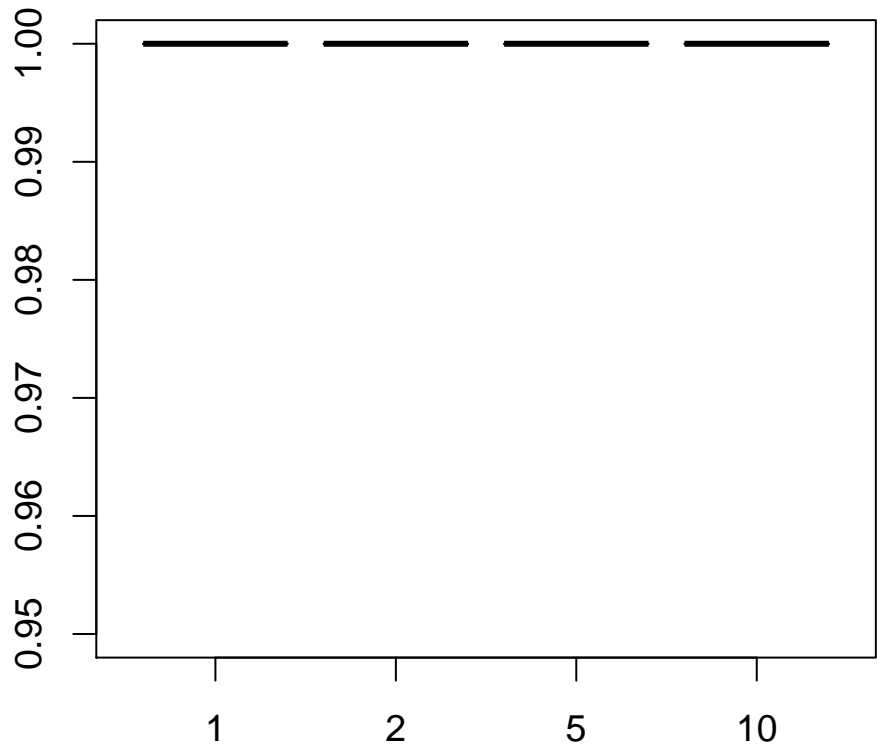
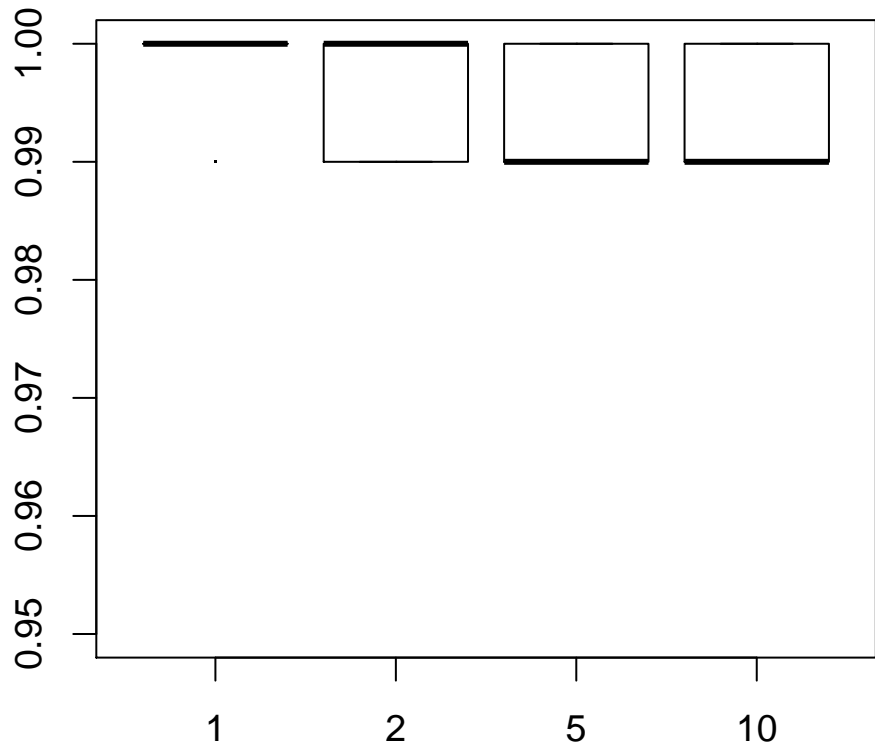


ratio of recovered collinear blocks



max number of mismatched genes

ratio of correctly called synteny



max number of mismatched genes