

	C34-1		
sc27	CACATTGATCCCGTTCATAAC	ATATTTCTACATAACCTTCCCTCACGATATTCGCTCTTT	1582
AvrM14-A	-----	-----ATATTTCTACATAACCTTCCCTCACGATATTCGCTCTTT	39
AvrM14-B	-----	-----ATATTTCTACATAACCTTCCCTCACGATATTCGCTCTTT	39
sc27	CAAAAATGAAGTTTGGTATCATCTTTTTAGCCCTCTTCTTTGTCACTATCAGTCACGTTT		1642
AvrM14-A	CAAAAATGAAGTTTGGTATCATCTTTTTAGCCCTCTTCTTTGTCACTATCAGTCACGTTT		99
AvrM14-B	CAAAAATGAAGTTTGGTATCATCTTTTTAGCCCTCTTCTTTGTCACTATCAGTCACGTTT		99
sc27	TATGCGCCGGCAATAATGATCTT	AAAAATGTGAAGGCAATCGCGATAGTTTACAGGGAGC	1702
AvrM14-A	TATGCGCCGGCAATAATGATCTT	AAAAATGTGAAGGCAATCGCGATAGTTTACAGGGAGC	159
AvrM14-B	TATGCGCCGGCAATAATGATCTT	AAAAATGTGAAGGCAATCGCGATAGTTTACAGGGAGC	159
sc27	TCTCAGACGGGTCTCAGACAGTCTCCTGGCGAAAATGAAAGGCCTGGCGGACGAGAAAAG		1762
AvrM14-A	TCTCAGACGGGTCTCAGACAGTCTCCTGGCGAAAATGAAAGGCCTGGCGGACGAGAAAAG		219
AvrM14-B	TCTCAGACGGGTCTCAGACAGTCTCCTGGCGAAAATGAAAGGCCTGGCGGACGAGAAAAG		219
sc27	GATGGATGTTTGTAAAGAGGACATGTCCGGA	AGGACGAGGAGGCTGACCCTGGGGTCGCCG	1822
AvrM14-A	GATGGATGTTTGTAAAGAGGACATGTCCGGA	AGGACGAGGAGGCTGACCCTGGGGTCGCCG	279
AvrM14-B	GATGGATGTTTGTAAAGAGGACATGTCCGGA	AGGACGAGGAGGCTGACCCTGGGGTCGCCG	279
sc27	CGATACGCGAAACGCAGGAAGAAA	GTCAGTTAACAGACATTCCAGCCTTTTCAGAGAGCAA	1882
AvrM14-A	CGATACGCGAAACGCAGGAAGAAA	GTCAGTTAACAGACATTCCAGCCTTTTCAGAGAGCAA	339
AvrM14-B	CGATACGCGAAACGCAGGAAGAAA	GTCAGTTAACAGACATTCCAGCCTTTTCAGAGAGCAA	339
sc27	ACTTTGGAGCTTTACTAACCCTCAGTCCTTCTCGACATCAG	CCGGCTTTACAGGAATGGT	1942
AvrM14-A	ACTTTGGAGCTTTACTAACCCTCAGTCCTTCTCGACATCAG	CCGGCTTTACAGGAATGGT	399
AvrM14-B	ACTTTGGAGCTTTACTAACCCTCAGTCCTTCTCGACATCAG	CCGGCTTTACAGGAATGGT	399
sc27	GAAGAAAAGCGGCGCACC GTTCACCCAACCGGGTTCCAAAGATA	CTCAGCGTGTTCATCAC	2002
AvrM14-A	GAAGAAAAGCGGCGCACC GTTCACCCAACCGGGTTCCAAAGATA	CTCAGCGTGTTCATCAC	459
AvrM14-B	GAAGCAAAGCGGCGCACC GTTCACCCAACCGGGTTCCAAAGATC	CTCAGCGTGTTCATCAC	459
sc27	AATACACCCTCATATTGTCCAAGTTCAAGAGGCTTCAAAGTCTAAGGACACAGAAGACAC		2062
AvrM14-A	AATACACCCTCATATTGTCCAAGTTCAAGAGGCTTCA-----		496
AvrM14-B	AATACACCCTCATATTGTCCAAGTTCAAGAGGCTTCA-----		496
sc27	AGTCAAACGTCAATTTCTCTGGGTCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAG		2122
AvrM14-A	-----		496
AvrM14-B	-----		462
sc27	CGGCGCACC GTTCACCCAACCGGGTTCCAAAGATCCTCAGCGTGTTCACAAATACACCC		2182
AvrM14-A	-----		496
AvrM14-B	-----		496
