Figure S2:
Number of read in plipastatin biosynthesis operon region for both genomes.

(A) Mapping reads from BEST195 to the pps operon region of 168 reference genome:

(B) Mapping reads to the corresponding region in our BEST195 genome draft:
Vertical axis measures read-depth and horizontal axis enlarged the region of Marburg 168 genome in Mbp with horizontal arrows for 5 genes in the pps operon. Complete loss of BEST195 reads in ppsB and other regions with small levels of read-depth around 40-60 are apparent in (A). Small read-depth observed in ppsA (5'-end half), ppsC (5'-end half) and ppsD (3'-end half) are all attributed to highly repetitive sequences characteristic of those genes. Mapping reads to the corresponding region in our BEST195 genome draft gave a flat read-depth profile. Thus, only ppsD and ppsE genes are remained in BEST195.