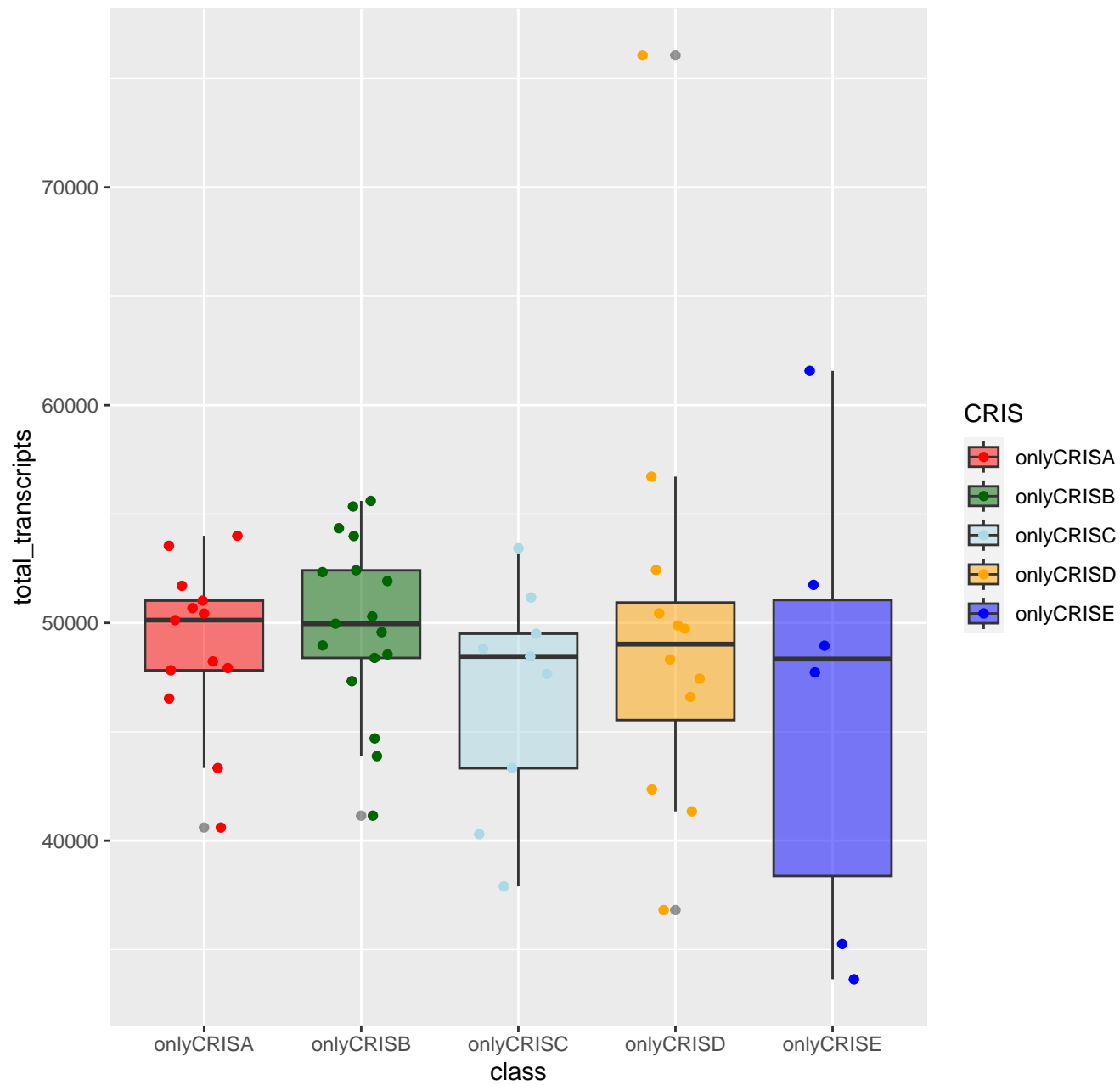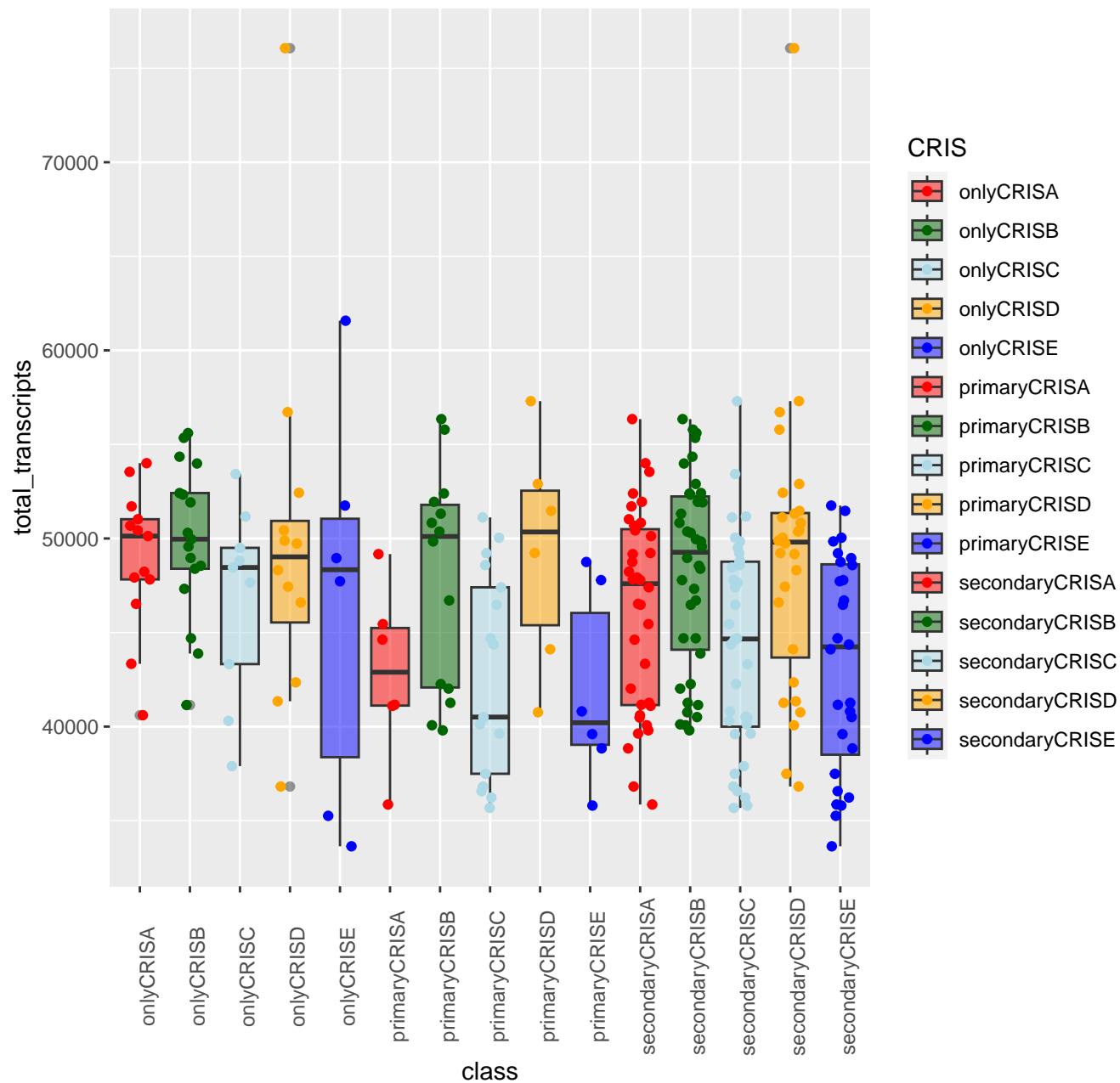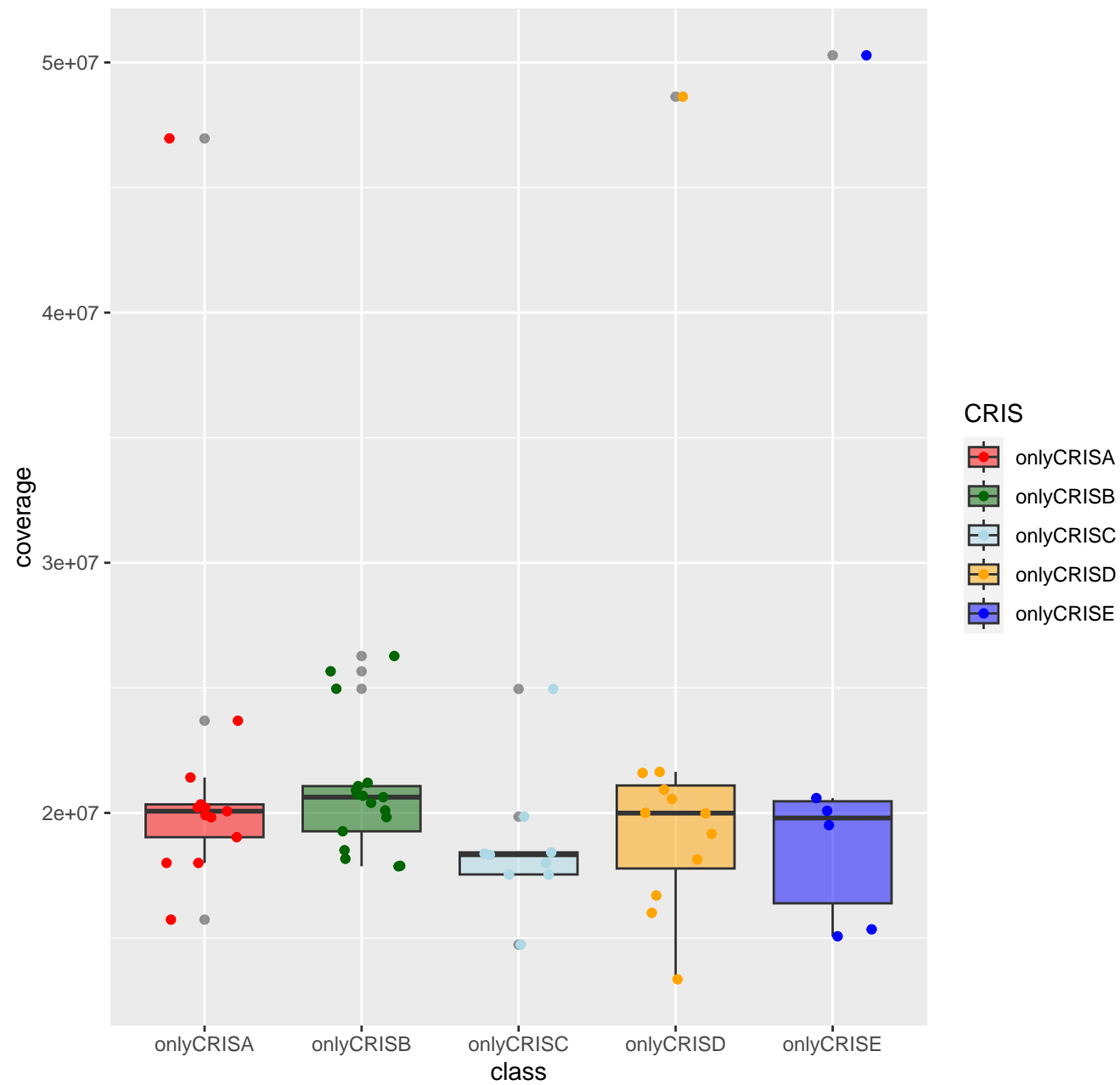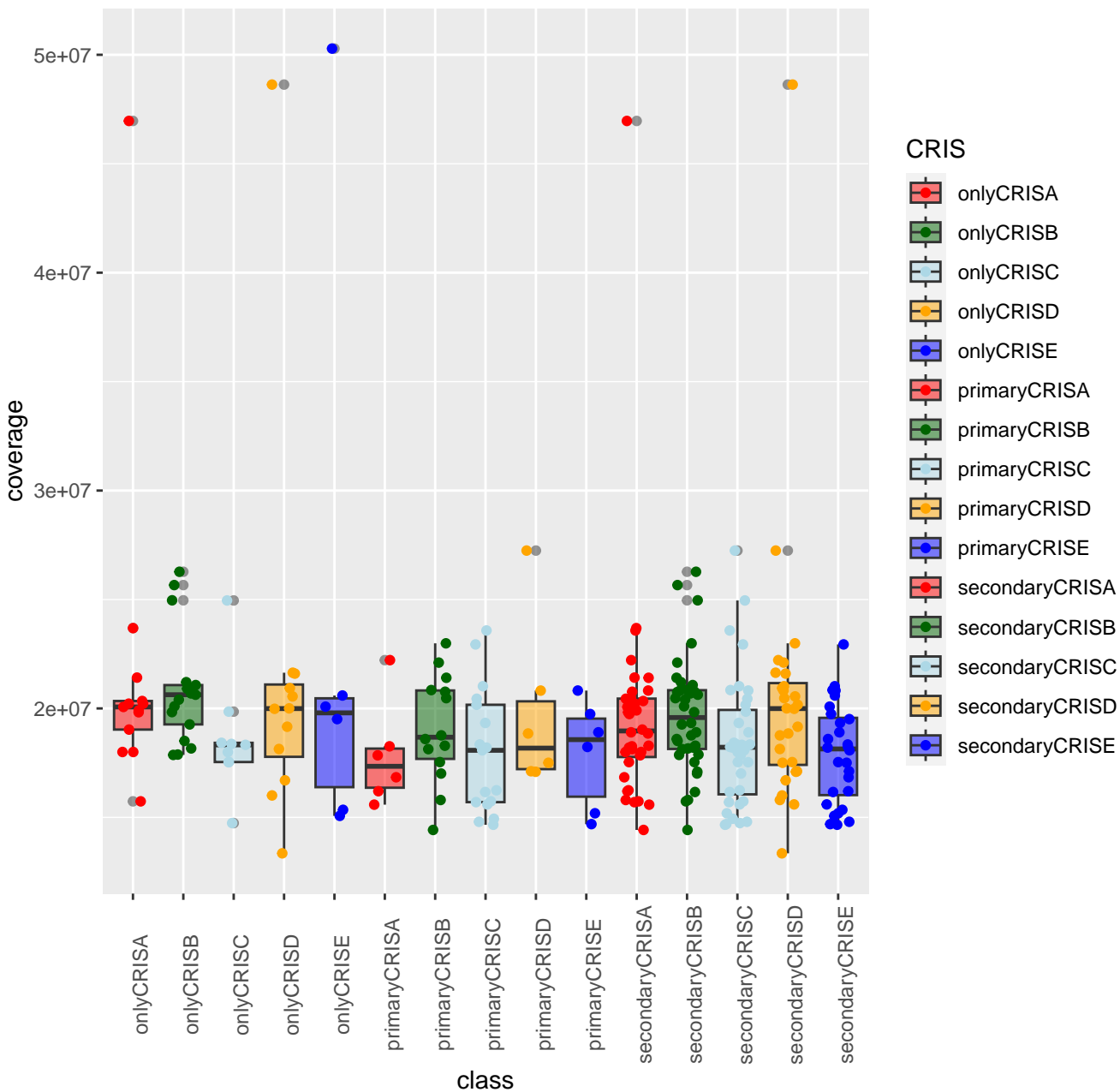Number of total transcripts for sample in each class

