



Supplementary Figure S4. MethGo analysis of Bisulfite NGS Data for C4MAPTR and β PTR coinfiltrated plant samples: A) Coverage map of ~2 million bisulfite NGS reads from C4MAPTR+ 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. High coverage (X) indicates high reliability of data. B) The genome wide methylation map showing the level of methylation at different regions of C4 mutant of BYVMV and betasatellite.