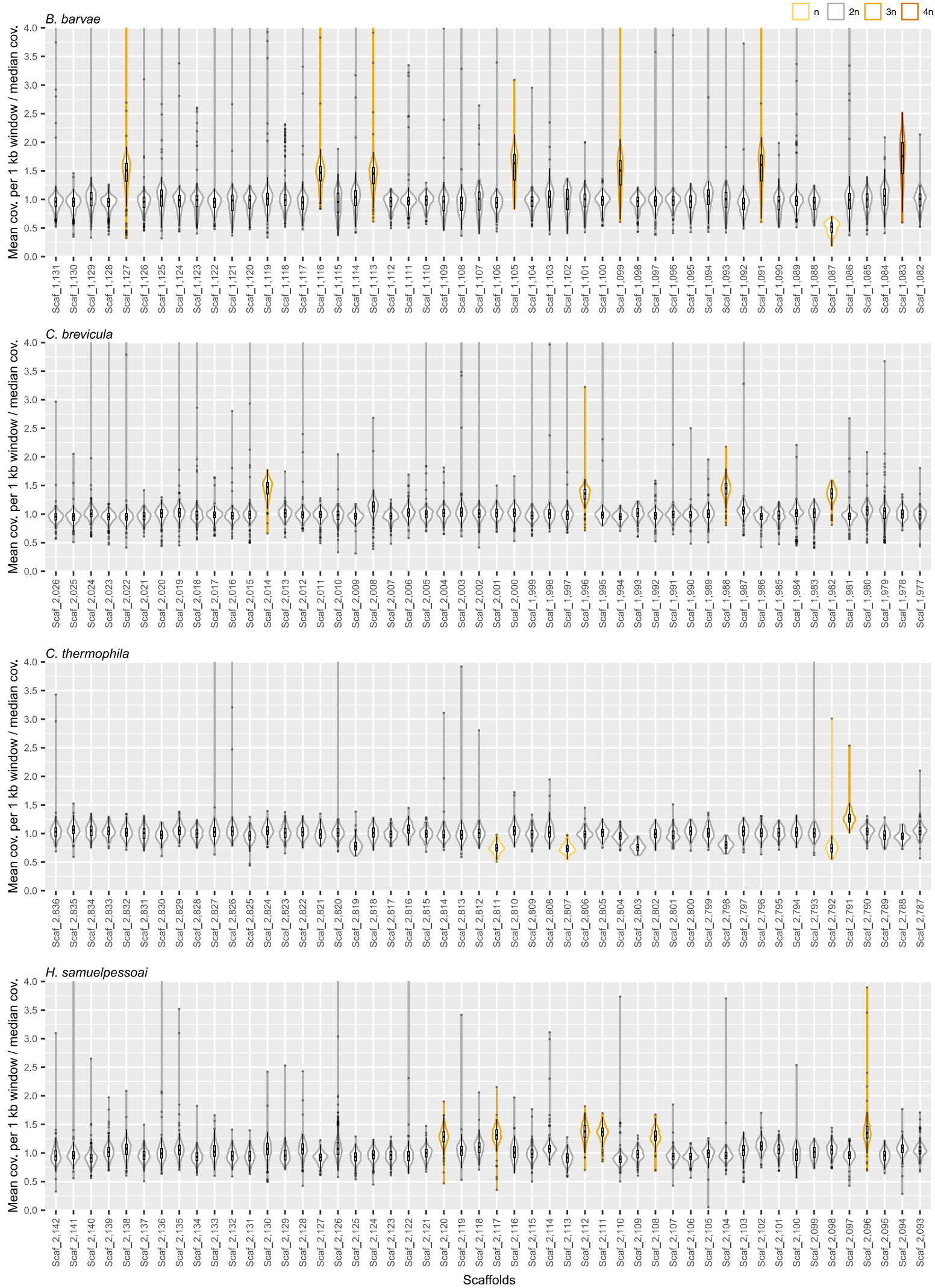
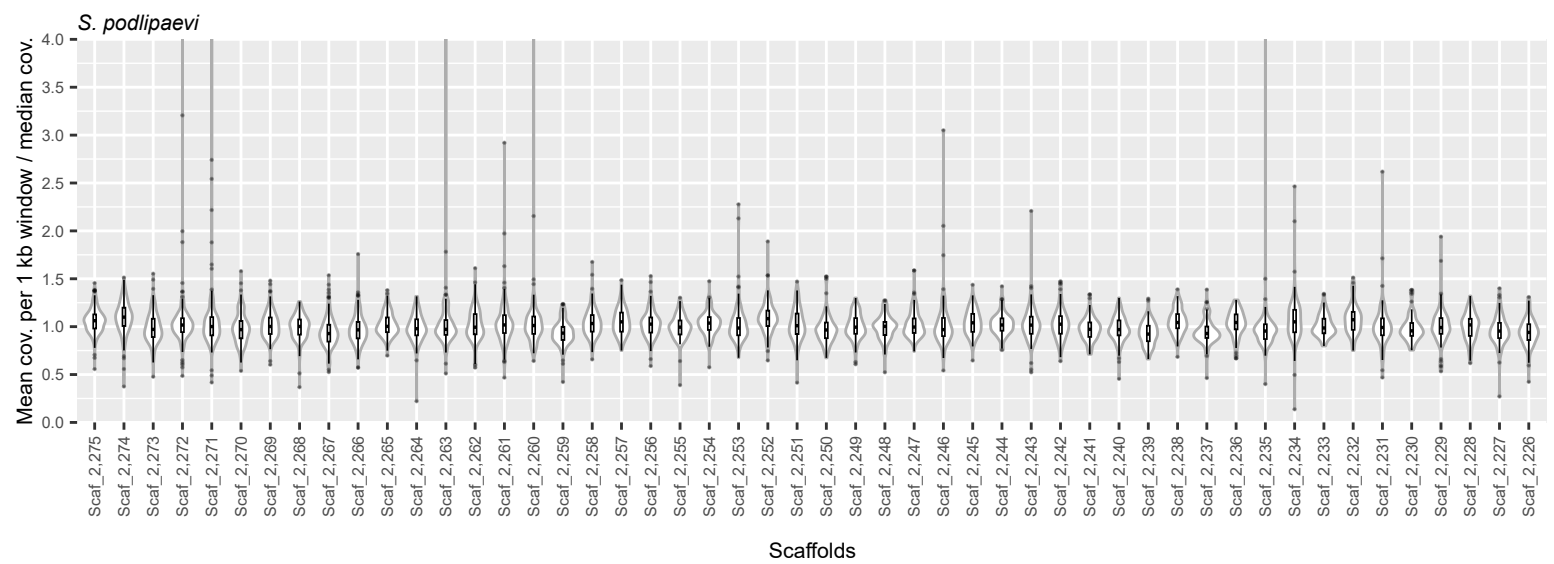
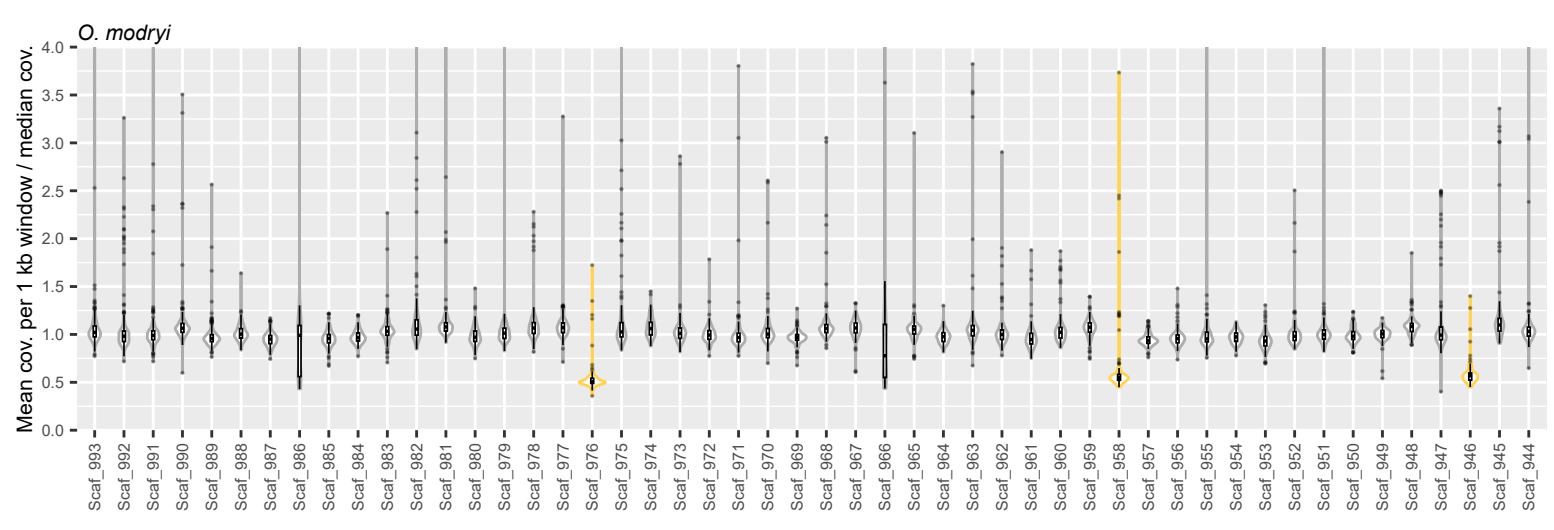
