

AvrL2-A	ATGGGCAAAGGAAATAACATTCAAACGCCGTGCTTTCGTGCATCTCAACTTCGAAGCTTT	60
sc8713_1	-----	0
sc8713_2	ATGGGCAAAGGAAATAACATTCAAACGCCGTGCTTTCGTGCATCTCAACTTCGAAGCTTT	3146
AvrL2-A	TGTTTAATTGCTTTCCTTATTGTGTCAATCCCTTCAATCCATCGTCTCACTGCCAGCACTT	120
sc8713_1	-----	0
sc8713_2	TGTTTAATTGCTTTCCTTATTGTGTCAATCCCTTCAATCCATCGTCTCACTGCCAGCACTT	3206
AvrL2-A	TCCTCCAAAGTGGAGTTGTCAGCACAAAAAATTAAGGTACAAGCACGGGTGAATCAGTTT	180
sc8713_1	-----AATCAGTTT	9
sc8713_2	TCCTCCAAAGTGGAGTTGTCAGCACAAAAAATTAAGGTACAAGCACGGGTGAATCAGTTT	3266
AvrL2-A	GTGAGAGAAAACAACCGTCCCCCTCGTCGAAGTGAACGATGTCATCCTTAGCCAGGAA	240
sc8713_1	GTGAGAGAAAACAACCGTCCCCCTCGTCGAAGTGAACGATGTCATCCTTAGCCAGGAA	69
sc8713_2	GTGAGAGAAAACAACCGTCCCCCTCG-----	3292
AvrL2-A	AATCTCAAACGAAAGCAGGTAAGCAATAAGACTTATATCACTATCACTATCTGAGCACT	300
sc8713_1	AATCTCAAACGAAAGCAGGTAAGCAATAAGACTTATATCACTATCACTATCTGAGCACT	129
sc8713_2	-----	3292
AvrL2-A	GATCCCAATCTTCTTCGACGCGGGTATCCAGGTTATCTTCCCCGCAATCGTCAACGTCG	360
sc8713_1	GATCCCAATCTTCTTCGACGCGGGTATCCAGGTTATCTTCCCCGCAATCGTCAACGTCG	189
sc8713_2	-----	3292
AvrL2-A	CACGAGGACAATTGGGAACTCTTGACAAGGAAATTGAGGAATATCGCAATGGCAAAAGT	420
sc8713_1	CACGAGGACAATTGGGAACTCTTGACAAGGAAATTGAGGAATATCGCAATGGCAAAAGT	249
sc8713_2	-----	3292
AvrL2-A	TTCAAGGTGGAAGATTTGCCTAAGGAAGAAGAACTCGTCAAATATAAAGCTGATGAGGTG	480
sc8713_1	TTCAAGGTGGAAGATTTGCCTAAGGAAGAAGAACTCGTCAAATATAAAGCTGATGAGGTG	309
sc8713_2	-----	3292
AvrL2-A	CCTCCTCCACGTTATGATGATTATTTTCATTAAACCCCTAAATGA	525
sc8713_1	CCTCCTCCACGTTATGATGATTATTTTCATTAAACCCCTAAATGA	354
sc8713_2	-----	3292
AvrL2-B	ATGTTACTAGTGCGGCATATGCCCTTCCTGACACCGTGCTTTCGTGCATCTCAACTTCGA	60
sc4334	ATGTTACTAGTGCGGCATATGCCCTTCCTGACACCGTGCTTTCGTGCATCTCAACTTCGA	11780
AvrL2-B	AGCTTTTGTTTAATTGCTTTCCTTATTGTGTCAATCCCTTCAATCCATCGTCTCACTGCCA	120
sc4334	AGCTTTTGTTTAATTGCTTTCCTTATTGTGTCAATCCCTTCAATCCATCGTCTCACTGCCA	11720
AvrL2-B	GCACTTCCCTCCAAAGTGGAGTTGTCAGCACCAAGAATTAAGGCACAAGCACGGGTGAAT	180
sc4334	GCACTTCCCTCCAAAGTGGAGTTGTCAGCACCAAGAATTAAGGCACAAGCACGGGTGAAT	11660
AvrL2-B	CAGTTTGTGAGAGAAAACAACCGTCCCCCTCGTCGAAGTGAACCAATGCCATCCTTCGC	240
sc4334	CAGTTTGTGAGAGAAAACAACCGTCCCCCTCGTCGAAGTGAACCAATGCCATCCTTCGC	11600
AvrL2-B	CAGGAAAATCTCAAACGTAACGCAGGTAAGCAATAAGACTTATATCACTATCACTATCTG	300
sc4334	CAGGAAAATCTCAAACGTAACGCAGGTAAGCAATAAGACTTATATCACTATCACTATCTG	11540
AvrL2-B	AGCACTGATCCCAATCTTCTTCGACGCGGGTATCCAGGTTATCTTCCCCGCAATCGTCA	360
sc4334	AGCACTGATCCCAATCTTCTTCGACGCGGGTATCCAGGTTATCTTCCCCGCAATCGTCA	11480
AvrL2-B	ACGTCGCACGAGGACAATTGGGAACTCTTGACAAGGAAATTGAGGAATATCGCAATGGC	420
sc4334	ACGTCGCACGAGGACAATTGGGAACTCTTGACAAGGAAATTGAGGAATATCGCAATGGC	11420
AvrL2-B	AAAAGTTTCAAGGTGGAAGATTTGCCTAAGGAAGAAGAACTCGTCAAATATAAAGCTGAT	480
sc4334	AAAAGTTTCAAGGTGGAAGATTTGCCTAAGGAAGAAGAACTCGTCAAATATAAAGCTGAT	11360
AvrL2-B	GAGGTGCCTCCTCCACGTTATGATGATTATTTTCATTAAACCCCTAAATGA	531
sc4334	GAGGTGCCTCCTCCACGTTATGATGATTATTTTCATTAAACCCCTAAATGA	11309

