



## Supplementary Material

# Identification and Genotyping of SNPs in *RKM1* and *RKM4* Genes of *Sordaria fimicola*

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Ref	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60	N6	CCTGCATTTTTATGGTGGCACTTATATTCATTTCAGAGCATTCCCTGAATATGTGTGA	480
S1	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60	N7	CCTGCATTTTTATGGTGGCACTTATATTCATTTCAGAGCATTCCCTGAATATGTGTGA	480
S2	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60		*****	
S3	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60		*****	
N5	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60		*****	
N6	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60		*****	
N7	ATGAAGTTTTTGGGCTAAGTGAATCCACTAAGAATATCAACGGATGCGTGAAGTTGTTTC	60		*****	
Ref	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120	N5	AACGAGAACTGTCTGACAACTCTATTTGACTGCTTCCCATCGTCGATCTTCTAAATCAT	540
S1	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120	N6	AACGAGAACTGTCTGACAACTCTATTTGACTGCTTCCCATCGTCGATCTTCTAAATCAT	540
S2	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120	N7	AACGAGAACTGTCTGACAACTCTATTTGACTGCTTCCCATCGTCGATCTTCTAAATCAT	540
S3	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120		*****	
N5	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120		*****	
N6	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120		*****	
N7	TTCCGAAAAATAAAATTTGATAGGATAATGATACTATCSTGGACAATGTCGFTGGAAT	120		*****	
Ref	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180	S1	GACTACCGTCCCAAAGTCAAATGGTATCCCTGAAATGGTGGTCTCTGTATGAAAAATC	600
S1	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180	S2	GACTACCGTCCCAAAGTCAAATGGTATCCCTGAAATGGTGGTCTCTGTATGAAAAATC	600
S2	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180	S3	GACTACCGTCCCAAAGTCAAATGGTATCCCTGAAATGGTGGTCTCTGTATGAAAAATC	600
S3	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180	N5	GACTACCGTCCCAAAGTCAAATGGTATCCCTGAAATGGTGGTCTCTGTATGAAAAATC	600
N5	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180	N6	GACTACCGTCCCAAAGTCAAATGGTATCCCTGAAATGGTGGTCTCTGTATGAAAAATC	600
N6	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180	N7	GACTACCGTCCCAAAGTCAAATGGTATCCCTGAAATGGTGGTCTCTGTATGAAAAATC	600
N7	GATAAATTTAAACCTTACTTGGATGCATTTGCCCTCCGCGCTAAATTCGCCCTTGGCTGG	180		*****	
Ref	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	Ref	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
S1	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	S1	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
S2	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	S2	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
S3	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	S3	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
N5	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	N5	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
N6	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	N6	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
N7	AACCCAAAGCGAGTTGAAGCGTTTATCATCTCAACAACATAGGGAATTCGATTCATGAAAAG	240	N7	GGTACCGCTCCCAATCAAGAGAACTCAATAAATTTGGCGTAAAGGAAATGAGGAG	660
Ref	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300	S1	TTACTCTCTGGATATGGATTTGTTTTAGAAGACAACATATTTGACTCAGTGGCTTTGAAA	720
S1	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300	S2	TTACTCTCTGGATATGGATTTGTTTTAGAAGACAACATATTTGACTCAGTGGCTTTGAAA	720
S2	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300	S3	TTACTCTCTGGATATGGATTTGTTTTAGAAGACAACATATTTGACTCAGTGGCTTTGAAA	720
S3	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300	N5	TTACTCTCTGGATATGGATTTGTTTTAGAAGACAACATATTTGACTCAGTGGCTTTGAAA	720
N5	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300	N6	TTACTCTCTGGATATGGATTTGTTTTAGAAGACAACATATTTGACTCAGTGGCTTTGAAA	720
N6	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300	N7	TTACTCTCTGGATATGGATTTGTTTTAGAAGACAACATATTTGACTCAGTGGCTTTGAAA	720
N7	TTCCGAGGTATATTTAAAGAGTGGTTTGAAGTGGTCAAGTCTTCCAGATATGTTGACTTG	300		*****	
Ref	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	Ref	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
S1	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	S1	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
S2	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	S2	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
S3	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	S3	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
N5	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	N5	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
N6	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	N6	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
N7	GAAGAGTGGCAGATGATGTCGAGACCTTCCCAATCTCGATGAGTTGACATAGAGGCT	360	N7	GTAAATGGCCATTAGATGTGGTATCTACAATCTTGAACAAGAACTAGTTTGAAGCTG	780
Ref	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420	S1	CCCTTACTTCGGATTACACCATTATGCTTTGAAAAAAGAACTGTGTCCAGCAAGAA	840
S1	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420	S2	CCCTTACTTCGGATTACACCATTATGCTTTGAAAAAAGAACTGTGTCCAGCAAGAA	840
S2	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420	S3	CCCTTACTTCGGATTACACCATTATGCTTTGAAAAAAGAACTGTGTCCAGCAAGAA	840
S3	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420	N5	CCCTTACTTCGGATTACACCATTATGCTTTGAAAAAAGAACTGTGTCCAGCAAGAA	840
N5	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420	N6	CCCTTACTTCGGATTACACCATTATGCTTTGAAAAAAGAACTGTGTCCAGCAAGAA	840
N6	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420	N7	CCCTTACTTCGGATTACACCATTATGCTTTGAAAAAAGAACTGTGTCCAGCAAGAA	840
N7	TTGTATGAGAGATTTTGAAGATACAGAACTTCAAAGACCAACTATCTGGTATTCCTTT	420		*****	
Ref	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	Ref	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900
S1	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	S1	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900
S2	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	S2	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900
S3	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	S3	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900
N5	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	N5	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900
N6	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	N6	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900
N7	CTCGCATTTTTATGGTCGACCTTATATTCATTTCAAAGAGCAATCCCTGAAATATGPGOTA	480	N7	AAGAAGGCTACTCGTAGTGTACAGACTACATCAATGGGGTGACTTACTTCATTAACATA	900