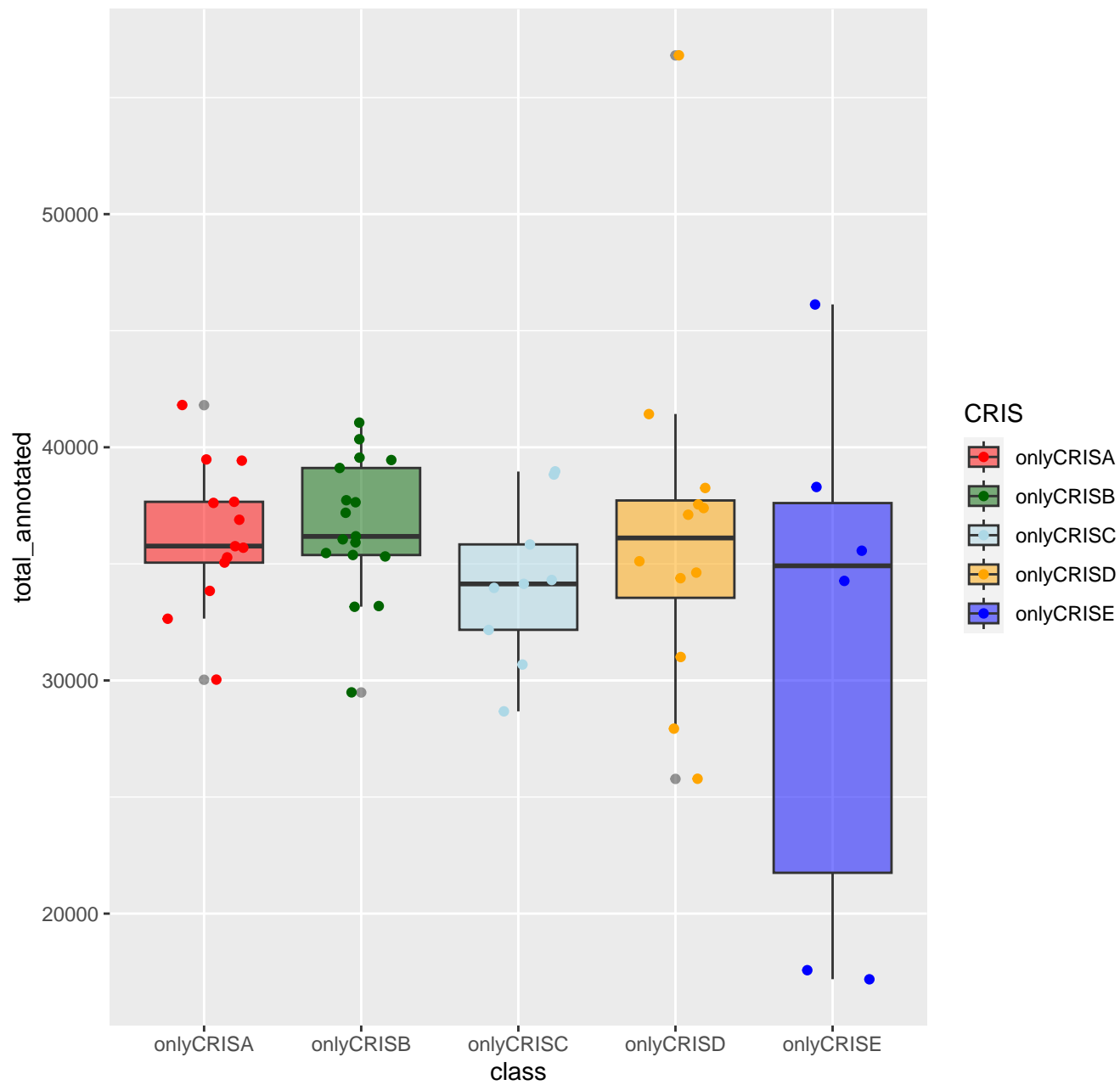Number of total transcripts for sample in each class