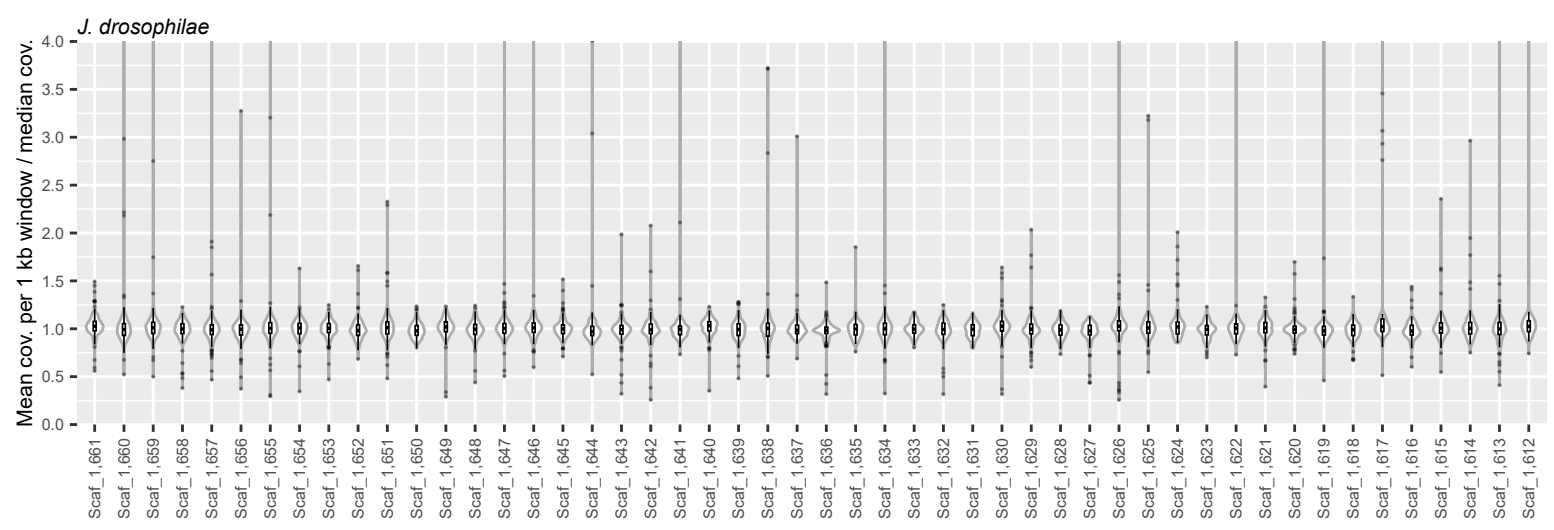
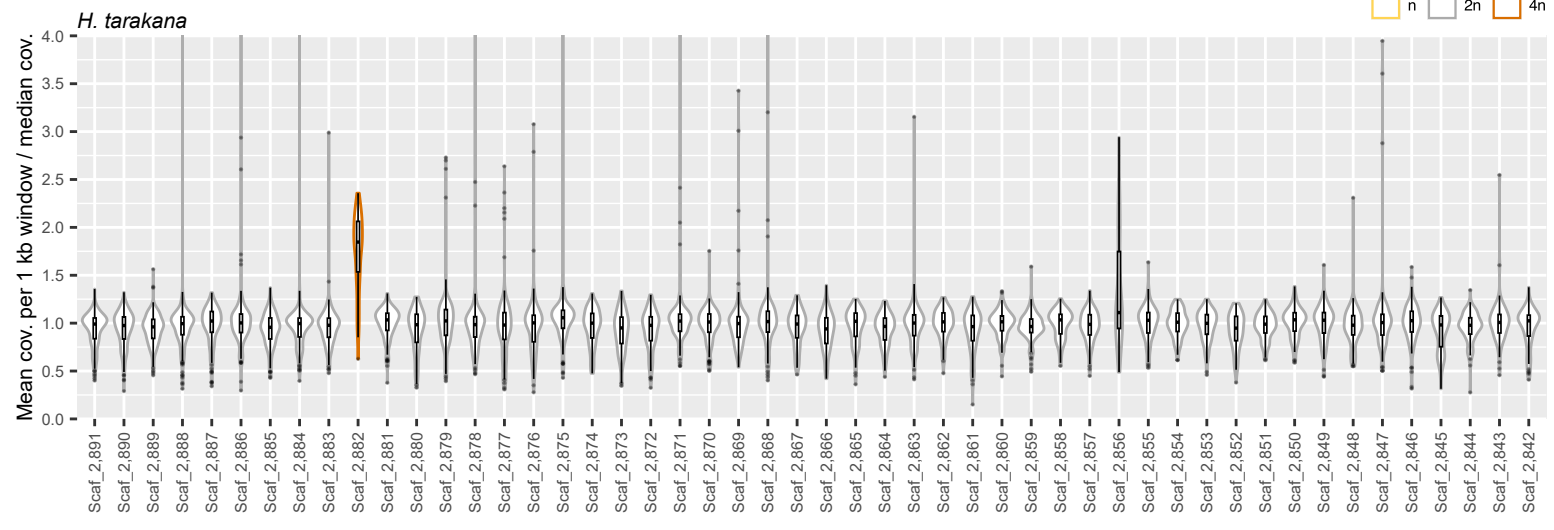


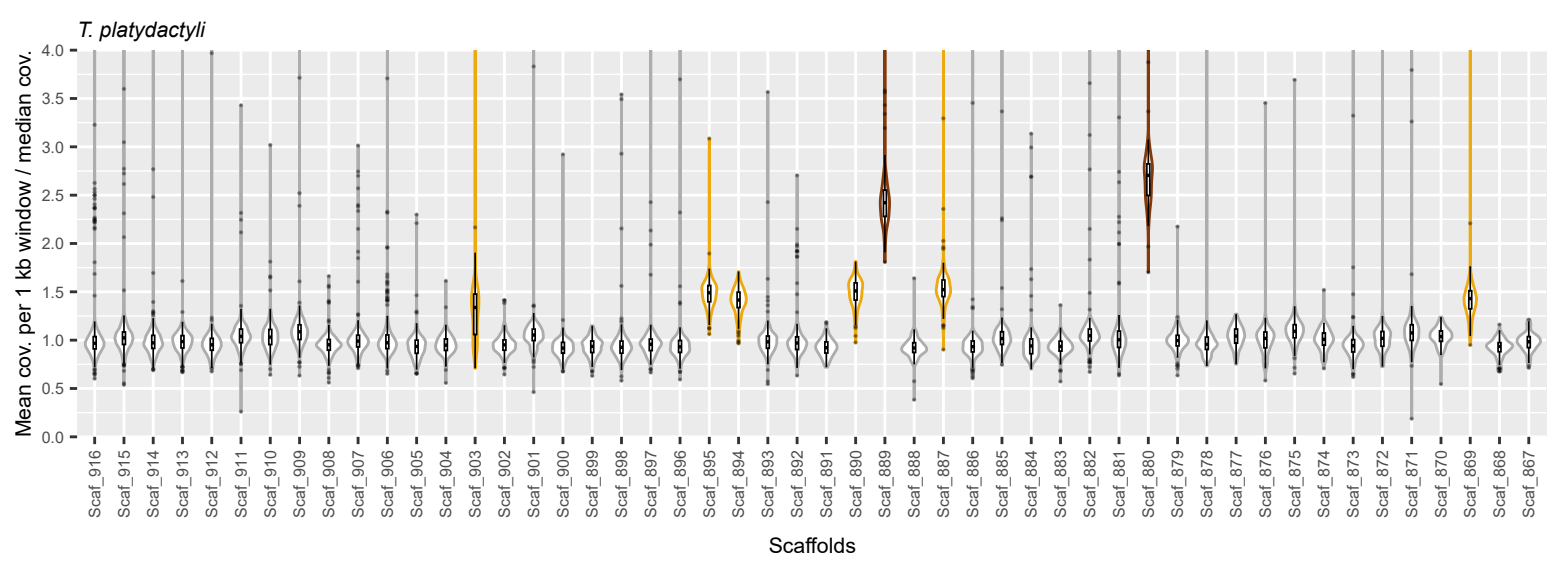
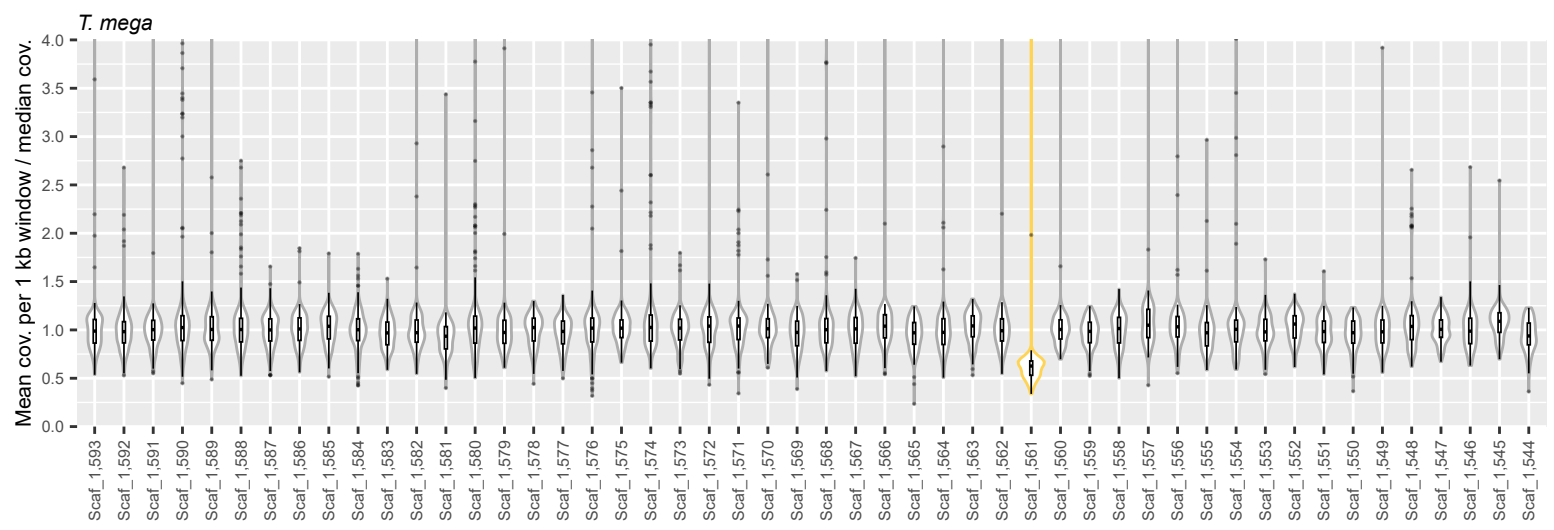