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Ref	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	Ref	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
S1	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	S1	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
S2	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	S2	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
S3	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	S3	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
N5	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	N5	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
N6	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	N6	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
N7	CAAAATGAACAATGTTTAGAACCACTTGGATCTTTTACCTACCTTTCTAAGGCCGAA	960	N7	MRFFGLSESTRNINWGLKLFPAKIKFDRDNDTIVDNVVRNDRFKFPVLDALPSRLNSPLW	60
Ref	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	Ref	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
S1	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	S1	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
S2	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	S2	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
S3	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	S3	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
N5	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	N5	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
N6	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	N6	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
N7	GAGGAGGATCTACAGATTGAGAGCCCGTTTGCAGGGTATACAAATGCTACGAAATGCA	1020	N7	NFSELKRLSSTNIGNSIHEKFEFIFKWFELVSSSDMFLERLVDVDTQPHNDELTYEA	120
Ref	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	Ref	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
S1	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	S1	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
S2	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	S2	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
S3	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	S3	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
N5	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	N5	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
N6	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	N6	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
N7	TTGCAGAGCAAACTCAACAGCATTACTGGACCACCTGCAACTGATGACTCTTATGCAATT	1080	N7	LYERILKITELRPTIYWSFFAFLMSHLIFISRAPEYVILNRNCPDNIIVLLPIVDLLNH	180
Ref	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	Ref	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
S1	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	S1	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
S2	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	S2	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
S3	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	S3	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
N5	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	N5	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
N6	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	N6	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
N7	GATCCTTACAGAGCTATTGTGCTGACGTTTATACTAAAGTCAAAAACAAATTTTAAAA	1140	N7	DYRSKVMYPENGFVCEKIGTASQSELSNYYGGKGNELLSSGYGFVLEDNI FDSVALK	240
Ref	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	Ref	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
S1	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	S1	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
S2	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	S2	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
S3	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	S3	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
N5	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	N5	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
N6	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	N6	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
N7	GAGCGTTTAAACGAGGTTGAAAAAATAGAAAAACAATGCTGTGACAGAACCAAGCACCA	1200	N7	VKLELDVVTILETEPFLKPLLSDYTYAFENKDCVQKEKATRSATDINGVTVFINI	300
Ref	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	Ref	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
S1	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	S1	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
S2	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	S2	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
S3	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	S3	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
N5	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	N5	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
N6	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	N6	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
N7	TTGCTAACCATGAGCAAAATTCCTTAAAGAAAGACCCCTGCTTTGACAGAACTGAATACCT	1260	N7	ONEQCLEPFLDLFFYLKSAEEDLDHLRLRQIQMLRNALQSKLNSITGFPATDDSYAI	360
Ref	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	Ref	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420
S1	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	S1	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420
S2	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	S2	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420
S3	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	S3	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420
N5	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	N5	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420
N6	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	N6	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420
N7	TCGCTGTCAGCAACGAAAGTGGTGAAGAGGTCATCTTTGAATCTACTTATGATTATTG	1320	N7	DEYRVYCADVYTRGQRIKLEALTRKLRITLSENKHLTMSRILKDKDAFAETELP	420