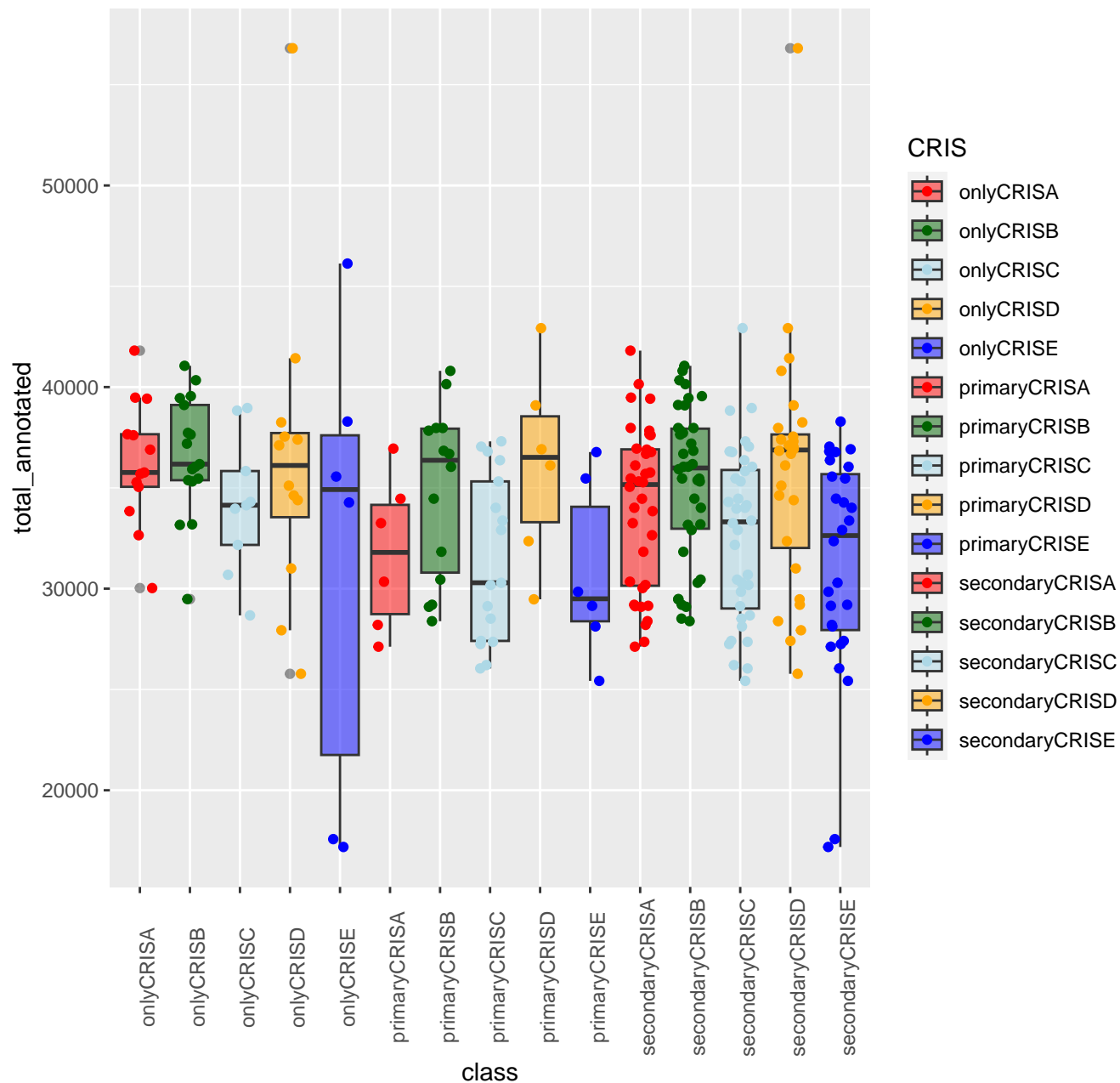Number of total reads for sample in each class
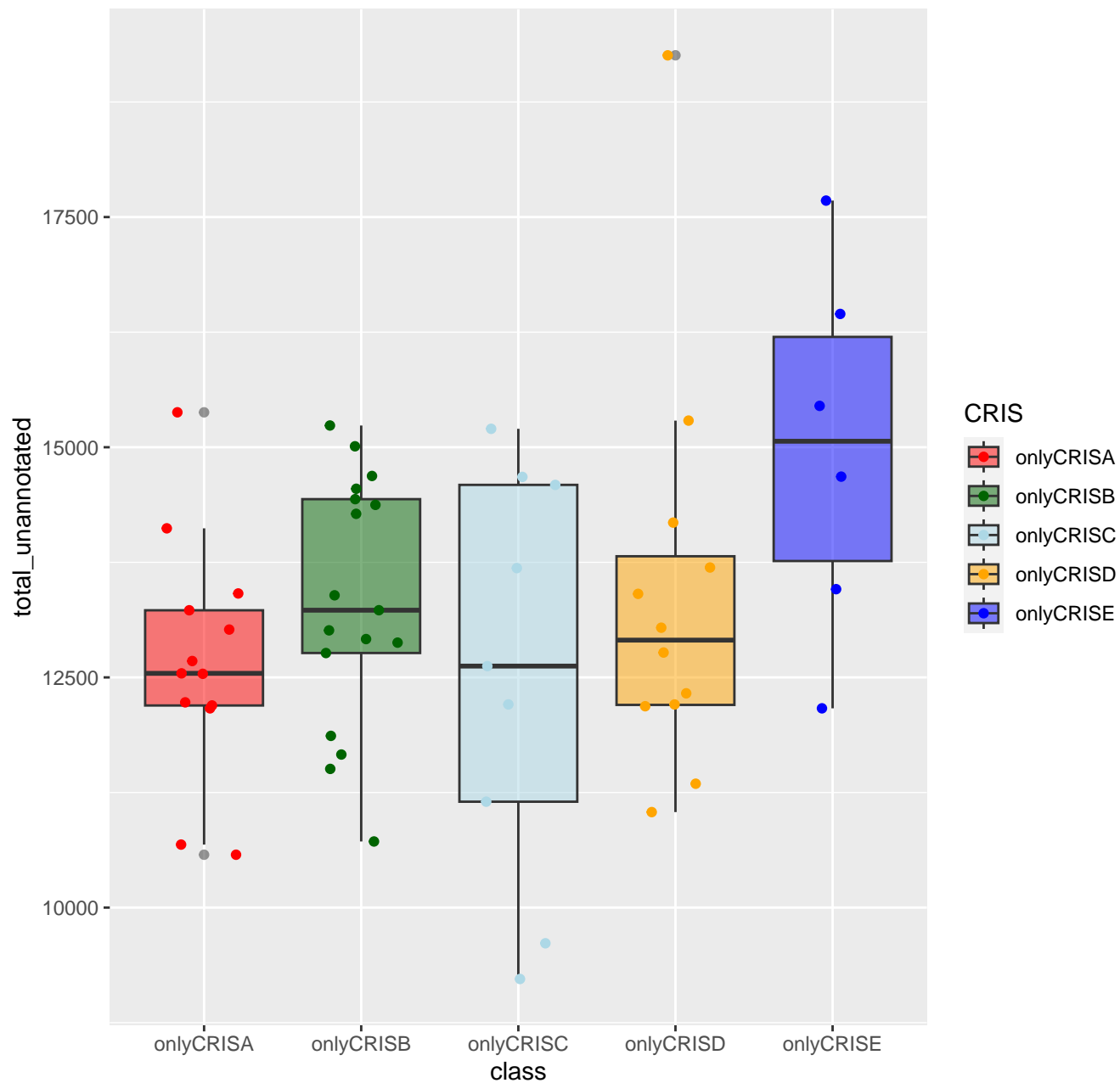
Number of total reads for sample in each class

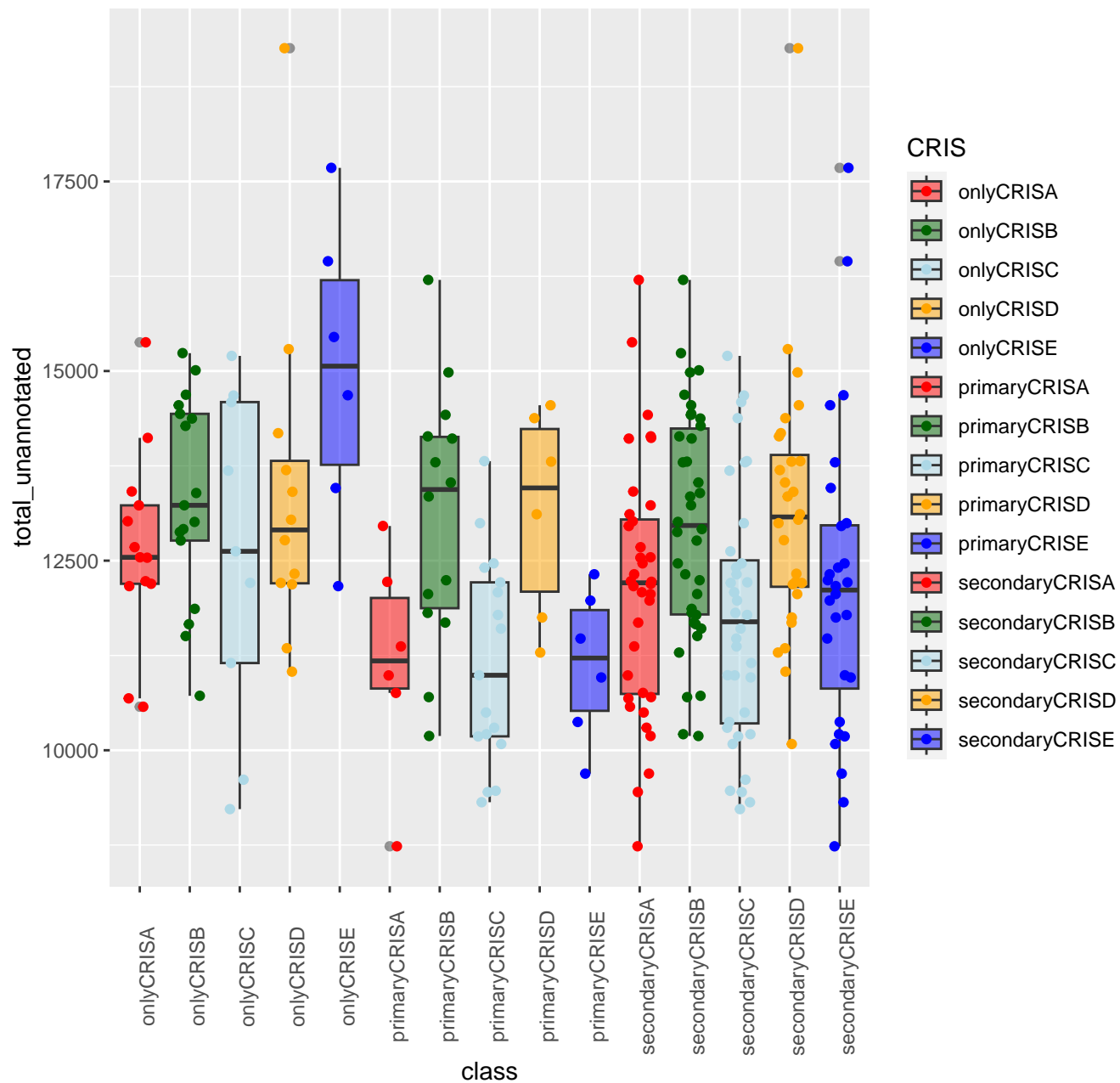Number of total annotated transcripts for sample in each class