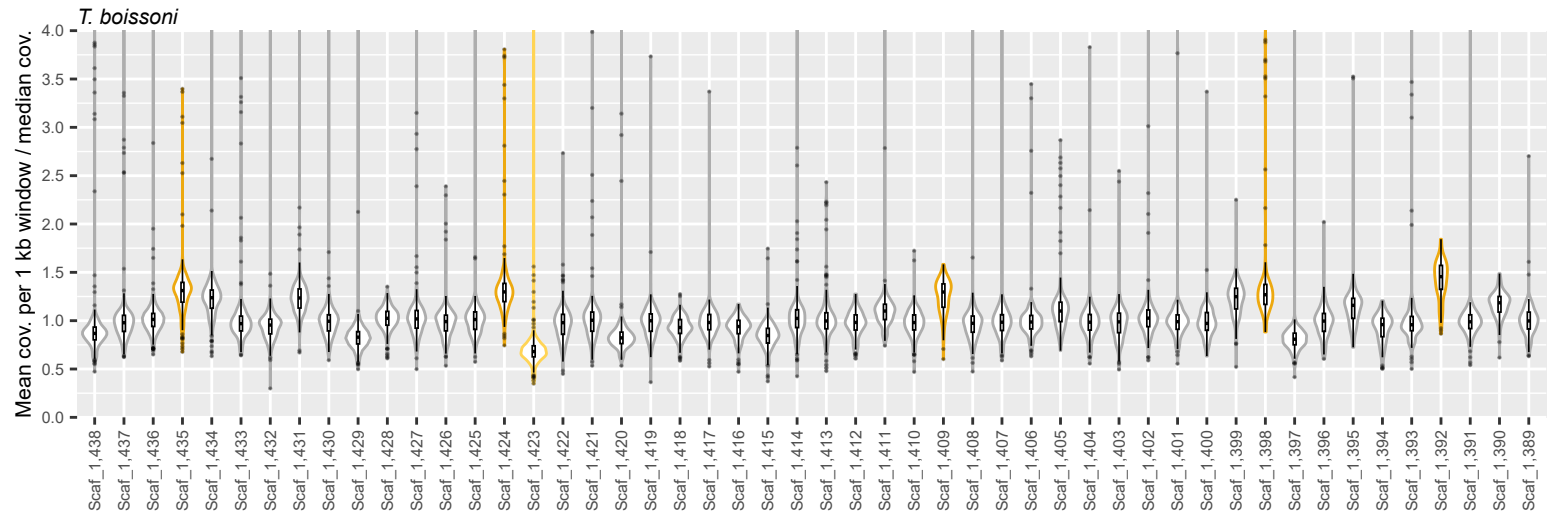
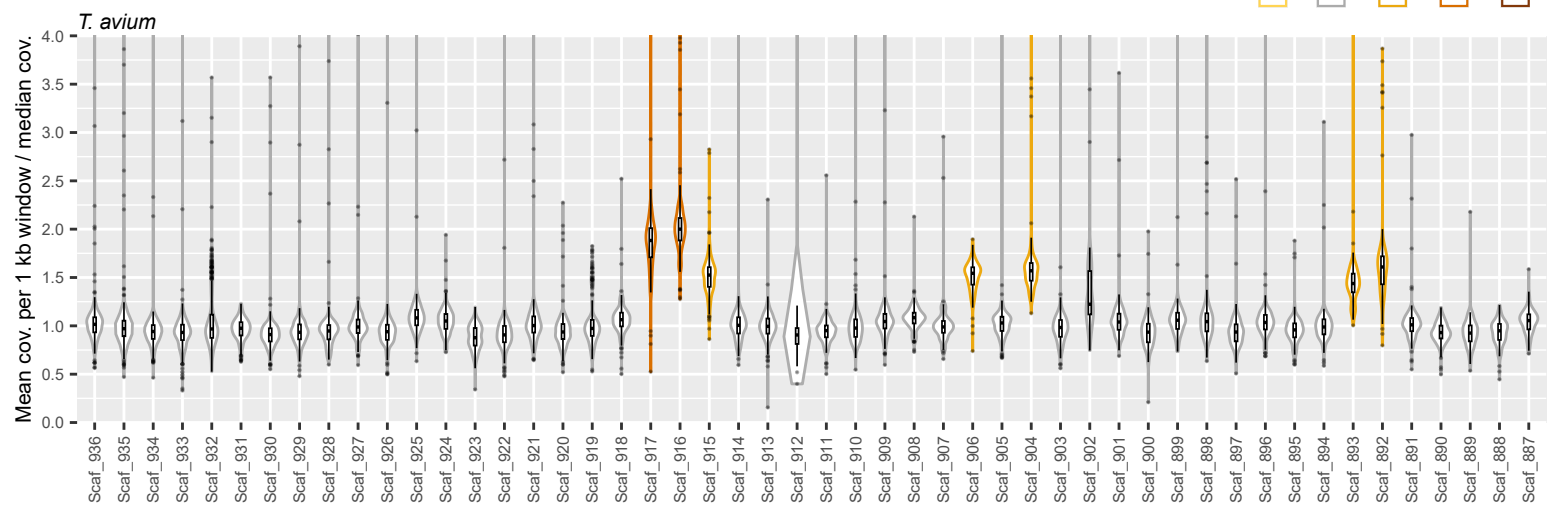
Additional file 6. Violin plot representation of