAC ATCCCTTCCA
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Sequence Report

Organism Name : HA Elk1 pShuttle A

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                                                          ApaI(2247)
2201  TCAGTGTGGA TGGCCTCTCG ACCCCCGTGG TGCTCTCCCC AGGGCCCCAG
                             AflII(2270)
                       KpnI(2265)
2251  AAGCCATGAG GTACCAAGCT TAAGTTTAAA CCGCTGATCA GCCTCGACTG
2301  TGCCTTCTAG TTGCCAGCCA TCTGTTGTTT GCCCCTCCCC CGTGCCTTCC
2351  TTGACCCTGG AAGGTGCCAC TCCCACTGTC CTTTCCTAAT AAAATGAGGA
2401  AATTGCATCG CATTGTCTGA GTAGGTGTCA TTCTATTCTG GGGGGTGGGG
2451  TGGGGCAGGA CAGCAAGGGG GAGGATTGGG AAGACAATAG CAGGCATGCT
2501  GGGGATGCGG TGGGCTCTAT GGCTTCTGAG GCGGAAAGAA CCAGCAGATC
                       EcoRI(2561)
2551  TGCAGATCTG AATTCATCTA TGTCGGGTGC GGAGAAAGAG GTAATGAAAT
2601  GGCATTATGG GTATTATGGG TCTGCATTAA TGAATCGGCC AACGCGCGGG
2651  GAGAGGCGGT TTGCGTATTG GGCGCTCTTC CGCTTCCTCG CTCACTGACT
2701  CGCTGCGCTC GGTCGTTCGG CTGCGGCGAG CGGTATCAGC TCACTCAAAG
2751  GCGGTAATAC GGTTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT
2801  GTGAGCAAAA GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC
2851  TGGCGTTTTT CCATAGGCTC CGCCCCCCTG ACGAGCATCA CAAAAATCGA
2901  CGCTCAAGTC AGAGGTGGCG AAACCCGACA GGACTATAAA GATACCAGGC
2951  GTTTCCCCCT GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG ACCCTGCCGC
3001  TTACCGGATA CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT GGCGCTTTCT
3051  CAATGCTCAC GCTGTAGGTA TCTCAGTTCG GTGTAGGTCG TTCGCTCCAA
3101  GCTGGGCTGT GTGCACGAAC CCCCCGTTCA GCCCGACCGC TGCGCCTTAT
3151  CCGGTAACTA TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA
3201  CTGGCAGCAG CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG
3251  TGCTACAGAG TTCTTGAAGT GGTGGCCTAA CTACGGCTAC ACTAGAAGGA
3301  CAGTATTTGG TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA
3351  GTTGGTAGCT CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT
3401  TTTTGTTTGC AAGCAGCAGA TTACGCGCAG AAAAAAAGGA TCTCAAGAAG
3451  ATCCTTTGAT CTTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAAACTCA
3501  CGTTAAGGGA TTTTGGTCAT GAGATTATCA AAAAGGATCT TCACCTAGAT
3551  CCTTTTGATC CTCCGGCGTT CAGCCTGTGC CACAGCCGAC AGGATGGTGA
3601  CCACCATTTG CCCCATATCA CCGTCGGTAC TGATCCCGTC GTCAATAAAC
3651  CGAACCGCTA CACCCTGAGC ATCAAACTCT TTTATCAGTT GGATCATGTC
3701  GGCGGTGTCG CGGCCAAGAC GGTCGAGCTT CTTCACCAGA ATGACATCAC
3751  CTTCCTCCAC CTTCATCCTC AGCAAATCCA GCCCTTCCCG ATCTGTTGAA
3801  CTGCCGGATG CCTTGTCGGT AAAGATGCGG TTAGCTTTTA CCCCTGCATC
3851  TTTGAGCGCT GAGGTCTGCC TCGTGAAGAA GGTGTTGCTG ACTCATACCA
3901  GGCCTGAATC GCCCCATCAT CCAGCCAGAA AGTGAGGGAG CCACGGTTGA
3951  TGAGAGCTTT GTTGTAGGTG GACCAGTTGG TGATTTTGAA CTTTTGCTTT
4001  GCCACGGAAC GGTCTGCGTT GTCGGGAAGA TGCGTGATCT GATCCTTCAA
4051  CTCAGCAAAA GTTCGATTTA TTCAACAAAG CCGCCGTCCC GTCAAGTCAG
4101  CGTAATGCTC TGCCAGTGTT ACAACCAATT AACCAATTCT GATTAGAAAA
4151  ACTCATCGAG CATCAAATGA AACTGCAATT TATTCATATC AGGATTATCA
4201  ATACCATATT TTTGAAAAAG CCGTTTCTGT AATGAAGGAG AAAACTCACC
4251  GAGGCAGTTC CATAGGATGG CAAGATCCTG GTATCGGTCT GCGATTCCGA
4301  CTCGTCCAAC ATCAATACAA CCTATTAATT TCCCCTCGTC AAAAATAAGG
4351  TTATCAAGTG AGAAATCACC ATGAGTGACG ACTGAATCCG GTGAGAATGG
4401  CAAAAGCTTA TGCATTTCTT TCCAGACTTG TTCAACAGGC CAGCCATTAC
4451  GCTCGTCATC AAAATCACTC GCATCAACCA AACCGTTATT CATTCGTGAT
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Sequence Report

Organism Name : HA Elk1 pShuttle A

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4501   TGCGCCTGAG CGAGACGAAA TACGCGATCG CTGTTAAAAG GACAATTACA
4551   AACAGGAATC GAATGCAACC GGCGCAGGAA CACTGCCAGC GCATCAACAA
4601   TATTTTCACC TGAATCAGGA TATTCTTCTA ATACCTGGAA TGCTGTTTTC
4651   CCGGGGATCG CAGTGGTGAG TAACCATGCA TCATCAGGAG TACGGATAAA
4701   ATGCTTGATG GTCGGAAGAG GCATAAATTC CGTCAGCCAG TTTAGTCTGA
4751   CCATCTCATC TGTAACATCA TTGGCAACGC TACCTTTGCC ATGTTTCAGA
                                           ClaI(4834)
4801   AACAACTCTG GCGCATCGGG CTTCCCATAC AATCGATAGA TTGTCGCACC
4851   TGATTGCCCG ACATTATCGC GAGCCCATTT ATACCCATAT AAATCAGCAT
                                  XhoI(4925)
4901   CCATGTTGGA ATTTAATCGC GGCCTCGAGC AAGACGTTTC CCGTTGAATA
4951   TGGCTCATAA CACCCCTTGT ATTACTGTTT ATGTAAGCAG ACAGTTTTAT
5001   TGTTCATGAT GATATATTTT TATCTTGTGC AATGTAACAT CAGAGATTTT
5051   GAGACACAAC GTGGCTTTGT TGAATAAATC GAACTTTTGC TGAGTTGAAG
5101   GATCAGATCA CGCATCTTCC CGACAACGCA GACCGTTCCG TGGCAAAGCA
5151   AAAGTTCAAA ATCACCAACT GGTCCACCTA CAACAAAGCT CTCATCAACC
5201   GTGGCTCCCT CACTTTCTGG CTGGATGATG GGGCGATTCA GGCCTGGTAT
5251   GAGTCAGCAA CACCTTCTTC ACGAGGCAGA CCTCAGCGCT AGATTATTGA
5301   AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT
5351   TTAGAAAAAT AAACAAATAG GGGTTCCGCG CACATTTCCC CGAAAAGTGC
5401   CACCTGACGT
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