

RTM1	44	-----SAYKNNVEKPKQEEQQP
RTM2 - 2	1	MHQRTLKTQNSTETSQKTTQPSTNQKPNPEISEKKVDGRKRGRFSAYKNNVEKPKQYEEQQP
RTM1	61	VSTPLPSEENGKLLQEPQTVINKQPRPEAKEVPISNTSISQRSNSNDSSSLNQNNHQ
RTM2 - 2	61	VSTPLPSEENCNLLQEPQMVINQPRPEAKEVPISNTSISQRSNSNDSSSLKQNNHQ
		C C C H
RTM1	121	HRHSSISRQESKPTLQEPKPELPTSIDIGNKIWKLCRFDAGMNGCRNSSQDCKFIHLDLI
RTM2 - 2	121	HRHSSISRQESKPALQEPKPELPTSIDIGNKIWKLCRFDAGMNGCRNSSQDCKFIHLDLI
RTM1	181	EQVALSDKKKLANVAIWNWDQAKLDSKYQPSDKDLLNSWVNSNSNEGNPLFTKYKTMIEE
RTM2 - 2	181	EQVALSDKKKLANVAIWNWDQAKLDSKYQPSDKDLLNSWVNSNSNEGNPLFIKYKTMIEE
		* *
RTM1	241	KDPEFVQLTKDLTAEQMELEELQNAFQVKKQRYMSELSSRLRQKILSKSRQKAFDKLLSE
RTM2 - 2	241	KDPEFVQLTKDLTAEQMELEELQNAFQVKKQRYMSELSSRLRQKILFKSRQKAFDKLLSE
RTM1	301	SAQKRAAASEAALSQESSSIEYLPSPQKYSNRYPMIPHHKDQYLPPENSQYSSLQQQPK
RTM2 - 2	301	SAQKRTAASEAALSQESSSIEYLPSPQKYSNRYQMIPHHKEQYLPPENSQYSSLQQQPK
RTM1	361	SPIRTSQQQHYQQNNTQSYQPQHVAHNWNPTYQHQQSNNQRFEPSPYKPSYY
RTM2 - 2	361	SPIRTSQQQHYQQNNTQSYQPQHVAHNWNPTYQHQQSNNQRFEPSPYKPSYY

Figure A: Pair-wise alignment of REP-1 and REP 2-2 ORF1 amino acid sequences. In all multiple sequence alignments in this study black and grey backgrounds indicate invariant and similar amino acid residues respectively. The CCCH zinc-finger is indicated above the aligned sequence. An asterisk marks the first and last amino acid of the predicted coiled coil.