some for the 50 longest scaffolds for each genome assembly. Estimated scaffold somy is color-coded. Scaffold IDs and the ratio of median-of-means coverage values to the median genome coverage are shown on X and Y axes, respectively. Bar plot shows the median coverage value and interquartile range.



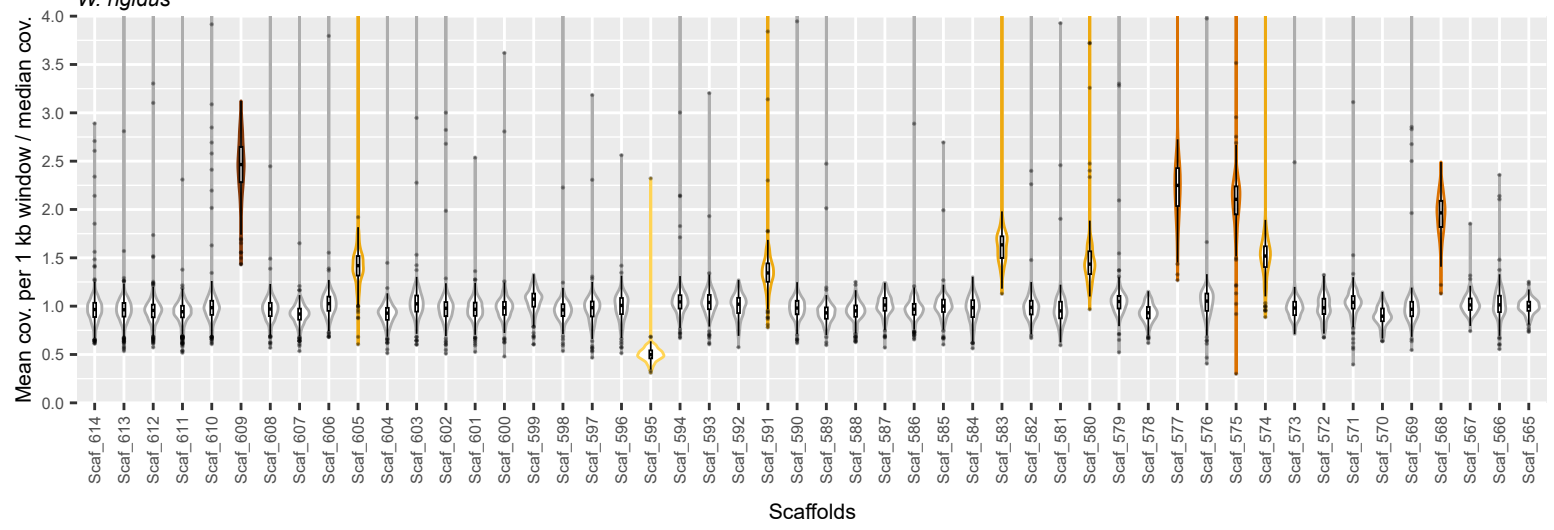
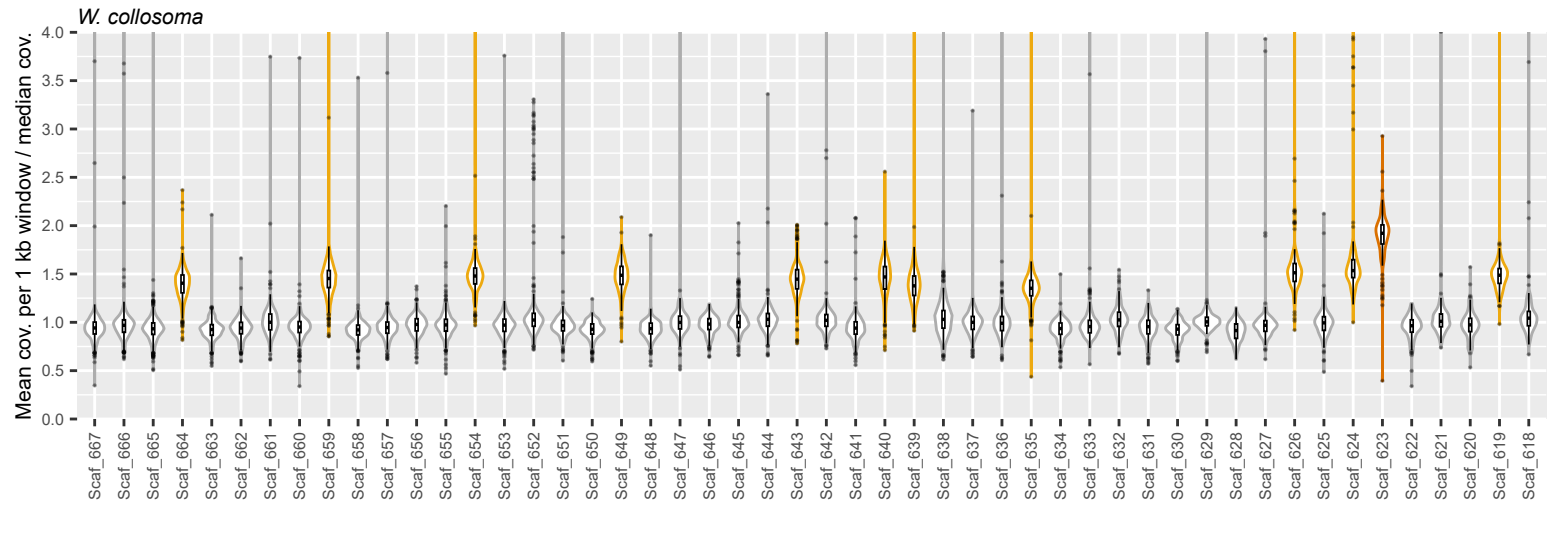
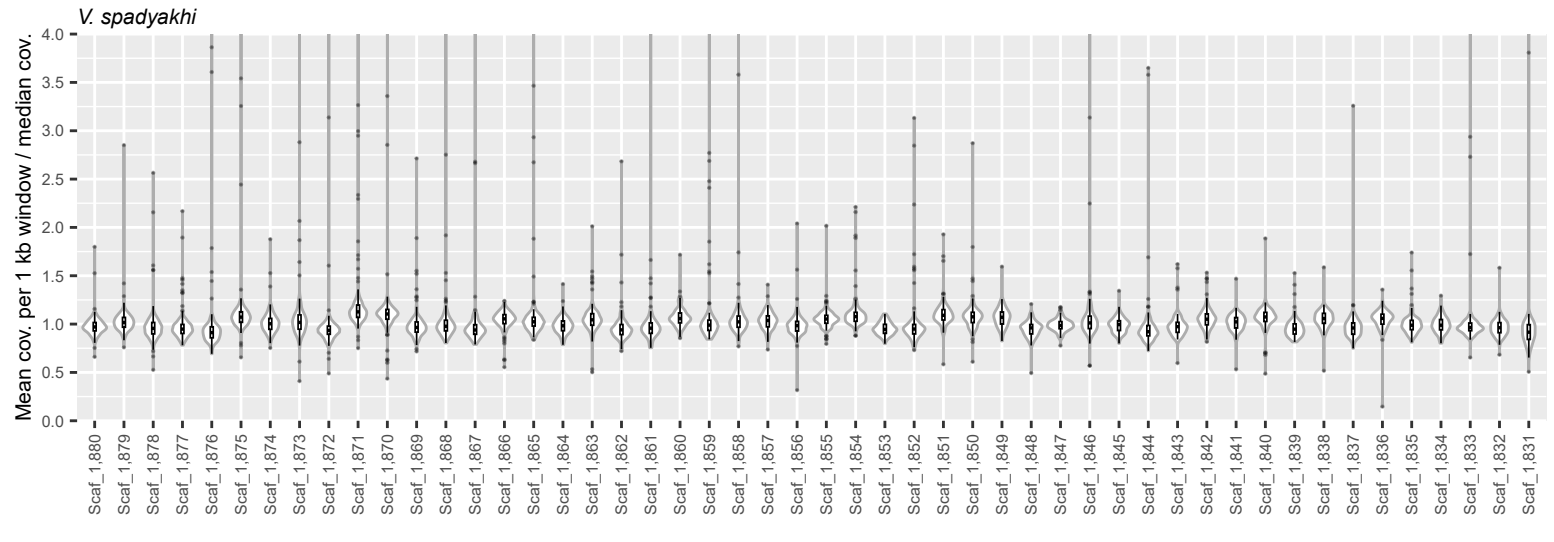
