

Figure S3 Spurious clustering of two segments in RR4049. (A) Schematic of inferred transformation intermediates. (B) Plot of donor-specific allele frequency against the recipient genome (top panel) and the donor genome (bottom panel); connecting lines between the plots show all syntenic SNV positions connecting the two references. The two donor segments in the top left appear to be ~50 kb apart but were derived from segments ~150 kb apart. A very similar pattern was seen for RR4050.