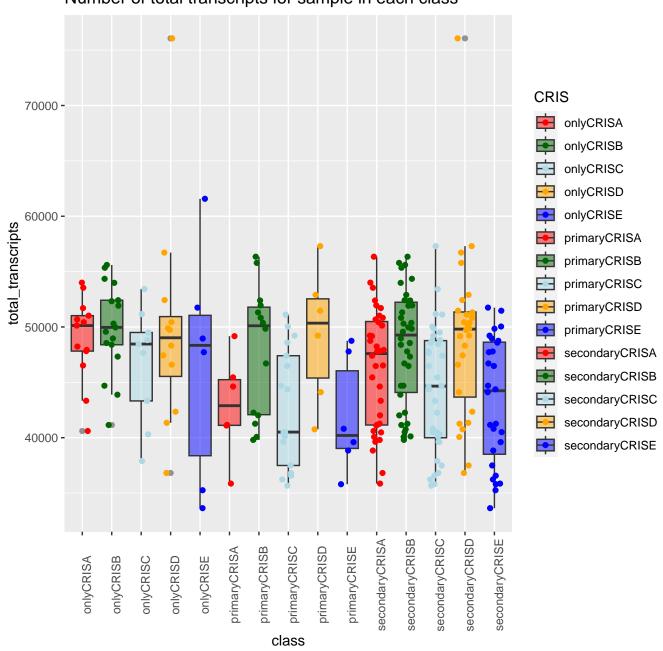
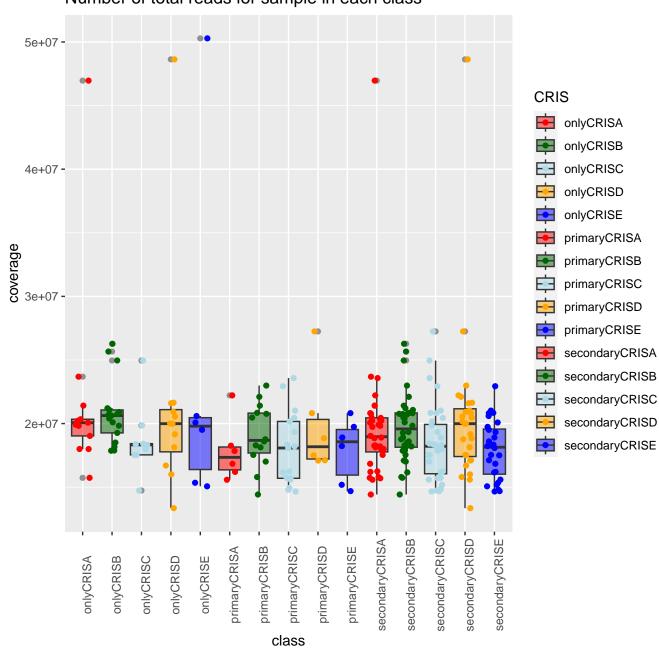
Number of total transcripts for sample in each class 70000 -60000 -**CRIS** total_transcripts onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE 50000 -40000 onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE class

Number of total transcripts for sample in each class



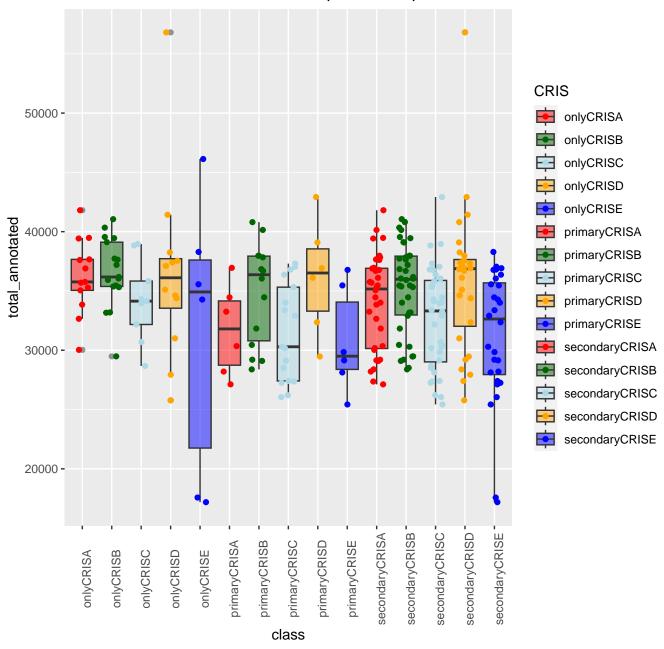
Number of total reads for sample in each class 5e+07 -4e+07 -**CRIS** onlyCRISA coverage onlyCRISB onlyCRISC 3e+07 onlyCRISD onlyCRISE 2e+07 onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE class