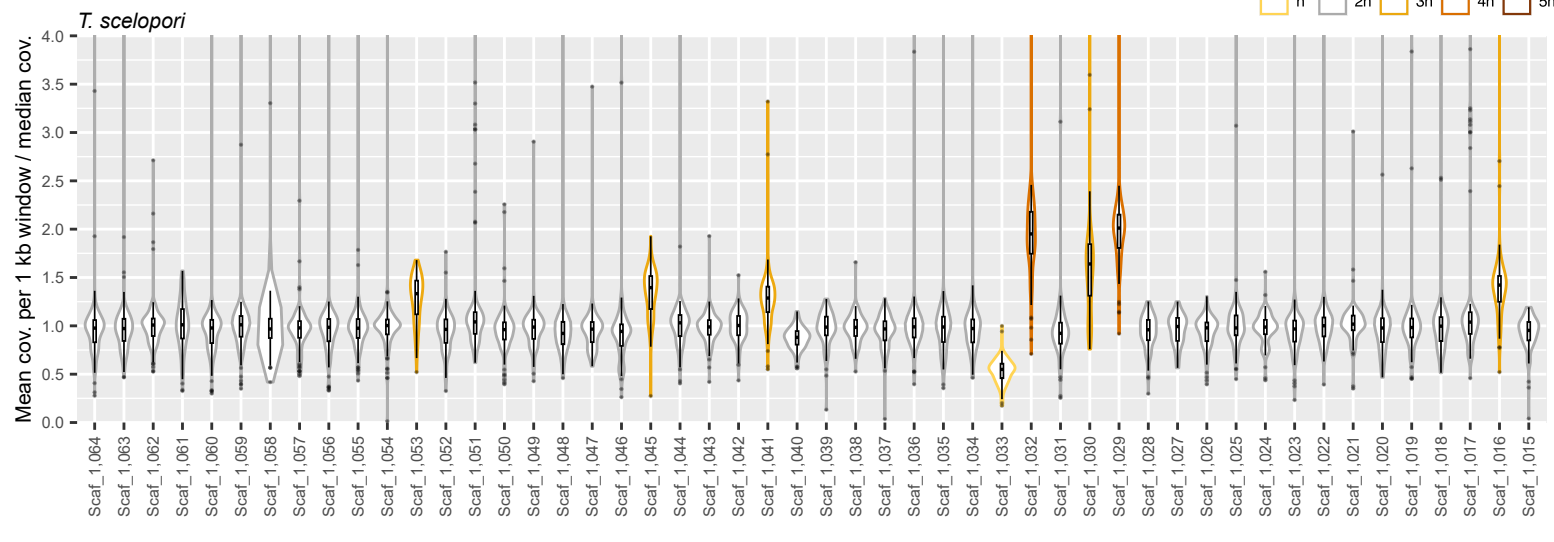
n 2n 4n



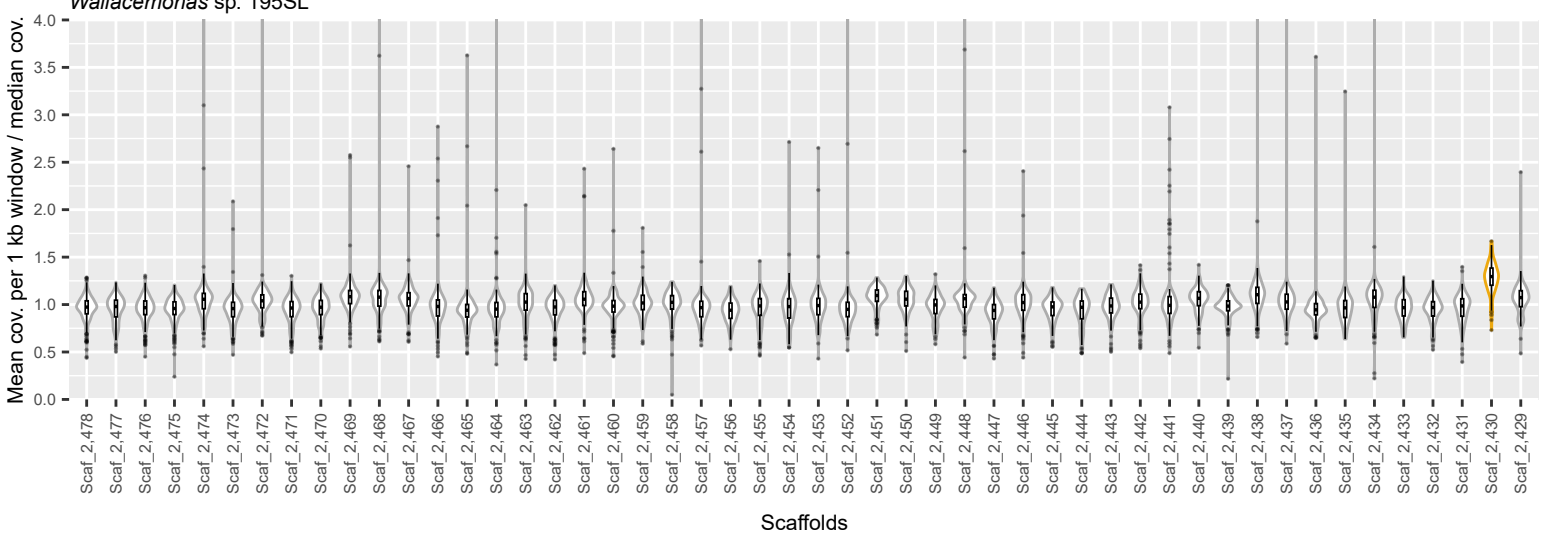
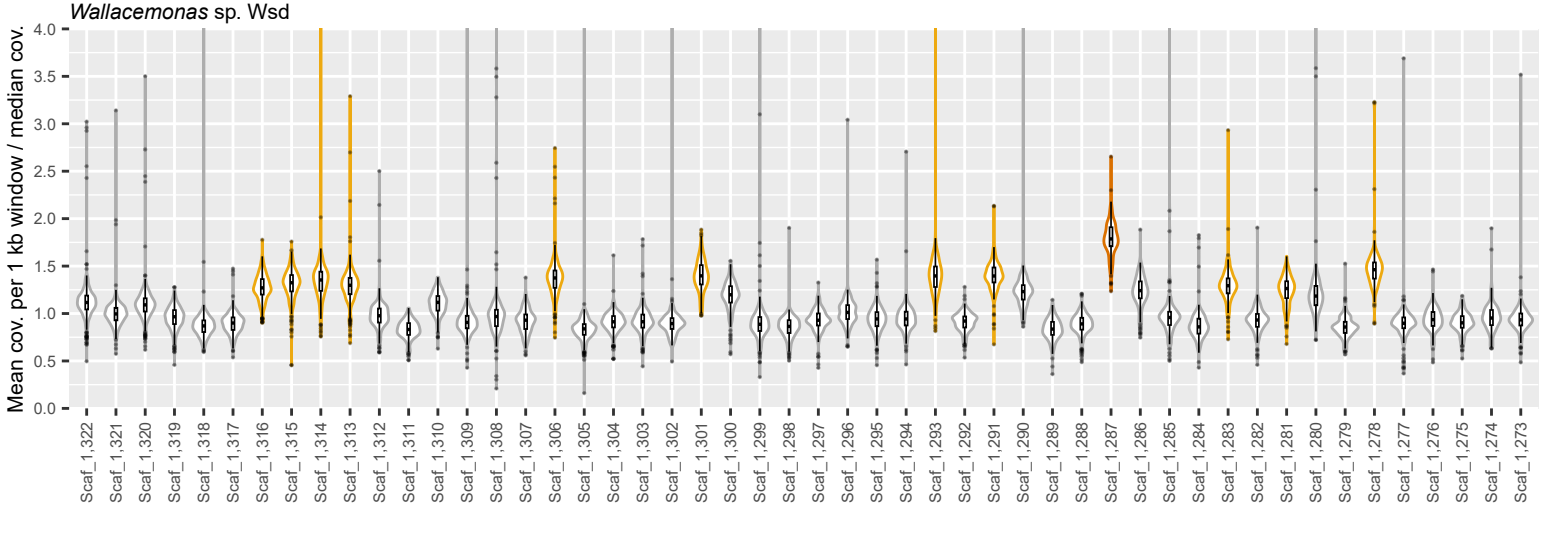