Number of total annotated transcripts for sample in each class

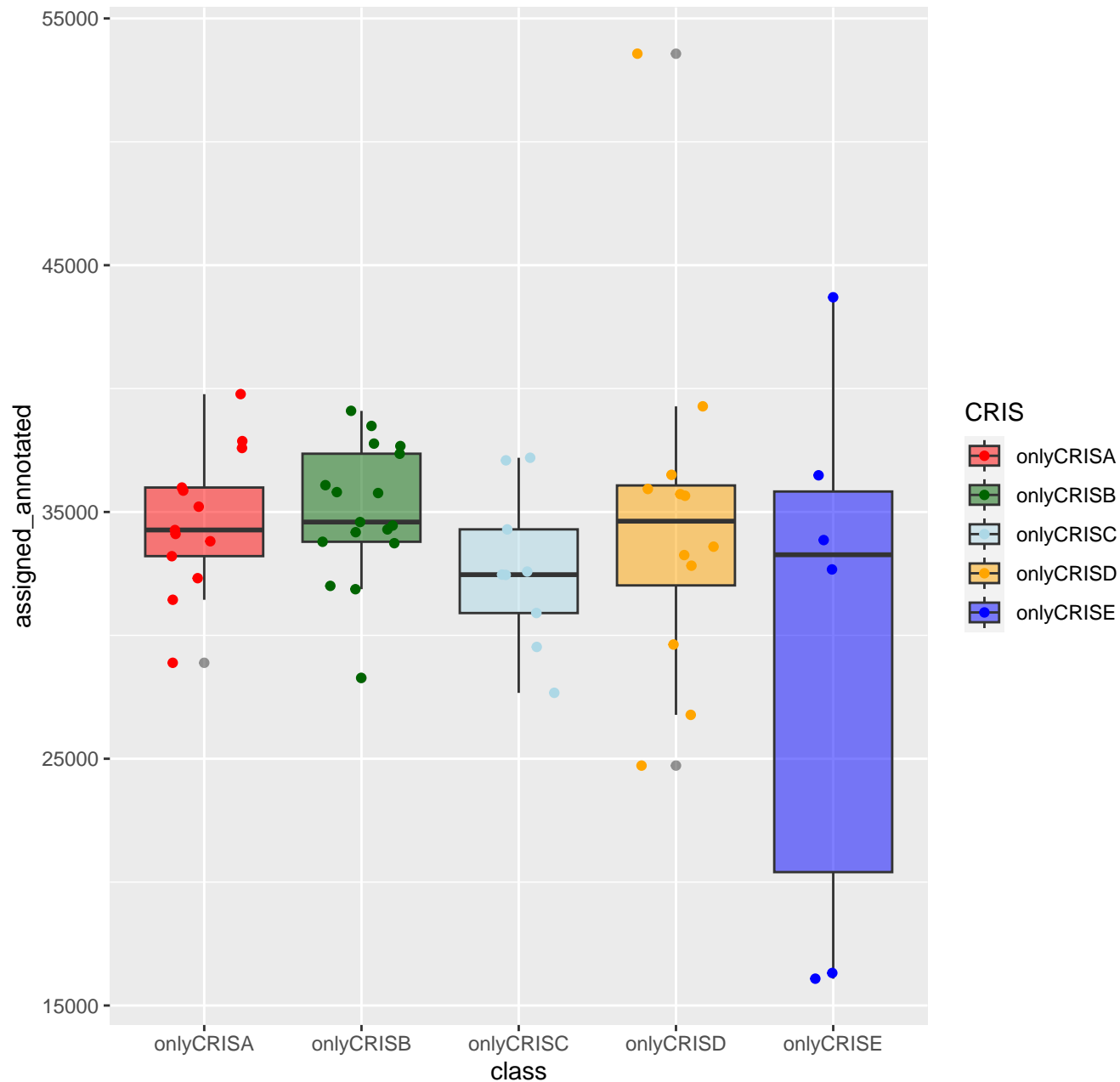Number of total not annotated transcripts for sample in each class

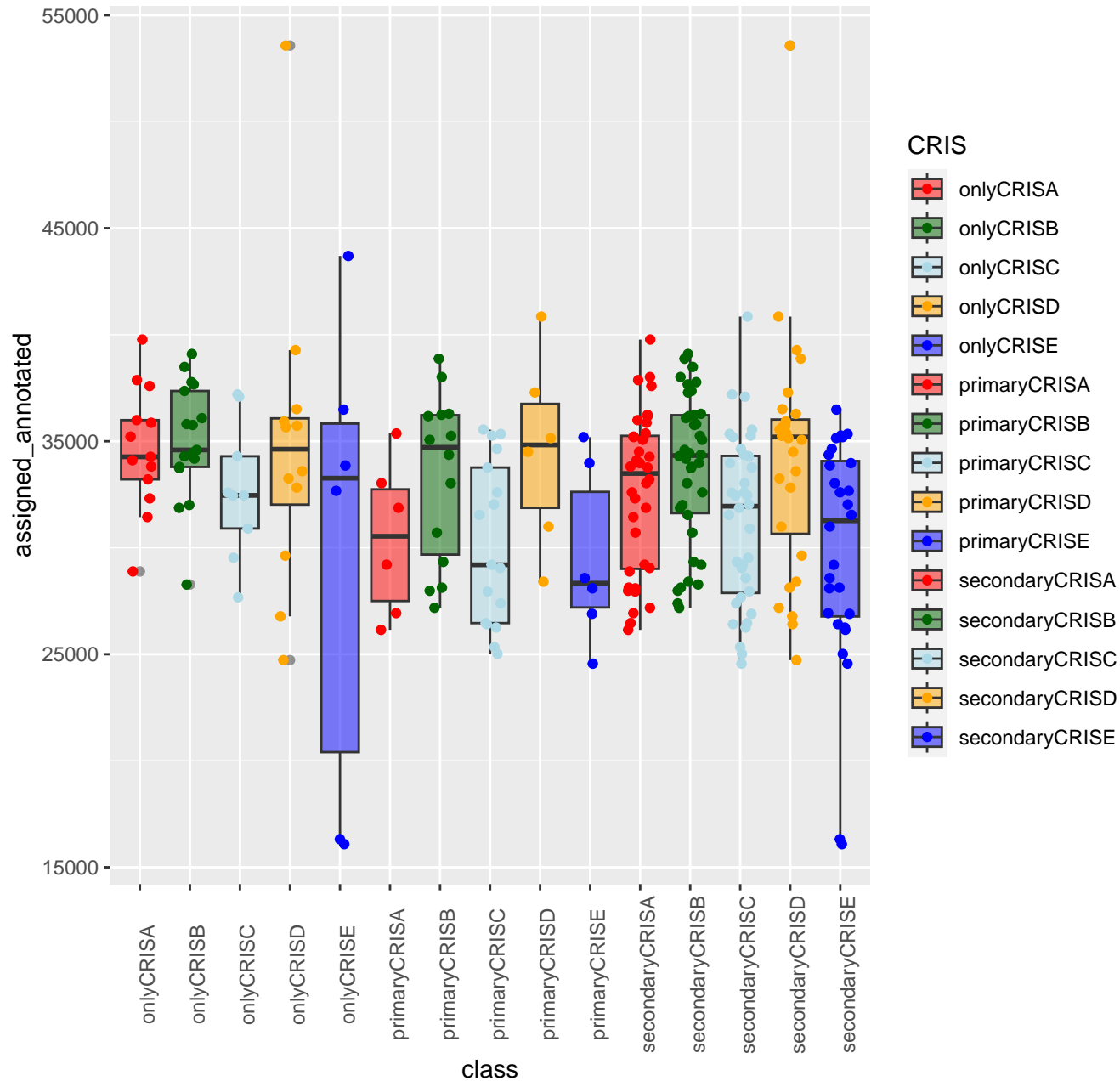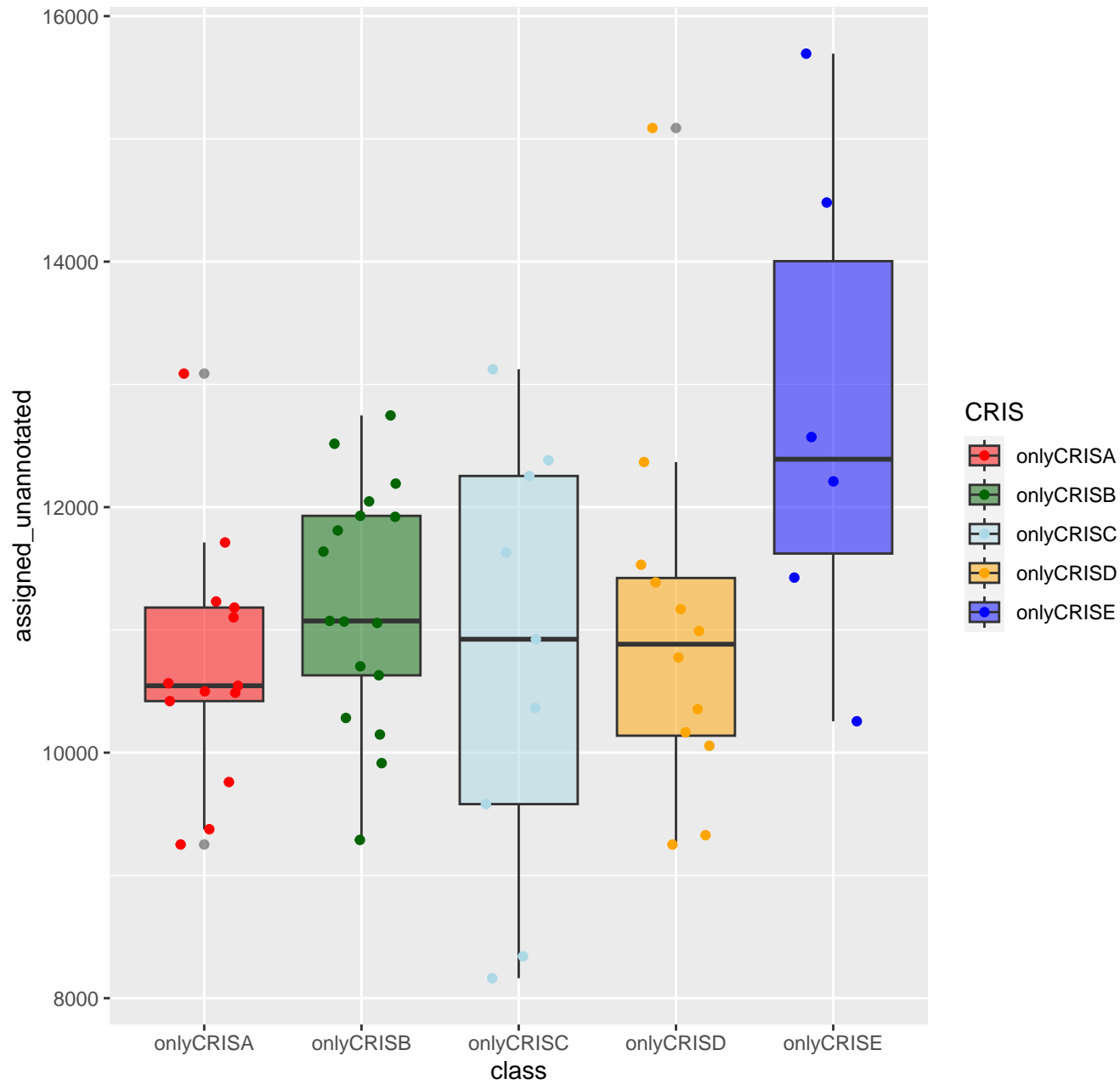Number of total not annotated transcripts for sample in each class