sc27	TCATATTGTCCAAGTTCAAGAGGCTTCAAAGTCTAAGGACACAGAAGACACAGTCAAACG		2242
AvrM14-A	-----	-----AAGTCTAAGGACACAGAAGACACAGTCAAACG	528
AvrM14-B	-----	-----AAGTCTAAGGACACAGAAGACACAGTCAAACG	528
sc27	CGAATTTCTCTGGGTCCGCCCATCCGAGGTCCGAAGTAAGCTACAAAGGGCGGAAATGAT		2302
AvrM14-A	TCAATTTCTCTGGGTCCACCCATCCGAGGTCCGAAGTAAGCTACAAAGGGCGGAAATGAT		588
AvrM14-B	CGAATTTCTCTGGGTCCGCCCATCCGAGGTCCGAAGTAAGCTACAAAGGGCGGAAATGAT		588
sc27	TCAAGCCTGGGATCAACTACACAGCTTTTTCTGAGAAACCTCGATGAAGTAAGTGTGCA		2362
AvrM14-A	TCAAGCCTGGGATCAACTACACAGCTTTTTCTGAGAAACCTCGATGAAGTAAGTGTGCA		648
AvrM14-B	TCAAGCCTGGGATCAACTACACAGCTTTTTCTGAGAAACCTCGATGAAGTAAGTGTGCA		648
sc27	AGTGTTCTGAATTGCCGCGGATCCATGATTGAATATCAACTGATATAGGGTCGGCTGTAGG		2422
AvrM14-A	AGTGTTCTGAATTGCCGCGGATCCATGATTGAATATCAACTGATATAGGGTCGGCTGTAGG		708
AvrM14-B	AGTGTTCTGAATTGCCGCGGATCCATGATTGAATATCAACTGATATAGGGTCGGCTGTAGG		708
sc27	ACAACGCTAGGTAGAGAACCGGAACGGTTCTTTGTGGCTCGATCCTTTACCACCTCAGGC		2482
AvrM14-A	ACAACGCTAGGTAGAGAACCGGAACGGTTCTTTGTGGCTCGATCCTTTACCACCTCAGGC		768
AvrM14-B	ACAACGCTAGGTAGAGAACCGGAACGGTTCTTTGTGGCTCGATCCTTTACCACCTCAGGC		768
sc27	TACAGTATAAAACCTTTTATCAAAAGACGACTACTATTCAATCATTTAATT	CATTCCTTT	2542
AvrM14-A	TACAGTATAAAACCTTTTATCAAAAGACGACT-----		800
AvrM14-B	TACAGTATAAAACCTTTTATCAAAAGACGACT-----		800
	C34-4		
sc27	GTTCCGAAAATC	2554	
AvrM14-A	-----	800	
AvrM14-B	-----	800	

Additional file 12. *AvrM14* sequences.

Alignment of *AvrM14-A* and *AvrM14-B* with the corresponding region of sc27. Note that the scaffold sequence contains 171 bp of additional sequence that is not present in the *AvrM14-A* and *AvrM14-B* genes. It is likely that this additional sequence prevented gene prediction by the annotation pipeline used by Nemri et al. [1]. As a result, *AvrM14* is not present in the list of *M. lini* effectors predicted by these authors. The C34-1 and C34-4 primer sites are shaded green, polymorphic nucleotides are shaded blue and a 77 bp intron is shaded yellow. Start (ATG) and stop (TGA) codons are shown in bold type. The position of a polymorphic *BspEI* restriction site is also shown.

References

[1] Nemri A, Saunders DGO, Anderson C, Upadhyaya NM, Win J, Lawrence GJ, et al. The genome sequence and effector complement of the flax rust pathogen *Melampsora lini*. Front Plant Sci. 2014;5:98.