Supplementary Fig. 1. Multiple sequence alignment of *RKM1* region of NFS and SFS strains of *S. fimicola* with respect to the *Saccharomyces cerevisiae*. Note: Symbol (\*) showing conserved sites, space and highlighted regions showing SNPs.

Supplementary Fig. 2. Multiple sequence alignment of amino acid sequence of *RKM1* protein of different strains of *S. fimicola* with respect to the *S. cerevisiae* amino acid sequence to observe the genetic variations. Symbol (\*) showing fully conserved sites, symbol (:): depicting conservation between groups of strongly similar properties, space and highlighted regions showing polymorphic sites.

Ref	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	Ref	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
N5	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	N5	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
N6	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	N6	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
N7	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	N7	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
S3	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	S3	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
S1	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	S1	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
S2	CTGAACGAAACCGGATCGTGGGAAGGTTAATTATCTGTATACCTTTAGAGATGGAAGTT	60	S2	AACGCCAATATCAAGAAATCTTAGAAGGTGAAGAAATAGTACTAGATTATATGATGTT	780
Ref	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	Ref	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
N5	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	N5	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
N6	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	N6	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
N7	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	N7	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
S3	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	S3	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
S1	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	S1	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
S2	TTGCAAGAAAGAACCGATGGGCGCTTACTTTAAAGTTTGGAAACAAACCAAGCGATATG	120	S2	TATAATAATGGTGAATTTGGCTCAACTAATACTTTTGGTCCAAATCTTGACAATTTCT	840
Ref	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	Ref	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
N5	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	N5	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
N6	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	N6	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
N7	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	N7	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
S3	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	S3	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
S1	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	S1	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
S2	AACGCGTAAATTTTTGGGATGATAAGTAACTGCAACTTTTAAACCCTCACTGTCCCT	180	S2	TGCCAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
Ref	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	Ref	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
N5	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	N5	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
N6	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	N6	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
N7	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	N7	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
S3	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	S3	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
S1	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	S1	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
S2	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	240	S2	TGCACAAATCCAGGTTTATGCAAACTGGCACTAAAGCAATGGAAGCGAATGGAGAGA	900
Ref	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	N6	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
N5	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	N7	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
N6	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	N5	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
N7	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	S2	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
S3	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	S3	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
S1	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	S1	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
S2	CAAAATGGTGGAGAAATTTACGCTGTAGCGACGCTCTTCCGAGTTTGATAAATTTGCCTAT	300	S2	-----LNETSWEGLIICILYEMEVLCERSRWAPYFKVWNKPSDM	40
Ref	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	N6	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
N5	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	N7	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
N6	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	S2	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
N7	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	S3	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
S3	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	S1	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
S1	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	S2	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