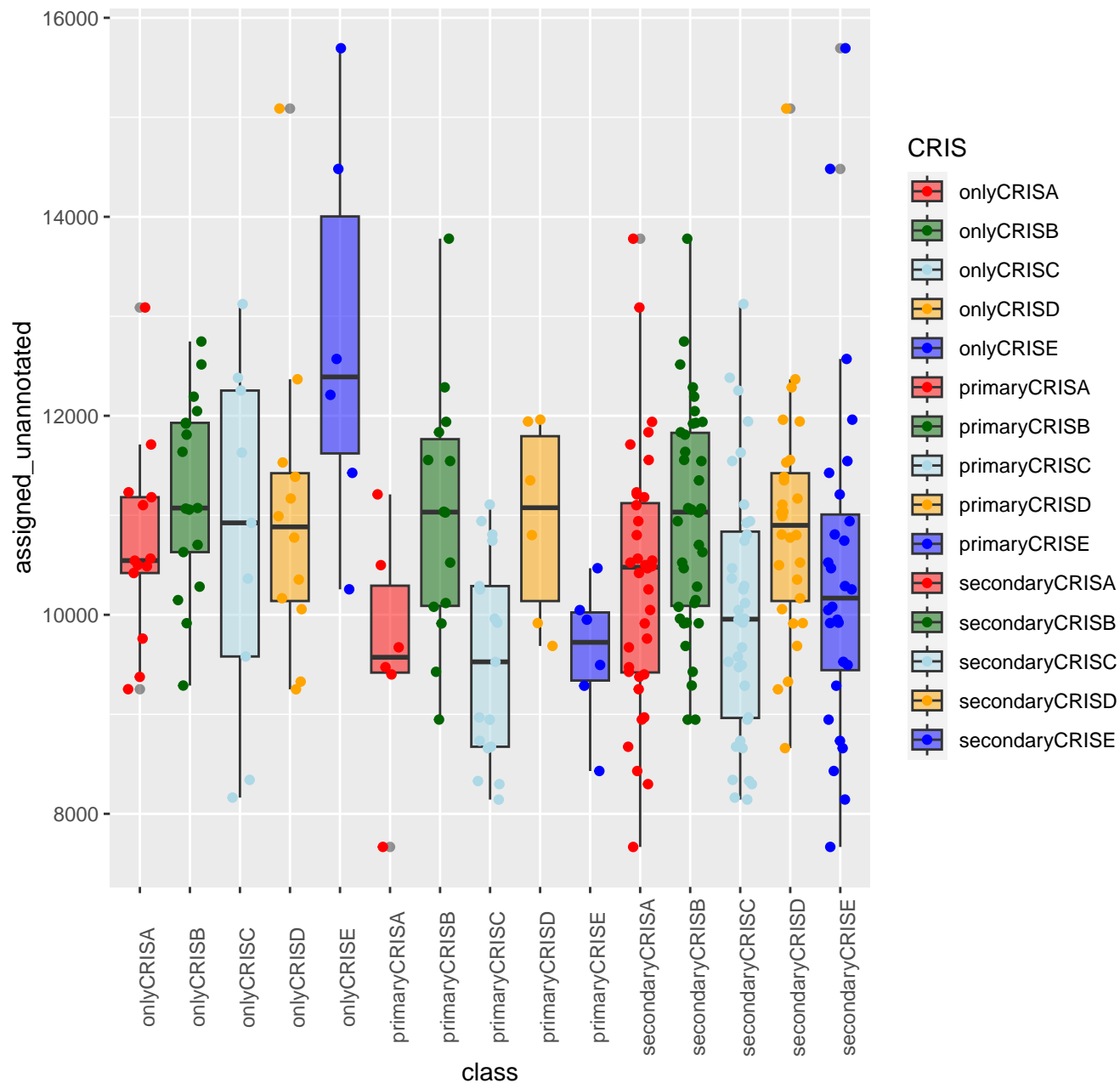Number of assigned annotated transcripts for sample in each class

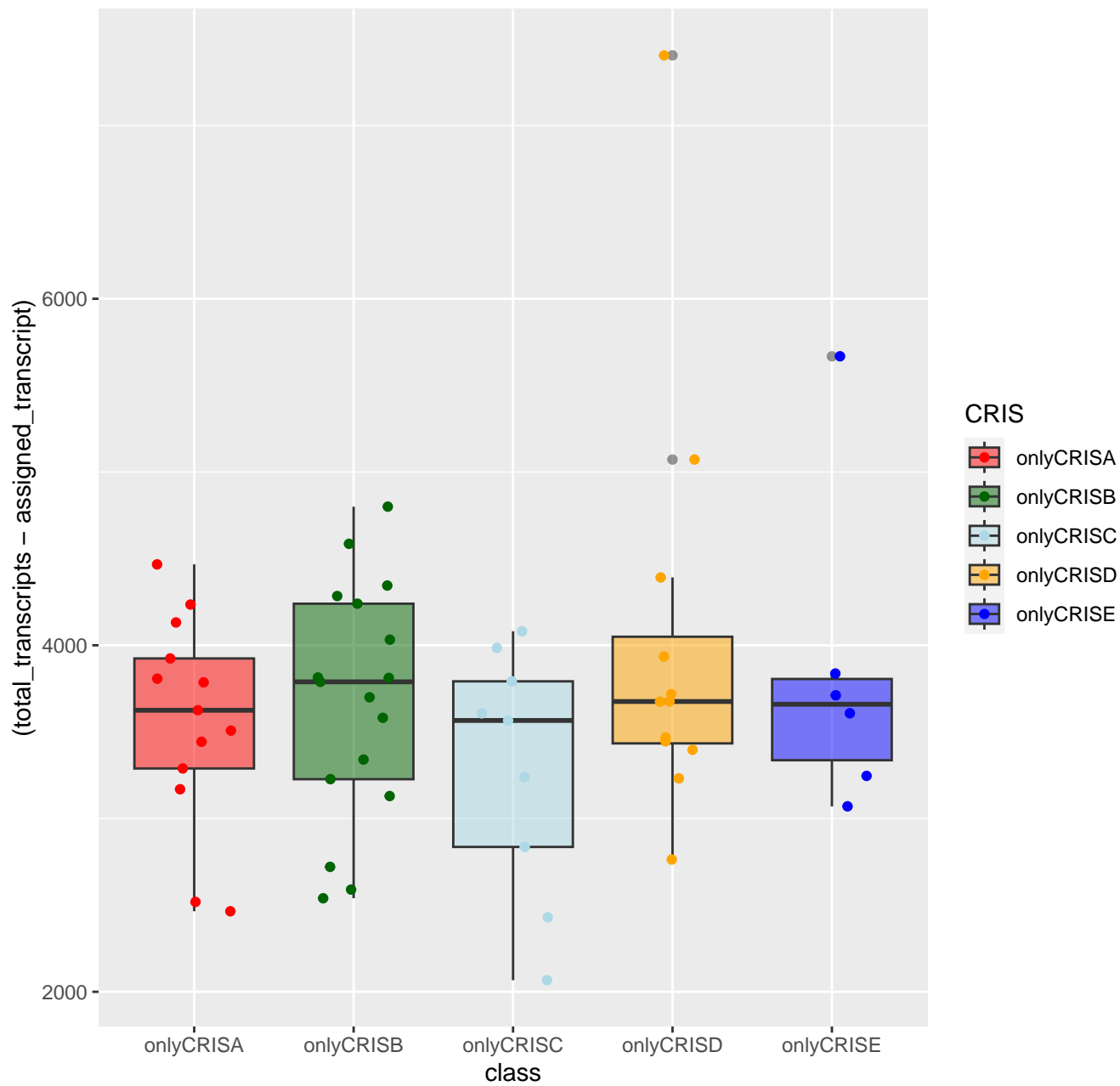Number of assigned annotated transcripts for sample in each class

