FVEG_03165

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Fv999  GCGAATGACCTGGGGAGCCATAATCGCCCATCCGCGTCGATTTGCAGTGGTACTTGGTAGTGAGGTCAAG  70
Fv149  GCGAATGACCTGGGGAGCCATAATCGCGC                                           29

Fv999  AGTGCAAGTGGGCCTTAAATCGCTCATGCCTTATTTGGGTTTCCGCAACTCAACTTAGCTTCAACAAGCT  140
Fv149                          GCTTCTTCCTTTTTCGGG                              47

Fv999  TTAATGGAGGAAGGTTTAACTCAAGAGTTCGCTTTTTATAAACCAGGCGTCCATCTTCTGTCTTCTGTTTA 210
Fv149                GGCTTGTCCGTAGACT          AATCGGGCGG                       73

Fv999  CTTTCTTCCTTACACACAATTCCATCAATCCACTACACAATTCCATCAATCCACTACACAATTCCATCAA  280
Fv149                                                                          73

Fv999  TCCACTACACAAACACAAGTTGTCTATCAAGAAATCATCTCTCATTCTATCTCCCAGATCACCAATCAAT  350
Fv149                                                                          73

Fv999  ACAGCCATGTCTACCAACTCAGACACCATGCCTGGCGTTATCCTCCACCTTTCATCAGATGATCTTGATG  420
Fv149                                GTGGTGGGCGCTGT                       AGTG  91

Fv999  TTTTTGCTTGATAAGAAGCTACAGCCTATTTACACTATGCTGGCTACTATTATCAAGAAACTTGATGATCT 490
Fv149  TTGCGCTTGCGGGCGATCG                   GCTGGAGAC GGGAGGGGAAAAGTTGA    CT  138

Fv999  TACCGACCGTGTTGAGGCAGTTGAAGGCCTGCGCGAAAAAGATCCCGGACATGGAAGTCGATATCCATTCT 560
Fv149  TAT    GT  TTGACTTGGTTTTAGGTCGGTGCTAAAGCTCCTGGA     GAAG                 183

Fv999  CAAGACTAGAGGCTGAAGAAGATTGAGGCGCAGCTTTTGTCCAGGACATGGTTAGTTCGTTCTCTAGAAT  630
Fv149                AGTTCCAGAAGACTG        CCTCTTTCGGG                         209

Fv999  GAATAATTATATGCTAATACCAAGACAGATTCAAGACTTTCTTTACGCTCATTCCCATGTCGGGCTGGAC  700
Fv149        TCACATGCT                                                   GAC   221

Fv999  CTTTGAAGAGGCGATCGTGACAAACGCCGAGGCCATGGTTGGGTGCGCTGATGGAGGTGGTGGAGAGATG  770
Fv149  CTTTGAAGAGGCGATCGTGACAAACGCCGAGGCGGTGGTTGGAATGCGCTGATGGAGGTGGTGGAGAGATG 291

Fv999  TCATATGGGCGTGGTTGGAGGTGAGGGACAGTAAATTGGGCACTGTACCCTACCTGAGTACTATGCCTG   840
Fv149  TTATATAGGCGTGGTTGGAGGTGAGGGACAGTAAATATGGGCACTGTACCCTACCTGAGTACTACGTCTG  361

Fv999  ACGCAGTATTCATATGGACATGCACTCATTCTTGTACGTCATGATAAGTCCATCCATCATATCATAGACT  910
Fv149  ACACAGTATTAATATGGACATGCACTCAGTCTTGTACGTCATGATAAGTCCATCCATCATATCAT       426

Fv999  ACCCCGCCATGAACTGGAGTGCTTGACTCTATCTCGGCGGCTTTAATCCCAATACGAAATTGTTATCTCG  980
Fv149  ACCCCGCCATGATCTGGAATGCTTGGCTCTATCTCGGCGGCTTTGATCCCAATACGAAAATCTTGTCTCA  496

Fv999  AGGTTTTCGTTTATCACAATCTCCATGTTACAGATCATTTATGCAAGTCATAAATCTAACATTAAATCAA 1050
Fv149  AGGTTTTCGTTTATCAGAATCCCCATGTCACAGATCATTTATGCAAGTCATAAATCTAACATGAAATCAA  566

Fv999  TTGTTTGTTGCCTATCGCTATGCGTACTCCATAATCCGTCCGAAATCGCAGCCAGTTCAATTTACAGCAG 1120
Fv149  TTGTTTGTTGCCTATCGCTATGCGTACTCCATAATCCATCCGAAATC CAGCCCCTTCAATTTACAGCAG  635

Fv999  TCTCC    CTCTGATGGTCTCA    CCACACCCACCATCAATAATTGTCGCGTGTTTCTAAGCCCCCAA 1183
Fv149  TCTCCTCCCTCTGAAGGTGTCAGTCACCACACCCACCATCAATAATTGTTGCGTGTT  CTGAACCCCCAA 704

Fv999  TGCTAAGCCATTCGCCATGATCTGATGTTTAGTGTACAACCTTTGCATCTACTCACTTCTAGATCTCGTC 1253
Fv149  TGCTAAGCCATTCGCCATGGTCTGATGTTTAGTGTACAAACTTTGCATCTACTCACTTCTAGATCTCGTC  774
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FVEG_03164

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Fv999  GTTTACTGCTTCTTCTTCTT 1273
Fv149  GTTTACTGCTTCTTCTTCTT  794
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Figure S2   A Clustal W alignment of the *FVEG_03165-FVEG_03164* intergenic region from Fv999-*Sk^K* and Fv149-*Sk^S*. The coding start site of flanking gene *FVEG_03165* is marked with a blue arrow. Similarly, the coding stop site of flanking gene *FVEG_03164* is marked with a blue line. The predicted coding sequence of *SKC1* is marked by a red line. This alignment shows that *SKC1* is present in Fv999-*Sk^K* but not Fv149-*Sk^S*.