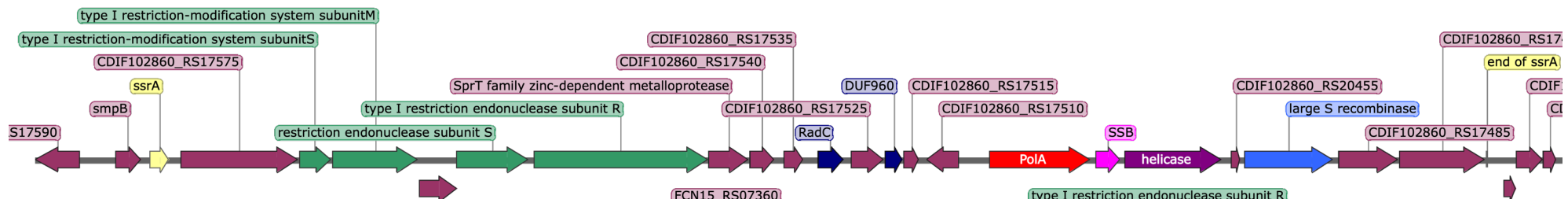
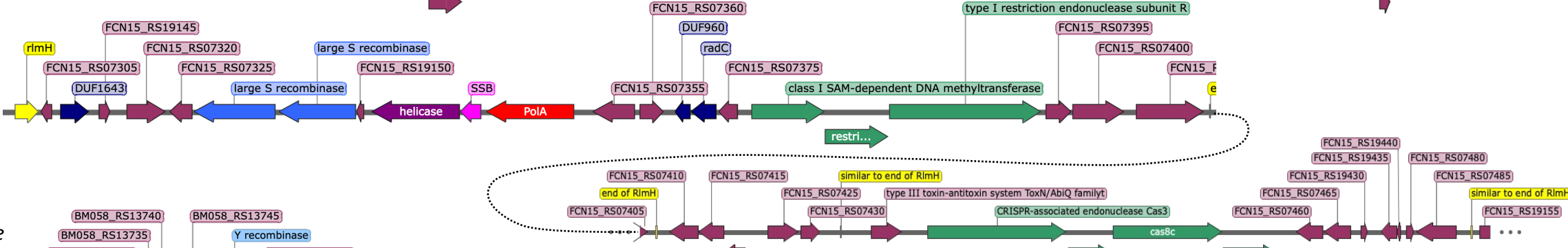


Figure S3. (legend on p4)