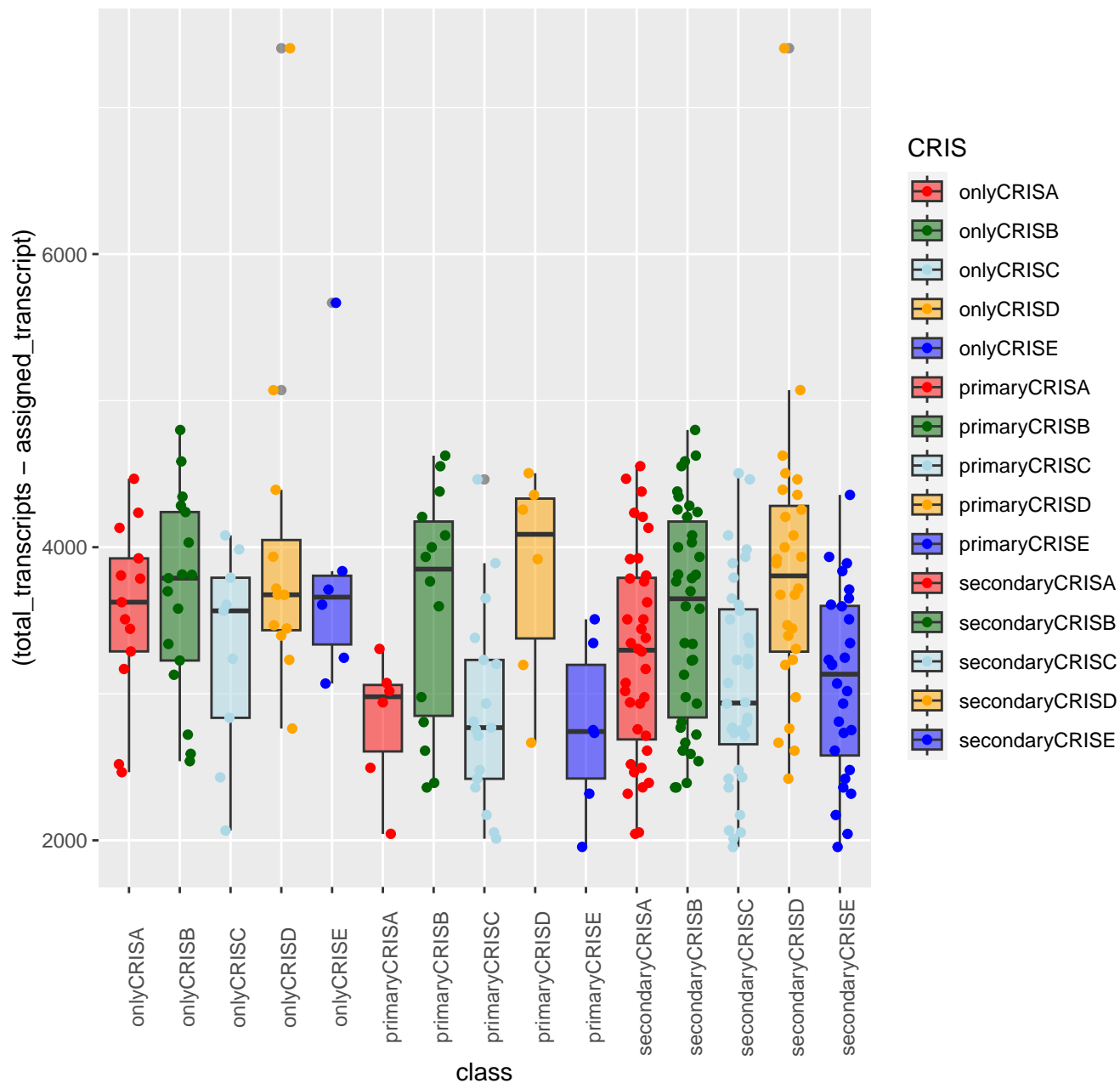Number of assigned not annotated transcripts for sample in each class

Number of assigned not annotated transcripts for sample in each class
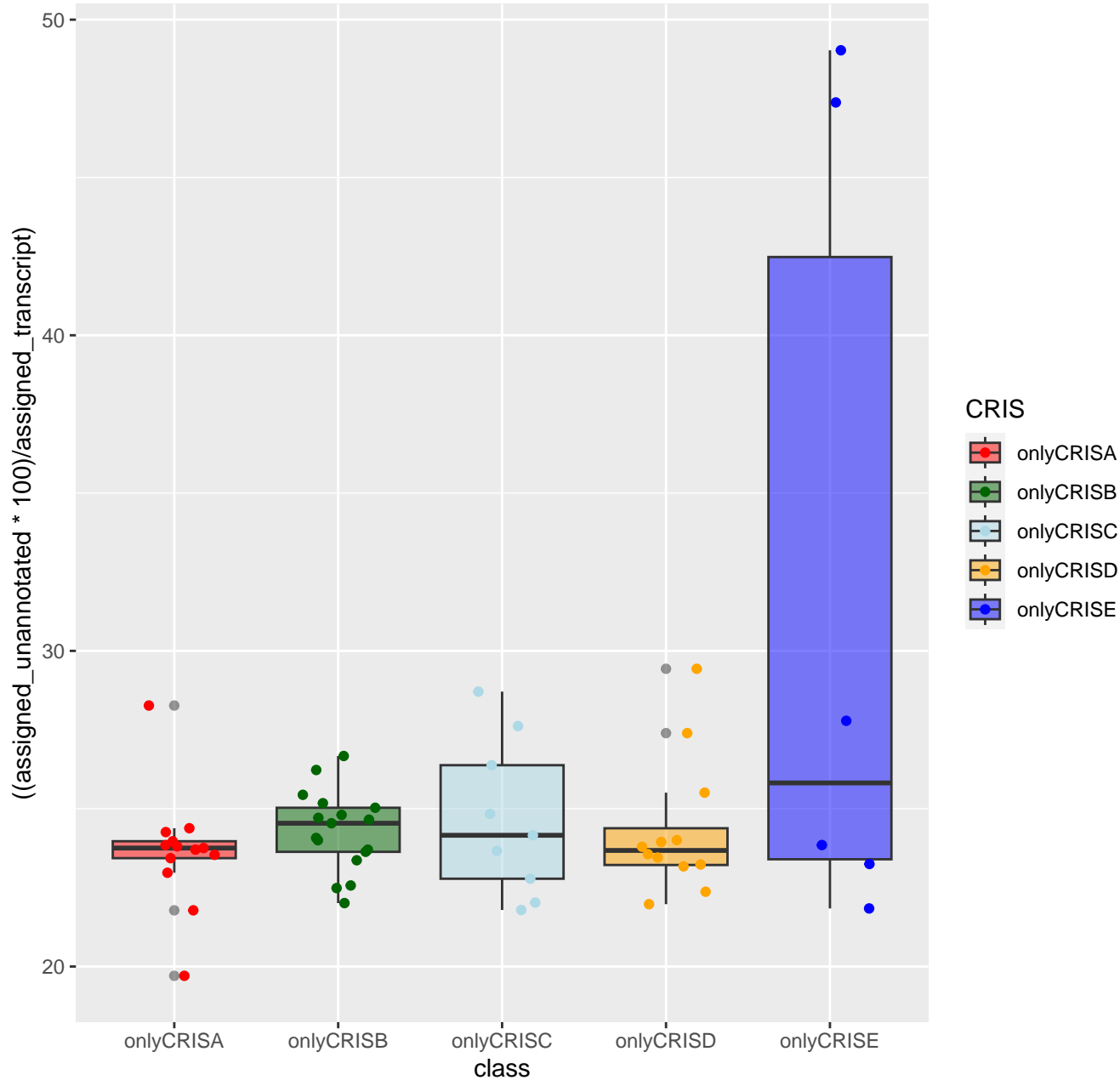
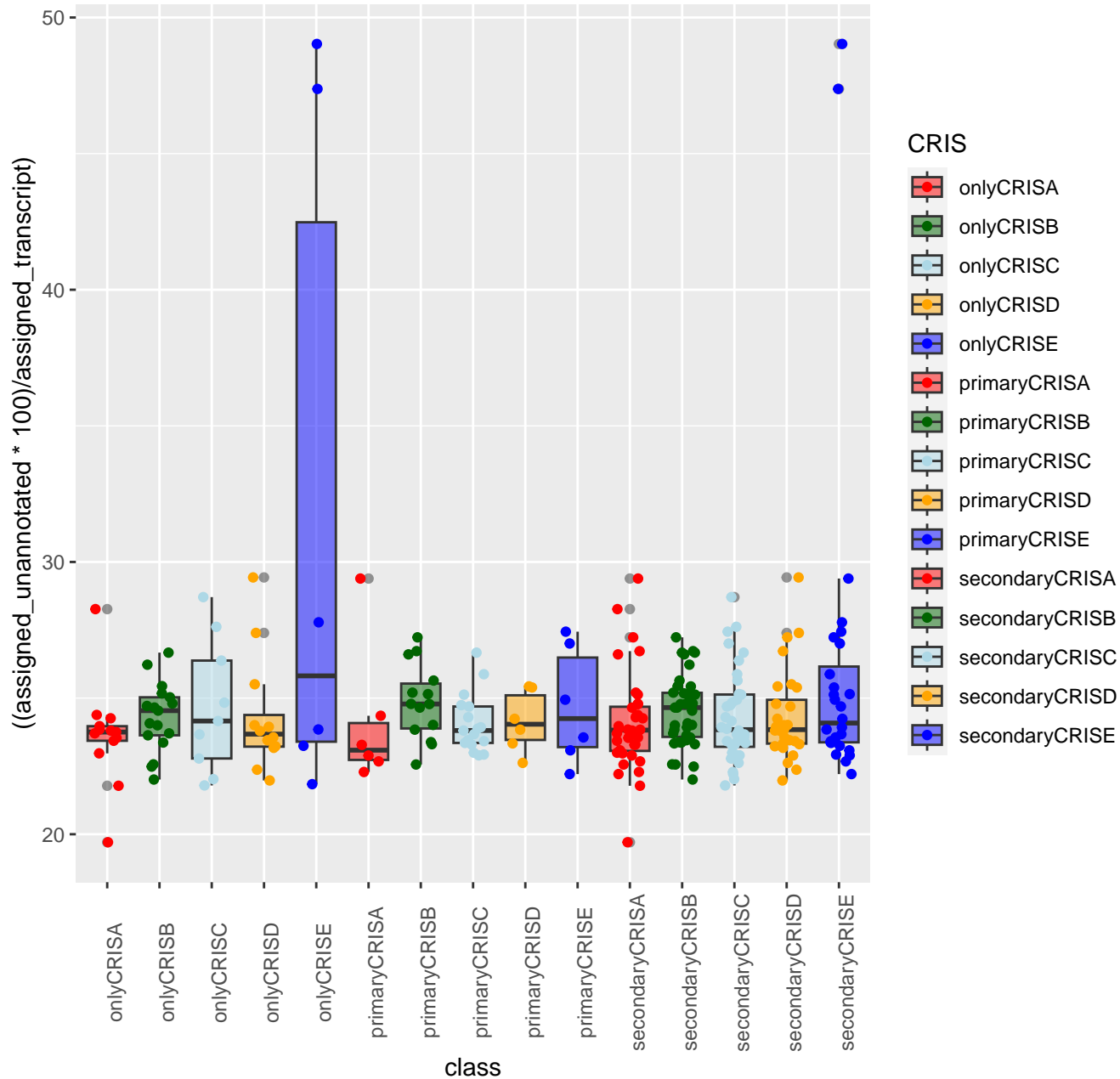Number of unassigned transcripts for sample in each class