S2	ATTGCAAGCATATATAGTACTCTTTGATTGGAAATGCAAGATAGTAGTGTAAAT	360	S3	NALIFWDDNELQLLPSLVERIGKKEAKEMHERIIRSIKQIGGEPFSRVATSFEDNFAY	100
Ref	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	N6	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
N5	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	N7	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
N6	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	N5	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
N7	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	S2	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
S3	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	S3	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
S1	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	Ref	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
S2	GAAGAANTGAAAAAGGAAAGCCAAAGAGATGCATGAAGAATTTAATCAATCAAA	420	S1	IASIILSYSFLEMQDSSVNEEEEESEELNERNVLSMIFLADLNADTSKCNANLT	160
Ref	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	N6	YDNSCLMVALRDIEKNEQVYNIYGEHNSLLRRYGVVWDGSKYDFGVEVLENIVEA*	219
N5	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	N7	YDNSCLMVALRDIEKNEQVYNIYGEHNSLLRRYGVVWDGSKYDFGVEVLENIVEA*	219
N6	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	N5	YDNSCLMVALRDIEKNEQVYNIYGEHNSLLRRYGVVWDGSKYDFGVEVLENIVEA*	219
N7	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	S3	YDNSCLMVALRDIEKNEQVYNIYGEHNSLLRRYGVVWDGSKYDFGVEVLENIVEA*	220
S3	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	S1	YDNSCLMVALRDIEKNEQVYNIYGEHNSLLRRYGVVWDGSKYDFGVEVLENIVEA*	220
S1	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	Ref	YDNSCLMVALRDIEKNEQVYNIYGEHNSLLRRYGVVWDGSKYDFGVEVLENIVEA*	220
S2	ATGATCCCACTTGCCTGATATGTTGAAGTCAAGATACCAAGTAAATGCAACGCTAAATTAAC	480	N6	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	279
Ref	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	N7	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	279
N5	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	N5	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	279
N6	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	S3	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	280
N7	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	S1	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	280
S3	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	Ref	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	280
S1	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	N6	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	280
S2	TACGACTCTAACTGTTTAAAGATGGTGTCTTTGAGGATATTGAAAAGATGAACAAGTG	540	N7	KETFETNTEFLDRCIDILRNANIQFLEGESEIVLSDYDCYNNSELLPQLILLVQILITL	280
Ref	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	Ref	KQIFGLKLDIKAMERQVER-----	299
N5	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	N5	KQIFGLKLDIKAMERQVER-----	299
N6	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	S2	KQIFGLKLDIKAMERQVER-----	300
N7	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	S3	KQIFGLKLDIKAMERQVER-----	300
S3	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	Ref	KQIFGLKLDIKAMERQVERIVKQKLLQLEGARATTCNSATWKRIMKRLADYPIKQVCS	340
S1	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	S1	KQIFGLKLDIKAMERQVER-----	300
S2	TACAACATATACGGAGAACATCCAAATTCGGAACACTAAGAAGATATGGGTATGTTGAA	600	Ref	KQIFGLKLDIKAMERQVER-----	300
Ref	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	Ref	KQIFGLKLDIKAMERQVER-----	300
N5	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	S1	KQIFGLKLDIKAMERQVER-----	300
N6	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	Ref	KQIFGLKLDIKAMERQVER-----	300
N7	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	Ref	KQIFGLKLDIKAMERQVER-----	300
S3	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	Ref	KQIFGLKLDIKAMERQVER-----	300
S1	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	Ref	KQIFGLKLDIKAMERQVER-----	300
S2	TGGGACGGTTCGAAGTATGATTTTGGAGAAAGTGTACTTGAATAATTTGCGAGGCGTTA	660	Ref	KQIFGLKLDIKAMERQVER-----	300
Ref	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	Ref	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720
N5	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	N5	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720
N6	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	N6	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720
N7	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	N7	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720
S3	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	S3	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720
S1	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	S1	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720
S2	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720	S2	AAAGAGACTTTTGGAGCAATCTGAATTTTGGACAGGTGATGATATCTTACGCCAAT	720

**Supplementary Fig. 3.** Multiple sequence alignment of RKM4 region of *S. fimicola* strains with respect to *S. cerevisiae* in order to observe single nucleotide polymorphism (SNP). Note: Symbol (\*) is showing fully conserved sites, space and highlighted regions showing SNPs.

**Supplementary Fig. 4.** Multiple sequence alignment of amino acid sequence of RKM4 protein of different strains of *S. fimicola* with respect to the reference strain *S. cerevisiae* amino acid sequence to spot genetic diversity. Symbol (\*) showing conserved sites, space and highlighted regions showing polymorphic sites.