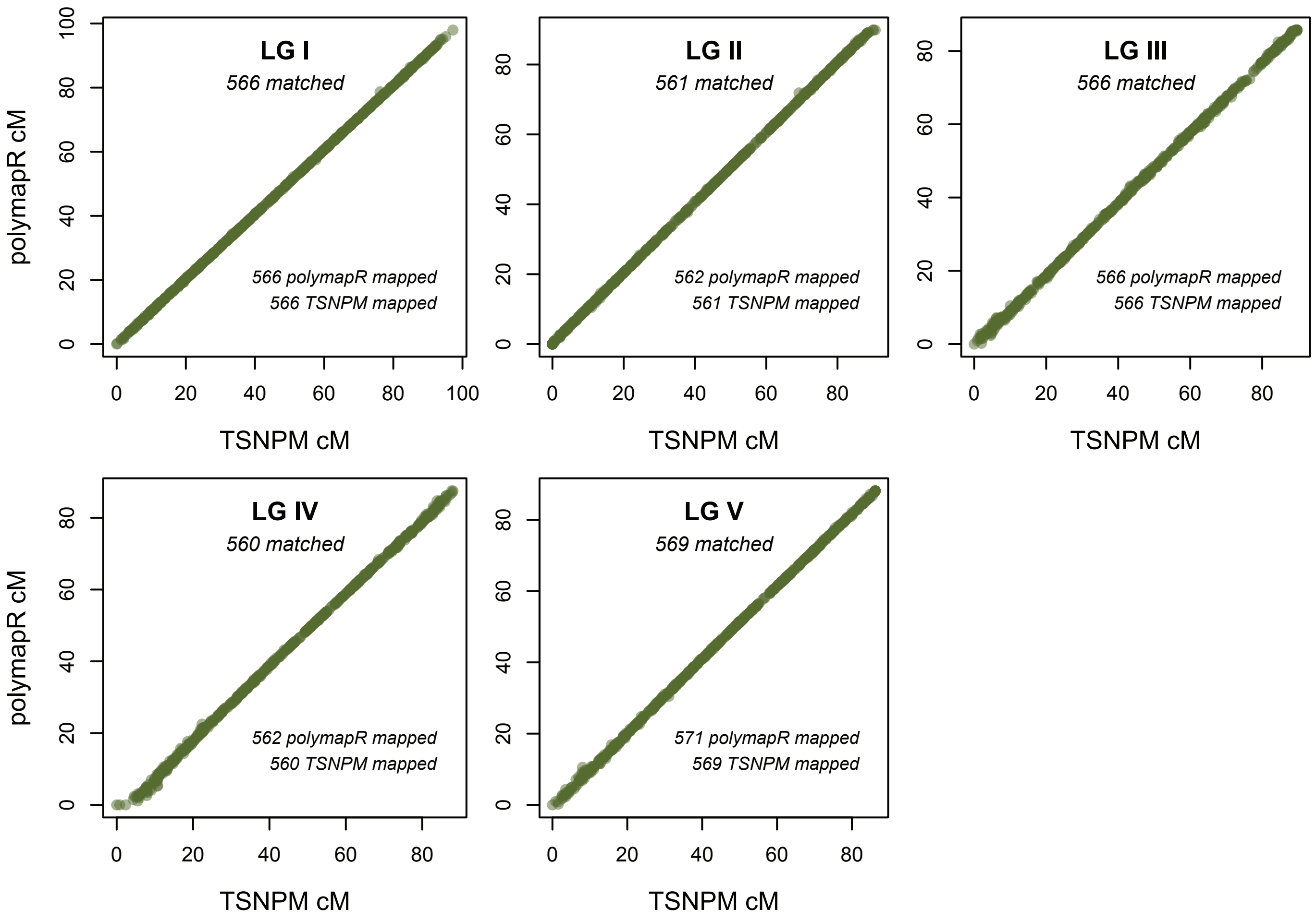
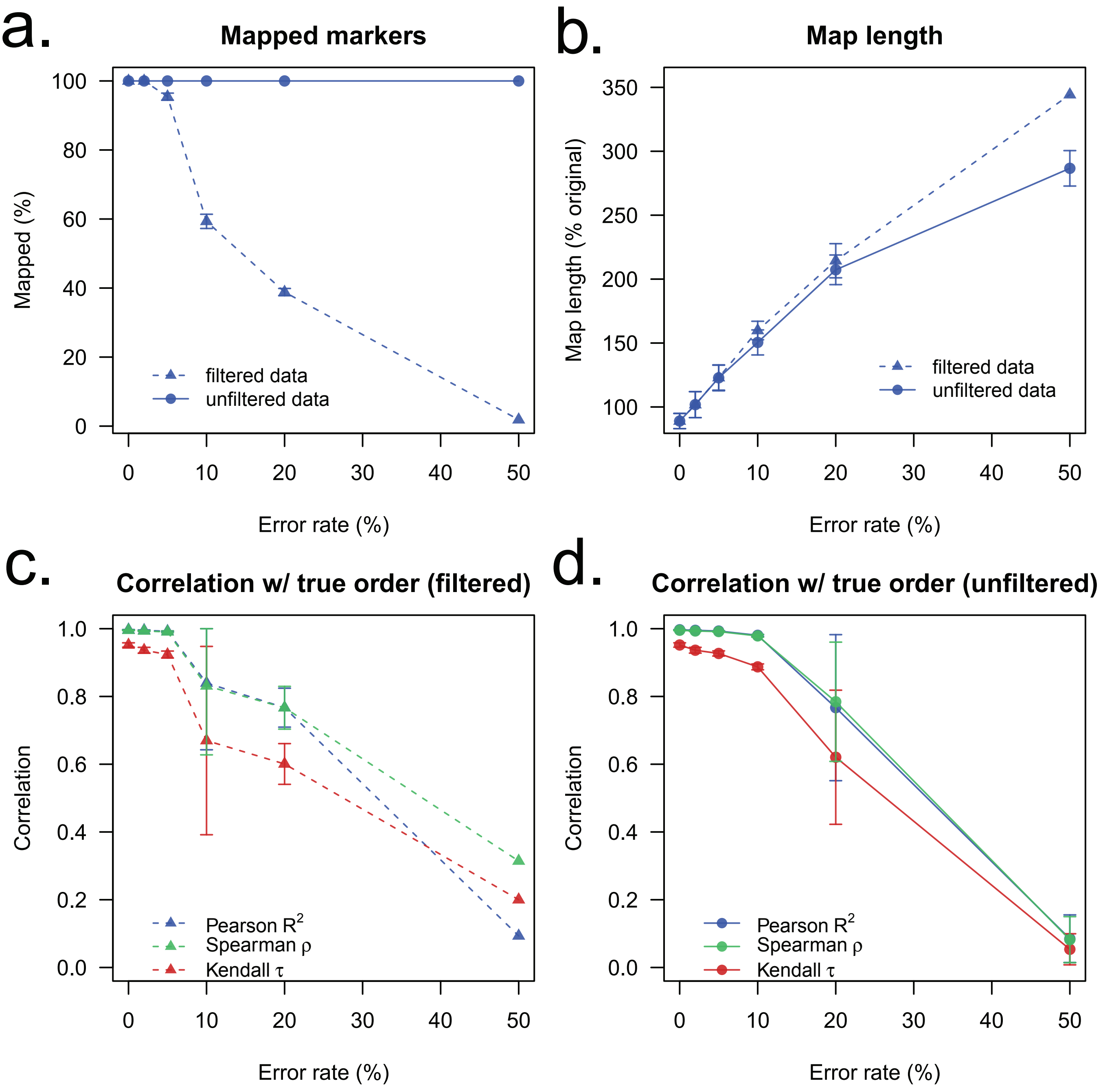


Supplementary Figure 1. Comparison of final linkage maps produced by polymapR (y-axis) and TetraploidSNPMap (x-axis) using the sample dataset provided with the polymapR package.
For all linkage groups, the marker order, map length and the number of mapped markers were almost identical between both software.



Supplementary Figure 2. Effect of genotyping errors on linkage map quality.
a. Rates of mapped markers at different error rates. Skewed markers (i.e. showing segregation distortion) or markers with poor concordance between parental and offspring scores can be detected and screened out in the early mapping steps of polymapR. At 50% random errors, almost all markers were removed prior to mapping (dashed line), and only 1 population produced a map. The user can also choose to keep “problematic” markers (solid line).
b. Map length increases with increasing numbers of genotyping errors.
c. & d. Errors can lead to poorer correlations between the true and estimated map orders, here using three of the most common correlation coefficients. Low error rates (< 5%) had almost no impact on the correctness of the maps produced. In this example, with random errors introduced into otherwise perfect simulated data, an error rate of 10% was tolerable (and suggests that filtering larger numbers of problematic markers might not always improve map quality).