Number of unassigned transcripts for sample in each class
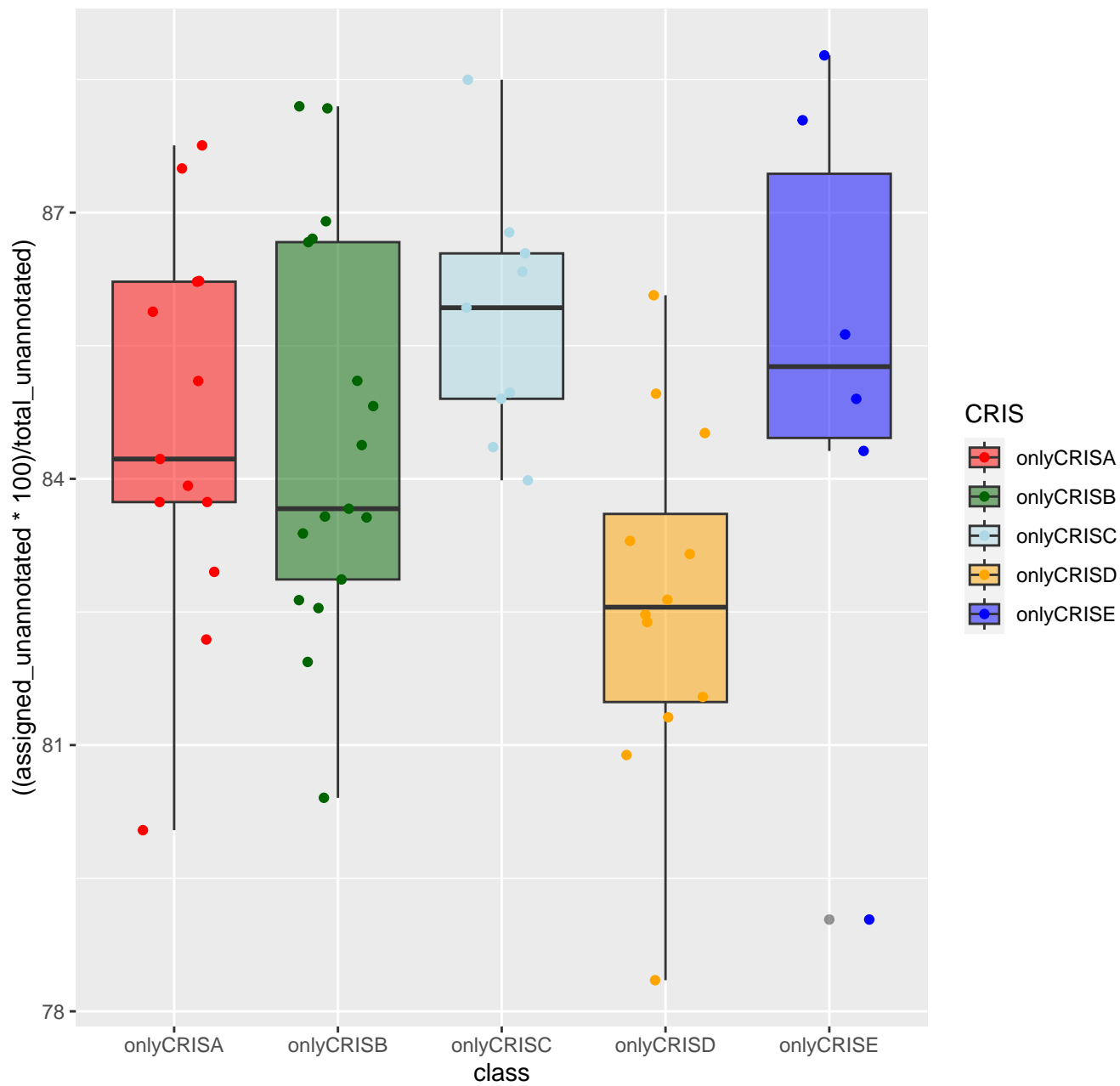
% of assigned not annotated transcripts for sample in each class

