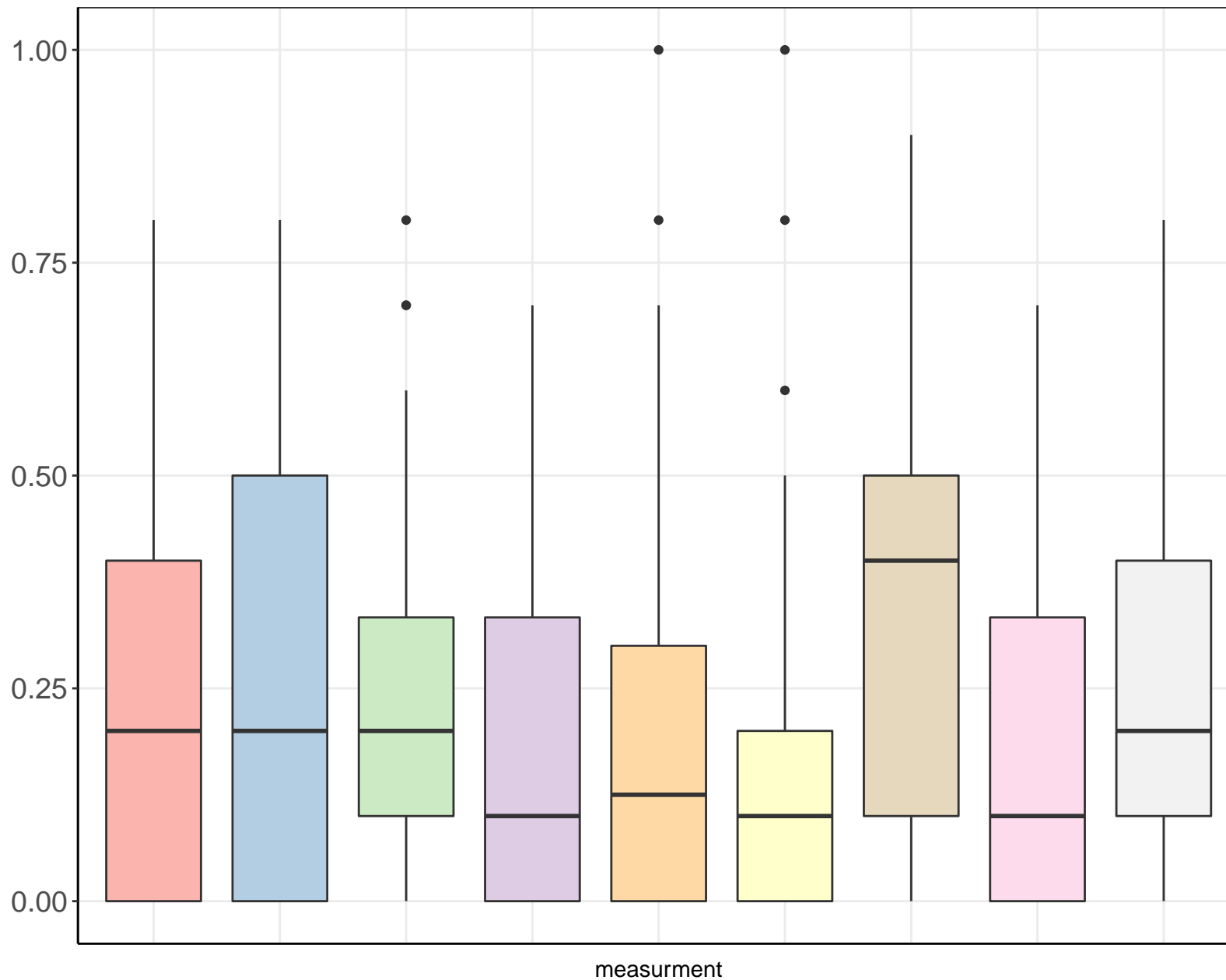


Number of binding positions in top 10 predicted – dna

hits fraction in top predicted



measurment

method

- aa_ref_overlap_individuals_change_ratio
- instances_individuals_change_ratio
- jsd_100way_aa_not_used_ratio
- jsd_100way_instances_major_ratio
- jsd_mul_aa_ref_SE
- jsd_SE_diff_ratio
- jsds_ratio
- jsds_subtraction
- SE_jsd_diff_ratio