



Figure 2-figure supplement 1. Expression of the *BRUSH* native genomic sequence in *brush*. (A) Complementation assay in *brush* by transformation of *BRUSH*_{2kbpro}:*BRUSH*_{genomic} or empty vector relative to Gifu wild type. No infected nodules were observed in *brush* roots expressing the *BRUSH* genomic sequence. Shown are DsRED fluorescence of rhizobia (middle panel) and GFP fluorescence (lower panel) for transformation control. Composite plants were sown in Weck jars, cultivated at 26°C, and inoculated with *M. loti* expressing DsRed. Roots were analyzed four weeks after inoculation. (B) Box plot showing the number of nodules per transformed plant (n=8) from (A). (C) Close-up of transformed roots. Scale bars in (A) represent 2 mm, 0.2 mm in (C). Different letters in (B) indicate different statistical groups (ANOVA followed by Tukey's HSD test, $F_{(2, 21)} = 33.60$, p-value < 0.001).