Apple replant disease has long been known as a major limitation to the establishment of new orchards on old orchard sites due to the long-term survival of soil-borne plant pathogens. A pathogen complex including necrotrophic fungi, oomycetes, and the root lesion nematode *Pratylenchus penetrans* functions as the primary cause of the disease in Washington State. Pre-plant soil fumigation continues to be the most common method employed by growers to control replant disease; however, problems arise as pathogen inoculum densities rebound quickly post-fumigation and the non-selective activity of fumigants may negatively affect the functional soil microbial community. Brassicaceous seed meal (SM) amendments can effectively control replant disease; however, significant material costs have limited commercial adoption of this practice. In the current study, a reduction in SM amendment rate from 6.6 t to 4.4 ha⁻¹ resulted in few significant differences in terms of disease control, composition of the soil microbiome and tree growth promotion in both greenhouse and field trials. Suppression of soil-borne pathogens such as *Pythium* spp. and *Pratylenchus penetrans* was improved when SM amendment was integrated with rootstock G.41 and G.210 relative to the Malling rootstocks. Functional annotation of differentially expressed genes (DEG) identified in roots of apple cultivated in SM amended soil indicated that both rootstock genotypes exhibited upregulation of DEGs that encoded proteins functioning in plant defense. In addition, gene regulation in plants cultivated in SM treated soil appeared to be associated with changes in composition of the rhizosphere microbiome. Findings from this study demonstrated that use of the appropriate apple rootstock genotype will allow for effective replant disease control at reduced SM application rate.