

Figure S1.

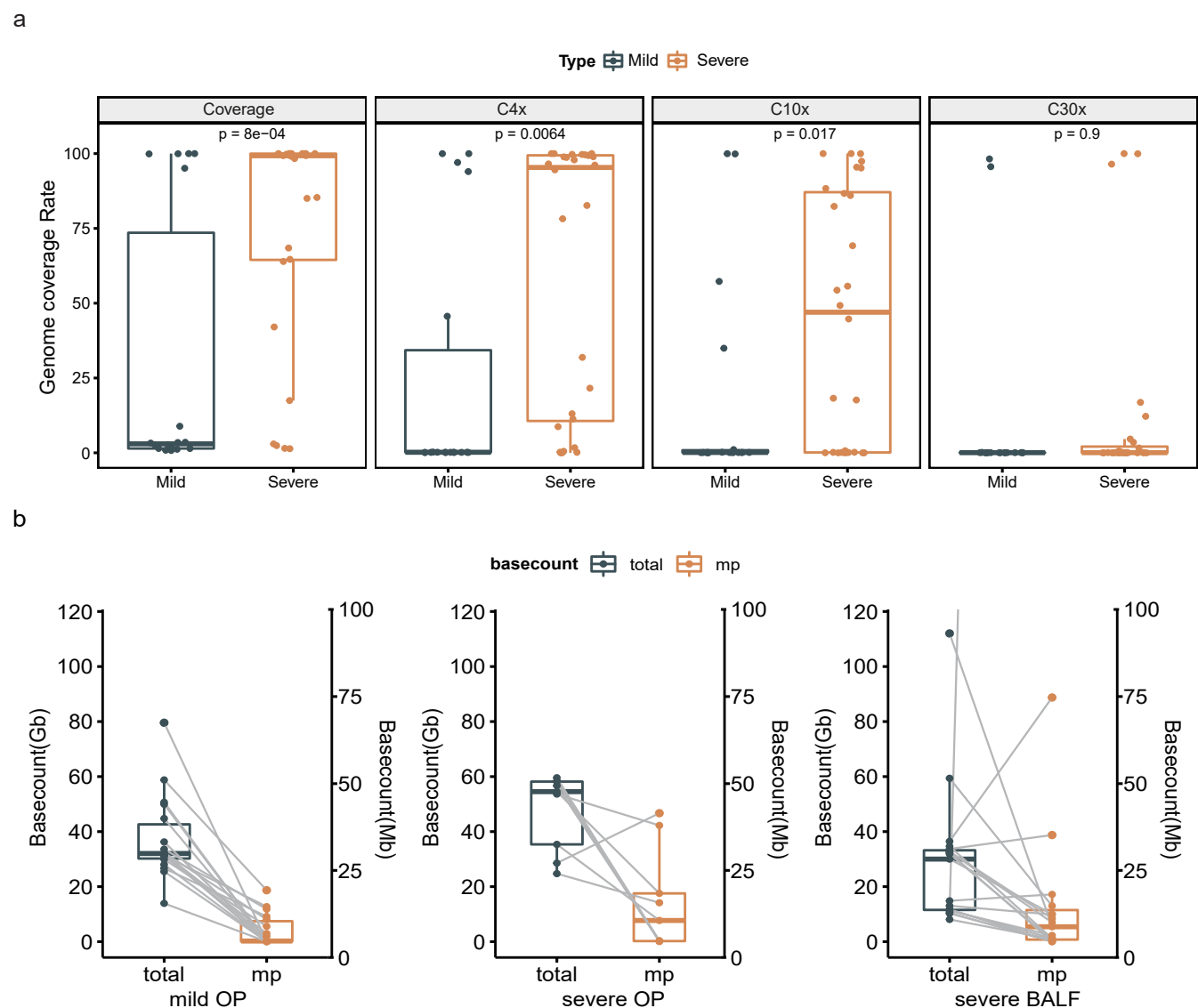


Figure S1. Evaluation of the *M. pneumoniae* genome obtained by metagenomic

sequencing. a. Genome coverage of *M. pneumoniae* achievable with samples from

patients with mild and severe symptoms. b. The relationship between the number of

M. pneumoniae bases and the total number of bases in whole metagenomic sequencing.