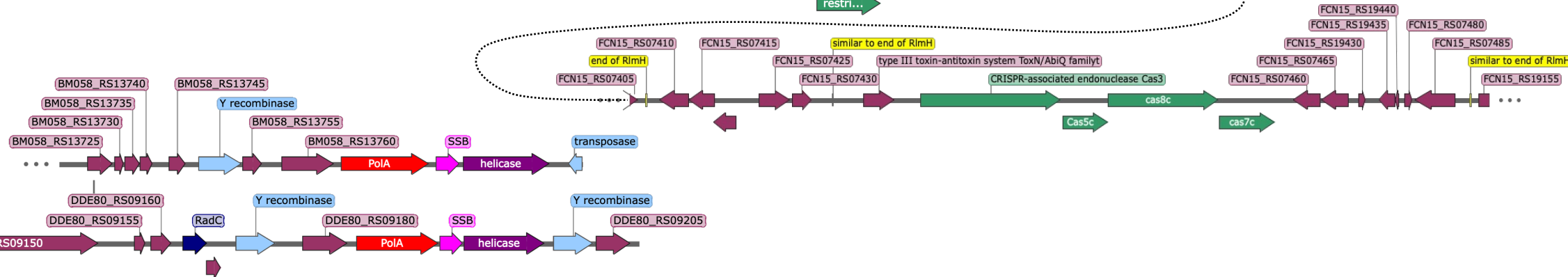
C. difficile



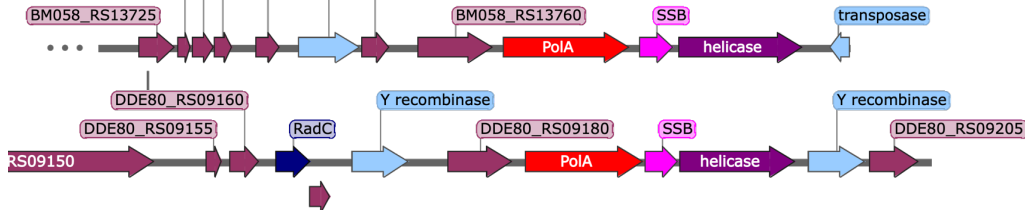
P. pinistramenti



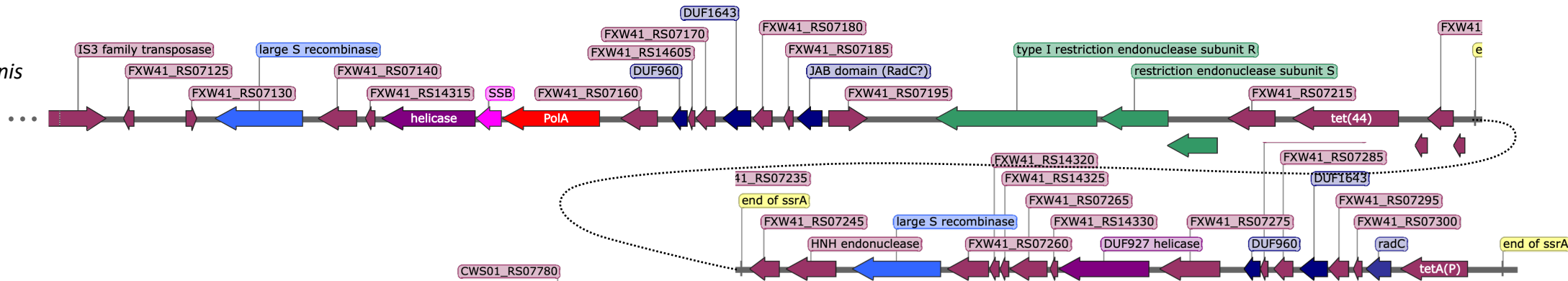
S. qingdaonense



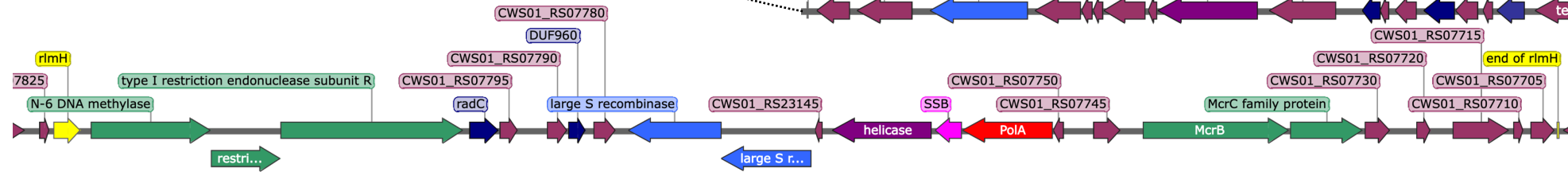
M. jejuensis



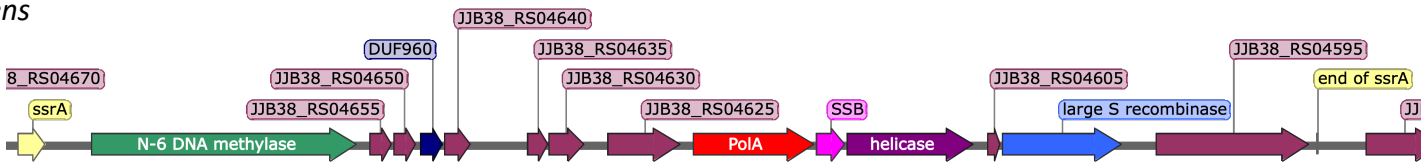
T. sanguinis



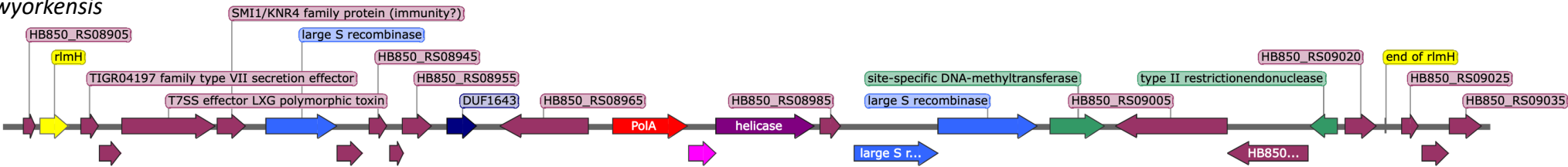
N. nealsonii



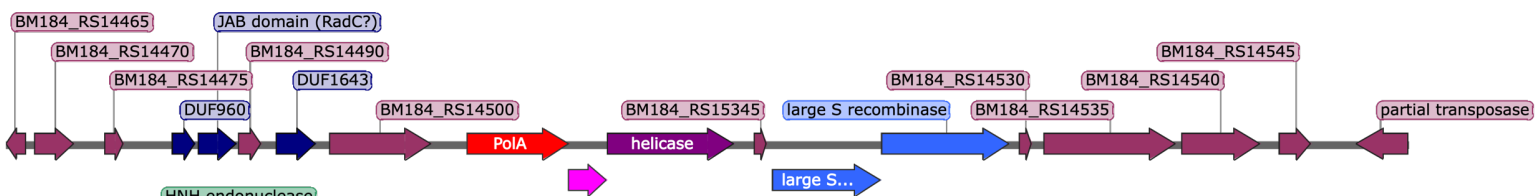
C. perfringens



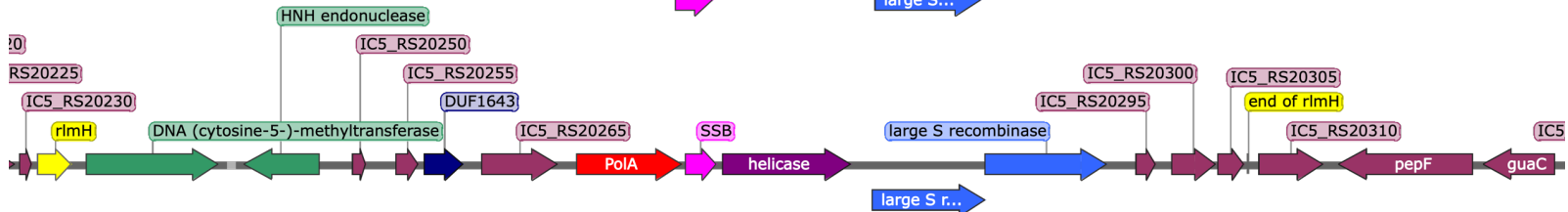
L. newyorkensis



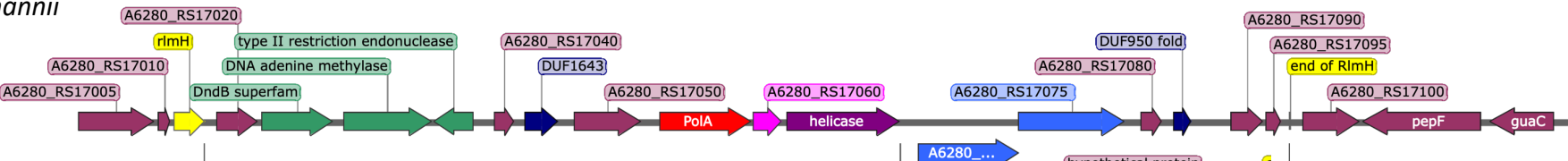
