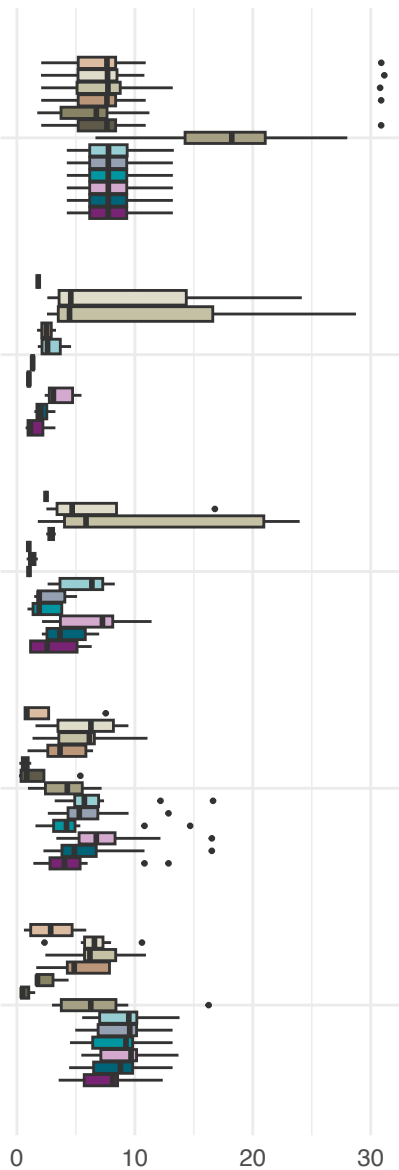
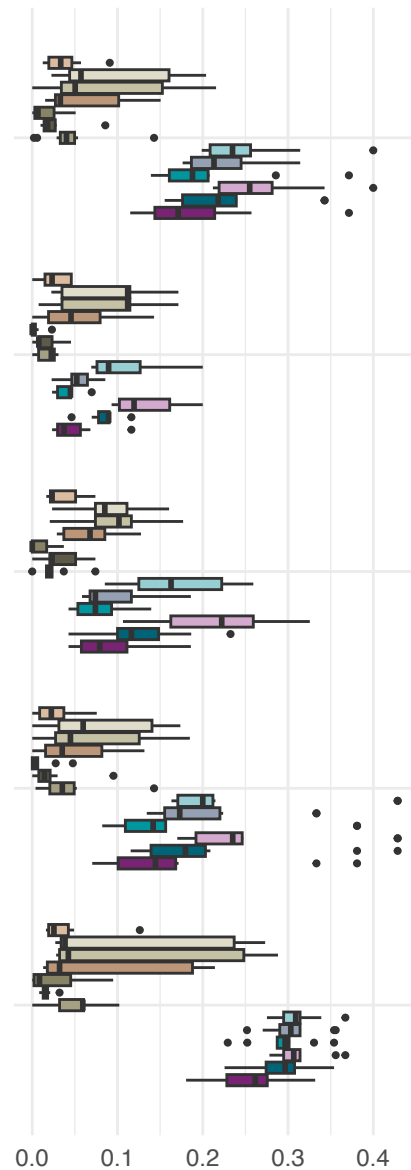


Enrichment of variants
in predicted enhancers

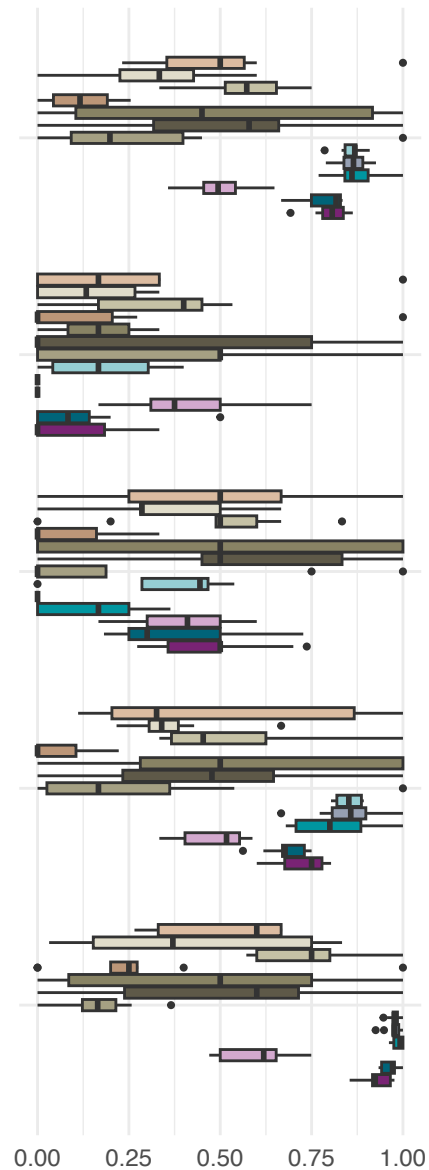
All variants
35–2846 variants
11–11 biosample pairs



Variants overlapping
predicted enhancers



Variants linked to correct gene,
given overlapping predicted enhancer



Predictor

- ArchR (high-confidence)
- DIRECTNET (high-confidence)
- SCENIC+ (importance)
- FigR (p-value)
- Cicero (co-accessibility)
- SnapATAC (p-value)
- SCENT (FDR)
- STARE (gABC, power law)
- In element (ABC (A=scATAC)) & distance to TSS
- ABC (A=scATAC, C=power law)
- Kendall correlation (access. at E x expr. at G)
- scE2G (scATAC)
- scE2G (Multiome)