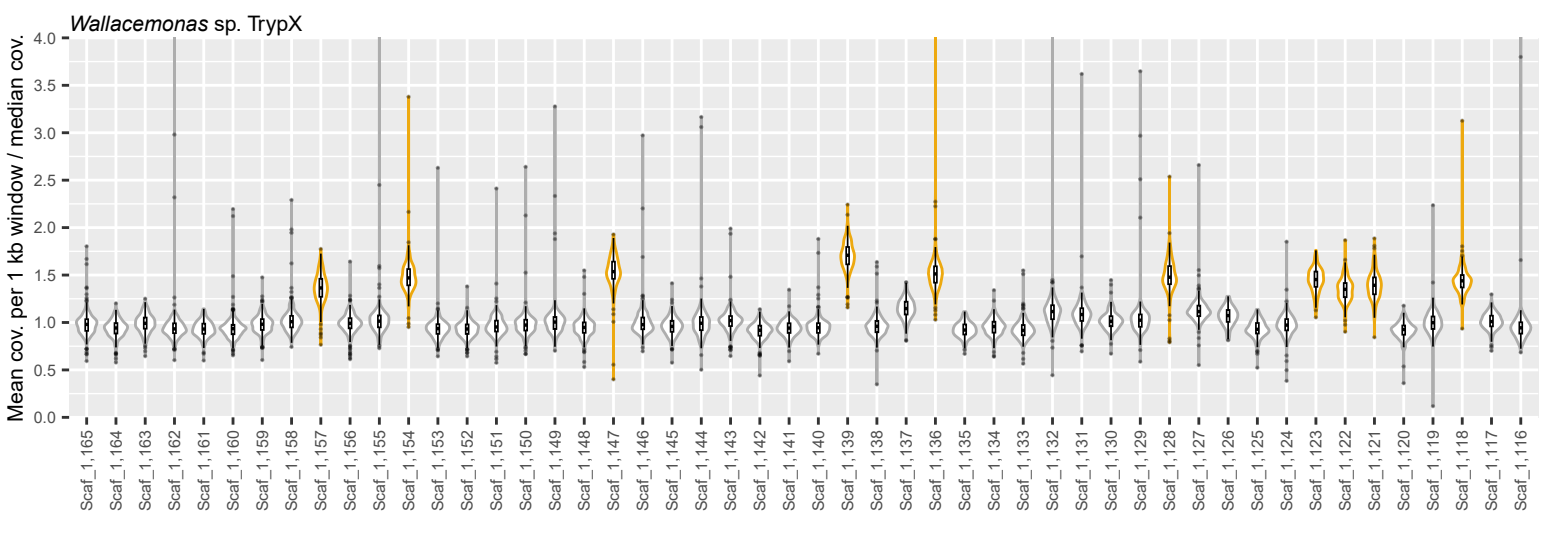
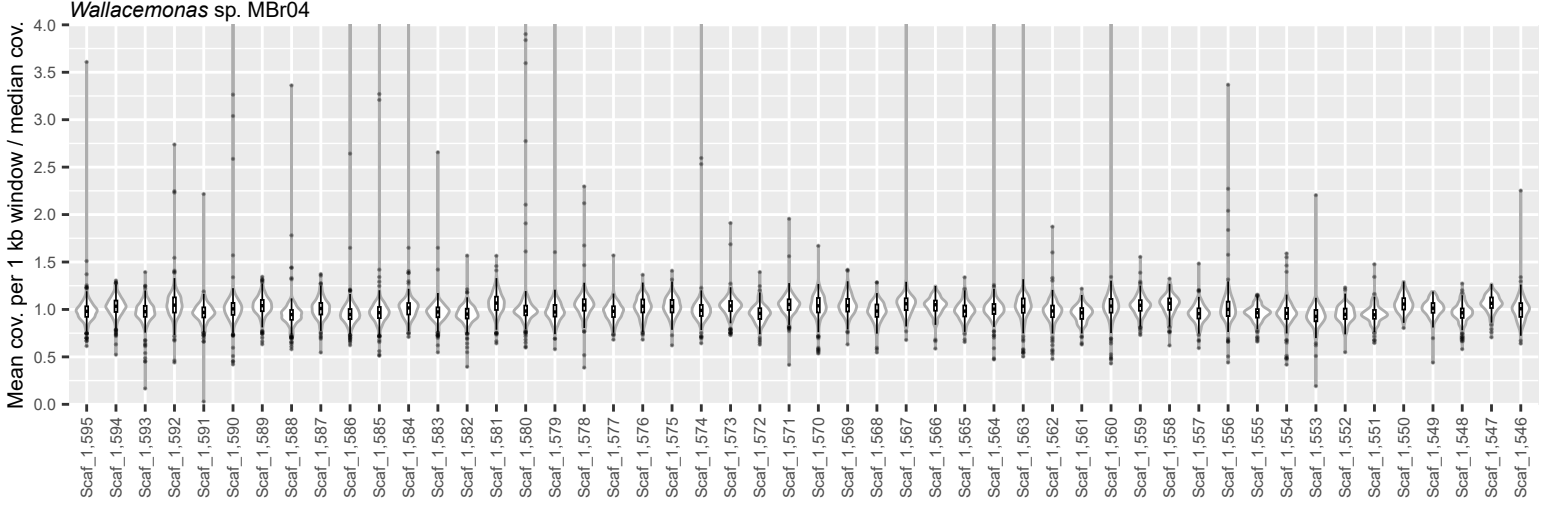
n 2n 3n 4n 5n



n 2n 3n 4n 5n



2n 3n 4n



Scaffolds