T. pasteurii



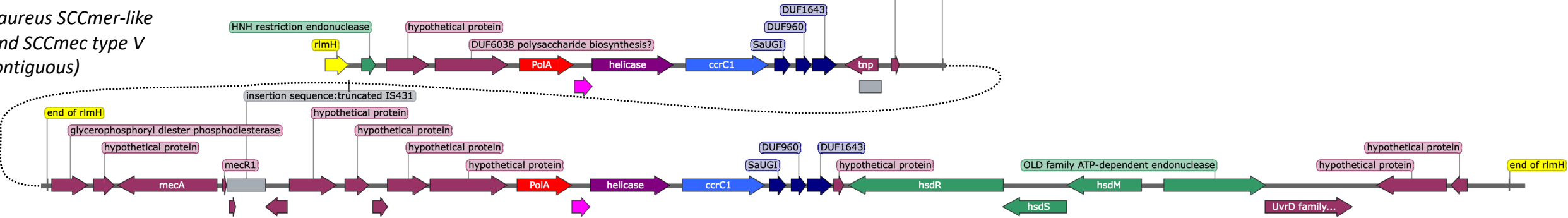
B. cereus



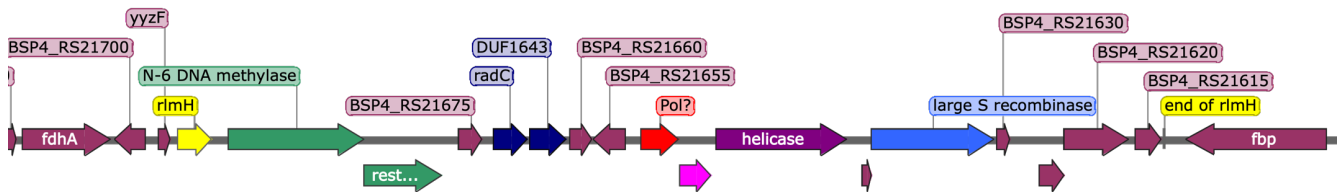
B. weidmannii



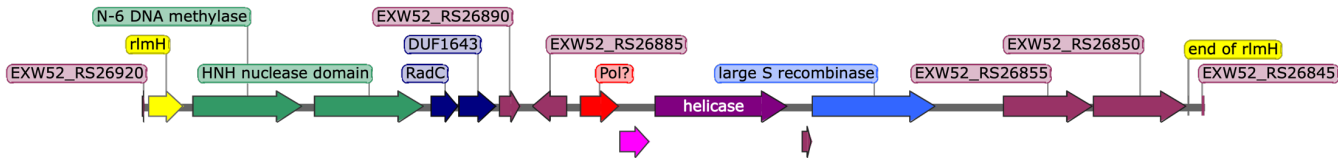
S. aureus SCCmer-like
and SCCmec type V
(contiguous)



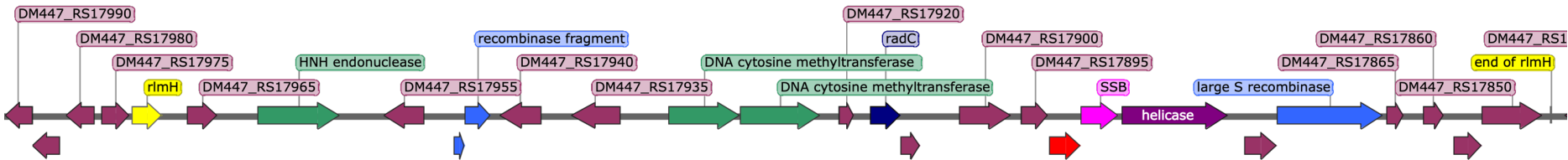
B. subtilis



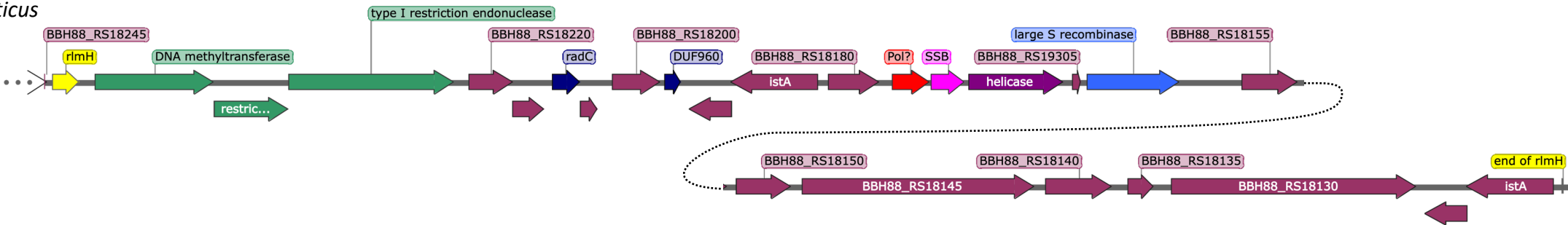
B. mycoides



P. zengyii



P. antarcticus



G. vulcani

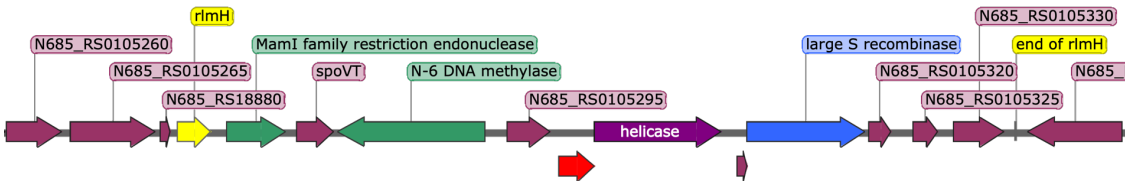


Figure S3. Genomic context of Pol-SSB pairs. Diagrams of the region encoding each pair are shown, colored to highlight relevant features (if found). Red, PolA (or minimal Pol-like protein); pink, SSB; purple, helicase; bright blue, large serine recombinase; yellow, putative insertion sites, pale blue, other recombinase possibly involved in mobility; dark blue, homology to genes found in the recombinase locus of SCC elements. For extremely long elements, dotted lines simply connect one segment to the next (they do not signify gaps). See table 1 for accession numbers.