

<b>RNA1</b>	5'- 1	<b>AGUAGUGAACUCCCUUUAU..20</b>	7012.. <u><b>AUUAAGGGAGUUCACUACU</b></u>	7031 -3'
<b>RNA2</b>	5'- 1	<b>AGUAGUGAACUCCUCAUA...19</b>	2225.. <u><b>UUAUGAGGAGUUCACUACU</b></u>	2225 -3'
<b>RNA3</b>	5'- 1	<b>AGUAGUGAACUCCCAUA.....17</b>	1467..... <u><b>UAUGGGAGUUCACUACU</b></u>	1483 -3'
<b>RNA4</b>	5'- 1	<b>AGUAGUGAACUCCUUACAA...19</b>	1500... <u><b>UUGUAAGGAGUUCACUACU</b></u>	1518 -3'
<b>RNA5</b>	5'- 1	<b>AGUAGUGAACUCCCUAUA...19</b>	1315... <u><b>UUAUAGGGAGUUCACUACU</b></u>	1333 -3'

**Figure S1.** Nucleotide sequences of the terminal complementarity regions of the five RNA genome segments of the novel emaravirus (E55270) infecting ash species are shown. Strictly conserved 13 terminal nucleotides (represented by the PDAP213 primer) are shown in bold. Sequences confirmed by tailing PCR are underlined.