<i>AvrL2-C</i>	ATGGGCAAAGGAAATAACATTCAAACGCCGTCCTTTTCGTGCATCTCGACTTCGAAGCTTT	60
<i>AvrL2-D</i>	ATGGGCAAAGGAAATAACATTCAAACGCCGTCCTTTTCGTGCATCTCGACTTCGAAGCTTT	60
<i>sc275_1</i>	ATGGGCAAAGGAAATAACATTCAAACGCCGTCCTTTTCGTGCATCTCGACTTCGAAGCTTT	11646
<i>sc275_2</i>	ATGGGCAAAGGAAATAACATTCAAACGCCGTCCTTTTCGTGCATCTCGACTTCGAAGCTTT	16625
<i>AvrL2-C</i>	TGTTTAATCGCTTTCTTATTGTGTCAATCACTTCAATCTATCGTCTCACTACCAAAAAATT	120
<i>AvrL2-D</i>	TGTTTAATCGCTTTCTTATTGTGTCAATCACTTCAATCTATCGTCTCACTACCAACAATT	120
<i>sc275_1</i>	TGTTTAATCGCTTTCTTATTGTGTCAATCACTTCAATCTATCGTCTCACTACCAAAAAATT	11586
<i>sc275_2</i>	TGTTTAATCGCTTTCTTATTGTGTCAATCACTTCAATCTATCGTCTCACTACCAAAAAATT	16565
<i>AvrL2-C</i>	TCCCCTGCTGAGGTGTGTCAGCATTGAAAACTCGCGTACGAGCACGGTTGGATCAGTTTTGC	180
<i>AvrL2-D</i>	TCCCCTGCTGAGGTGTGTCAGCATTGAAAACTCGCGTACGAGCACGGTTGGATCAGTTTTGC	180
<i>sc275_1</i>	TCCCCTGCTGAGGTGTGTCAGCATTGAAAACTCGCGTACGAGCACGGTTGGATCAGTTTTGC	11526
<i>sc275_2</i>	TCCCCTGCTGAGGTGTGTCAGCATTGAAAACTCGCGTACGAGCACGGTTGGATCAGTTTTGC	16505
<i>AvrL2-C</i>	AGAGAACAAGGCTATAGACCTGAAAACAGTCAATTCTTTGCCATCCTT-----	228
<i>AvrL2-D</i>	AGAGAACAAGGCTATAGACCTGAAGACAGTCAATTCTTTGCCATCGTT-----	228
<i>sc275_1</i>	AGAGAACAAGGCTATAGACCTGAAGACAGTCAATTCTTTGCCATCGTTTCNGTACTTTTTG	11466
<i>sc275_2</i>	AGAGAACAAGGCTATAGACCTGAAACAGTCAATTCTTTGCCATCCTT-----	16457
<i>AvrL2-C</i>	-----	228
<i>AvrL2-D</i>	-----	228
<i>sc275_1</i>	ATATTAGTCTGTATGTTTTTTTCAATATGCCACTTGCAGAGTAGGTGATGTGAATGTGGG	11406
<i>sc275_2</i>	-----	16457
<i>AvrL2-C</i>	-----	228
<i>AvrL2-D</i>	-----	228
<i>sc275_1</i>	AGTACATGATTCAAACATTTCATTAAGGCTAACTCTCGATCGGTACAAACAGCGCTTATC	11346
<i>sc275_2</i>	-----	16457
<i>AvrL2-C</i>	-----CGCGAGGAATATGCGCAGATCAAACCGCAATTTGGA	264
<i>AvrL2-D</i>	-----CGCGAGGAATATGCGCAGATCAAACCGCAATTTGGA	264
<i>sc275_1</i>	TGTAGTGACTTTGAGCCCAAGGANC GCGAGGAATATGCGCAGATCAAACCGCAATTTGGA	11286
<i>sc275_2</i>	-----CGCGAGGAATATGCGCAGATCAAACCGCAATTTGGA	16421
<i>AvrL2-C</i>	CACGCGCAGTACGCTCCAGCACACTCGCGCGACTCAGCTCCAAGTCACCAGGCAGAACAG	324
<i>AvrL2-D</i>	CACGCGCAGTACGCTCCAGCACACTCGCGCGACTCAGCTCCAAGTCACCAGGCAGAACAG	324
<i>sc275_1</i>	CACGCGCAGTACGCTCCAGCACACTCGCGCGACTCAGCTCCAAGTCACCAGGCAGAACAG	11226