% of assigned not annotated transcripts for sample in each class

CRIS
- onlyCRISA
- onlyCRISB
- onlyCRISC
- onlyCRISD
- onlyCRISE
- primaryCRISA
- primaryCRISB
- primaryCRISC
- primaryCRISD
- primaryCRISE
- secondaryCRISA
- secondaryCRISB
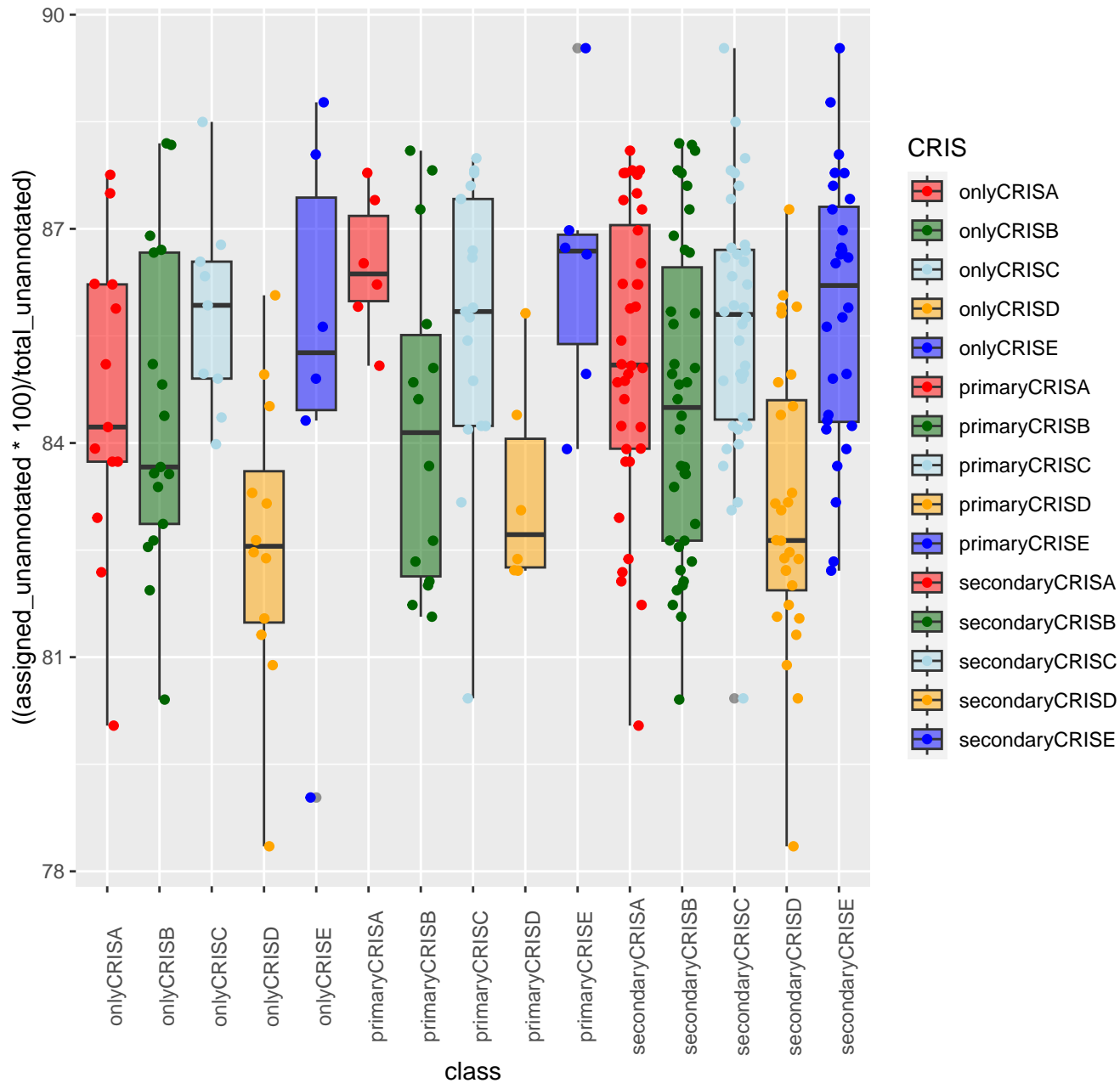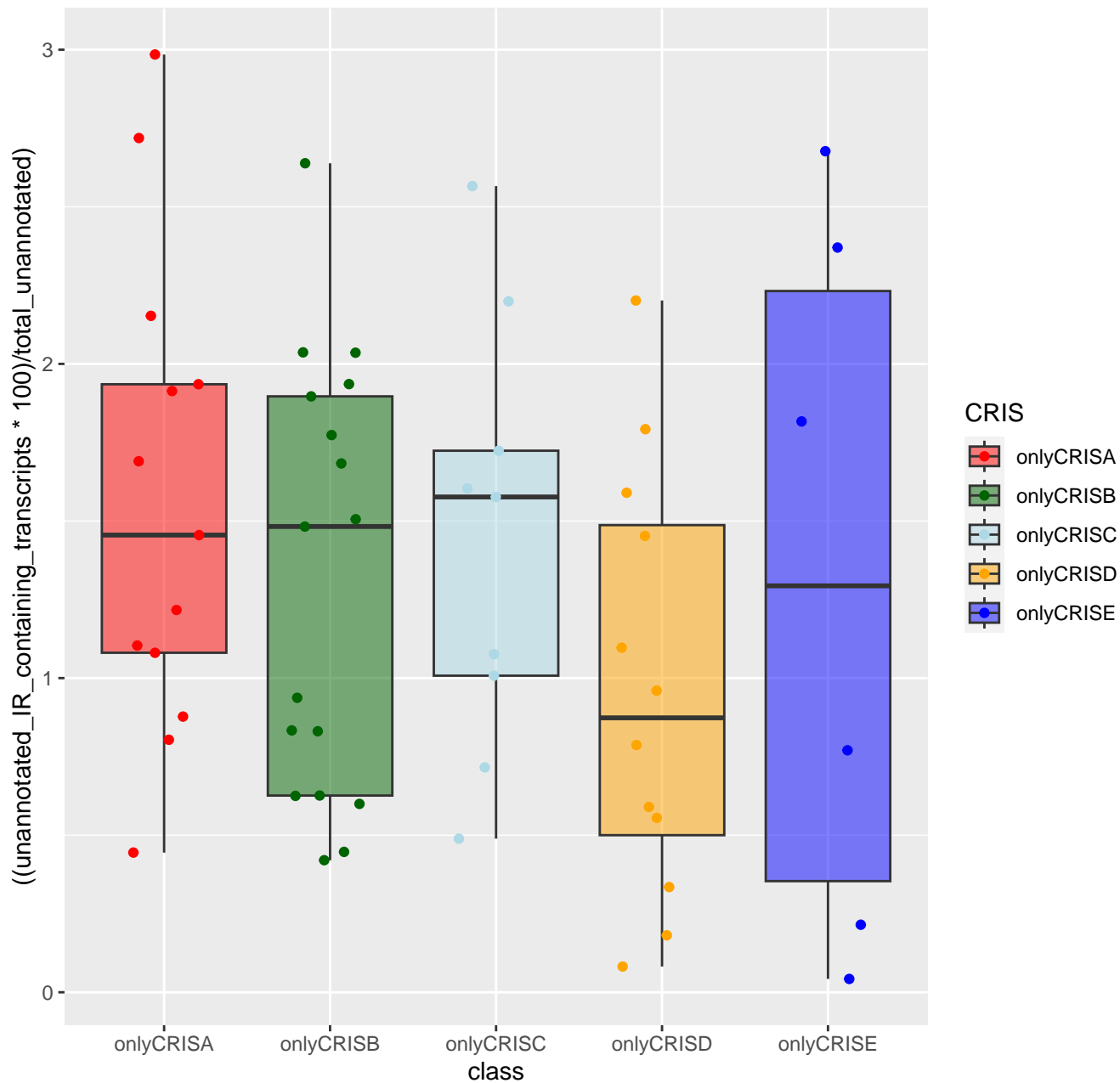- secondaryCRISC
- secondaryCRISD
- secondaryCRISE
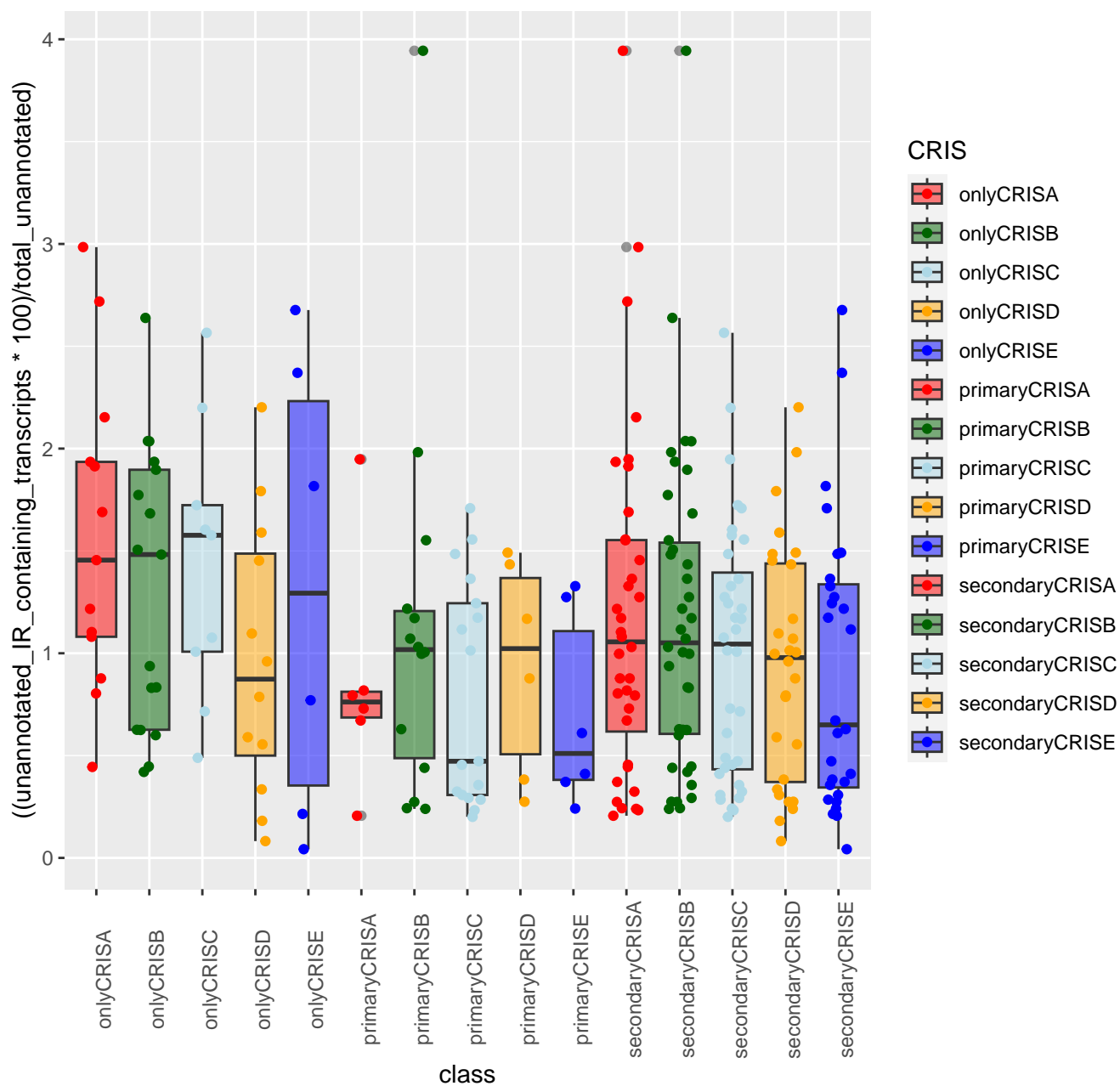
Rate of assignment for not annotated transcripts

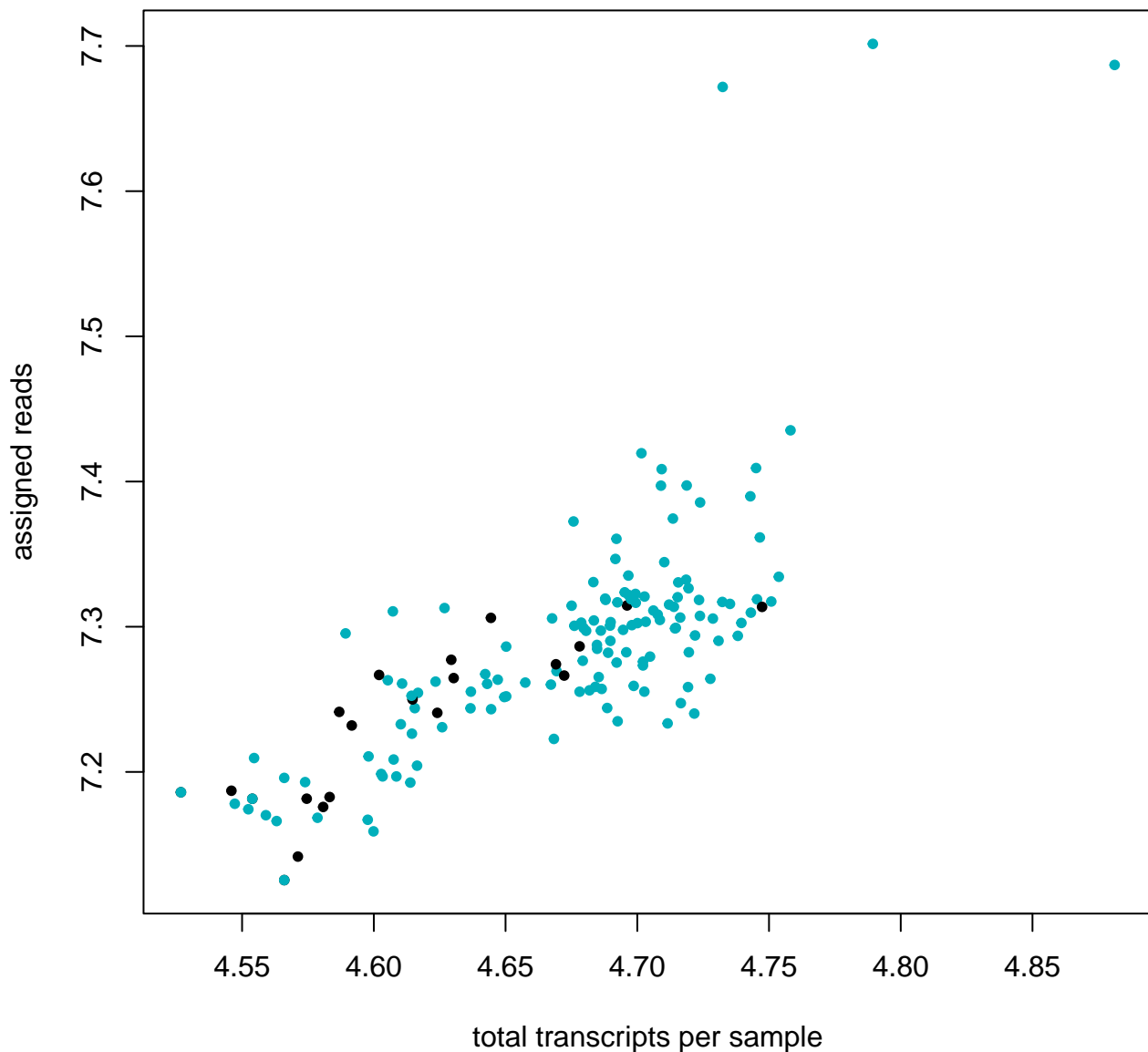Rate of assignment for not annotated transcripts

% IR containing not annotated transcripts for sample in each class

% of IR containing not annotated transcripts for sample in each class

Pearson correlation between transcript number and assigned reads: 0.688022400952397

total transcripts per sample

assigned reads

Distribution of number of isoforms per gene per sample

Number of isoforms per gene