



Supplementary figure S6. MethGo analysis of bisulfite NGS data for C2MAPTR and β PTR coinfiltrated plant samples: A) Coverage map of ~3.2 million bisulfite NGS reads from C2MAPTR+ β PTR co-infiltrated plant sample. Y-axis represents the percentage of methylation sites covered in the genome. X-axis represents the depth of coverage (X) in multiples of fifty. B) The genome-wide methylation map showing the level of methylation at different regions of C2 mutant **BYVMV** and betasatellite.