<i>sc275_2</i>	CACGCGCAGTACGCTCCAGCACACTCGCGCGACTCAGCTCCAAGTCACCAGGCAGAACAG	16361
<i>AvrL2-C</i>	AATTATGGCACAGGTAAGCAATAAGACTTAAATCACTATCACTATCTGAGCACTAATCCC	384
<i>AvrL2-D</i>	AATTATGGCACAGGTAAGCAATAAGACTTAAATCACTATCACTATCTGAGCACTAATCCC	384
<i>sc275_1</i>	AATTATGGCACAGGTAAGCAATAAGACTTAAATCACTATCACTATCTGAGCACTAATCCC	11166
<i>sc275_2</i>	AATTATGGCACAGGTAAGCAATAAGACTTAAATCACTATCACTATCTGAGCACTAATCCC	16301
<i>AvrL2-C</i>	AATCTTCTTCGACGTGGGTTTCCAGGTGTTTTTCCCTCGCGAGTGACCCAGGCATTGAA	444
<i>AvrL2-D</i>	AATCTTCTTCGACGTGGGTTTCCAGGTGTTTTTCCCTCGCGAGTGACCCAGGCATTGAA	444
<i>sc275_1</i>	AATCTTCTTCGACGTGGGTTTCCAGGTGTTTTTCCCTCGCGAGTGACCCAGGCATTGAA	11106
<i>sc275_2</i>	AATCTTCTTCGACGTGGGTTTCCAGGTGTTTTTCCCTCGCGAGTGACCCAGGCATTGAA	16241
<i>AvrL2-C</i>	GATTGGGAAAAAAGAAATGCACGACCAAGATTGGGAACATTATGAACGTGCCATTGTGGAG	504
<i>AvrL2-D</i>	GATTGGGAAAAAAGAAATGCACGACCAAGATTGGGAACATTATGAACGTGCCATTGTGGAG	504
<i>sc275_1</i>	GATTGGGAAAAAAGAAATGCACGACCAAGATTGGGAACATTATGAACGTGCCATTGTGGAG	11046
<i>sc275_2</i>	GATTGGGAAAAA-----	16230
<i>AvrL2-C</i>	TTTATGAATGACAAAGGTATTTGGCTGCCTGATATTGATGAGGTCCACGGTATTCGCCCG	564
<i>AvrL2-D</i>	TTTATGAATGACAAAGGTGCTTGGCTGCCTGATATTGATGAGGTCCACGGTATTCGCCCG	564
<i>sc275_1</i>	TTTATGAATGACAAAGGTGCTTGGCTGCCTGATATTGATGAGGTCCACGGTATTCGCCCG	10986
<i>sc275_2</i>	-----	16230
<i>AvrL2-C</i>	CCTGAACCTTATATTTTTTTCATCCCAAAAAAATTAG	600
<i>AvrL2-D</i>	CCTGAACCTTATATTTTTTTCATCCCAAAAAAATTAG	600
<i>sc275_1</i>	CCTGAACCTTATATTTTTTTCATCCCAAAAAAATTAG	10950
<i>sc275_2</i>	-----	16230

Additional file 15. *AvrL2* family DNA sequences.

Alignment of *AvrL2* coding regions with their closest matching scaffolds in the *M. lini* genome assembly. Polymorphic nucleotides are shaded blue.

Note that sc4334 and sc8713 are short scaffolds of 13,347 bp and 3,292 bp, respectively, suggesting that they might be located in a repetitive region of the genome that is difficult to assemble. Also sc8713 contains partial coding regions at the 5' and 3' ends of the scaffold that are homologous to the candidate identified on sc4334, which is characteristic of scaffolds formed from collapsed repeats.