Number of total reads for sample in each class

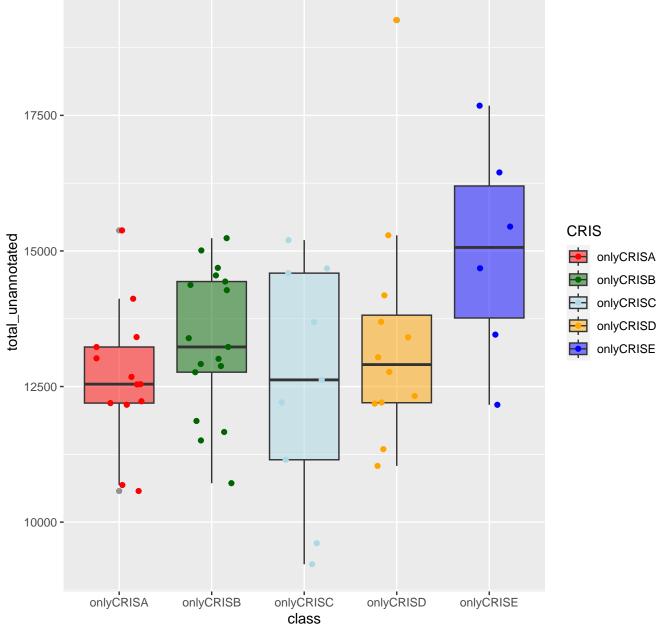


Number of total annotated transcripts for sample in each class 50000 -**CRIS** total_annotated 40000 onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE 30000 -20000 onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE class

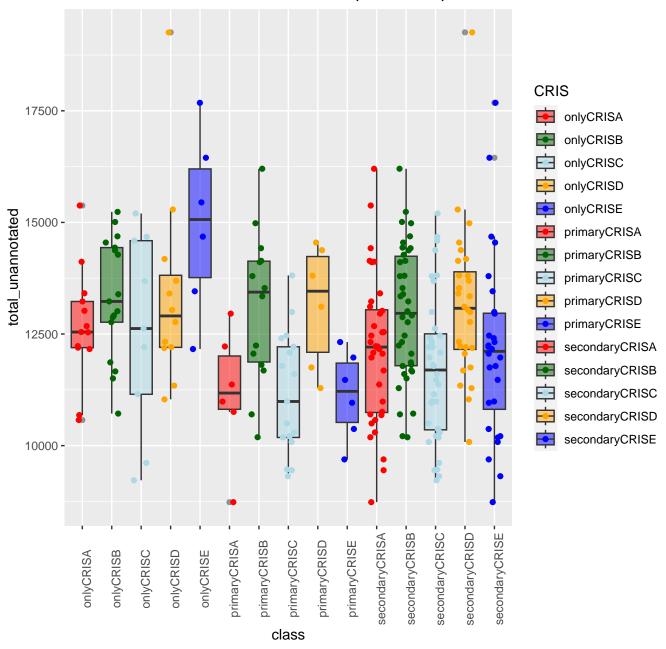
Number of total annotated transcripts for sample in each class



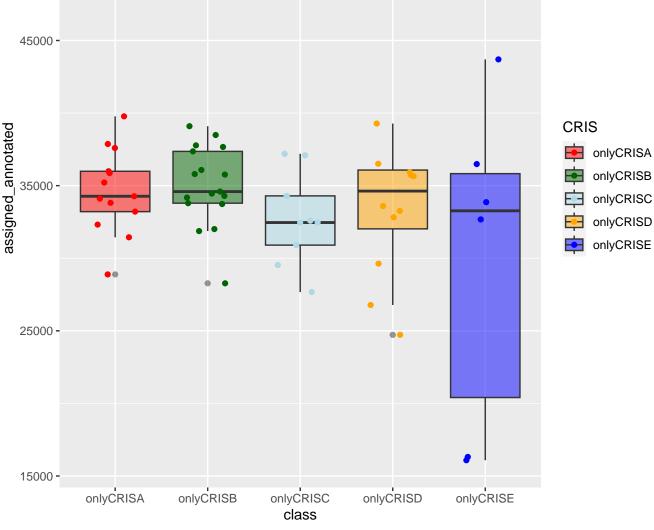
Number of total not annotated transcripts for sample in each class



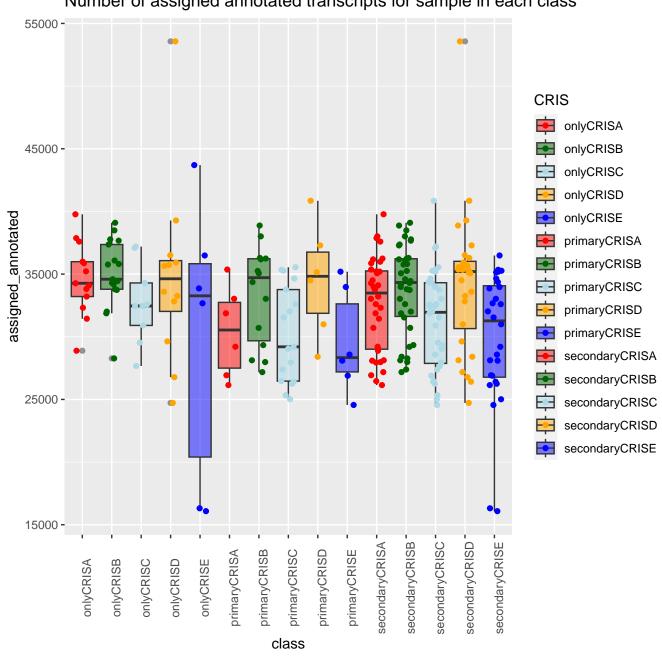
Number of total not annotated transcripts for sample in each class



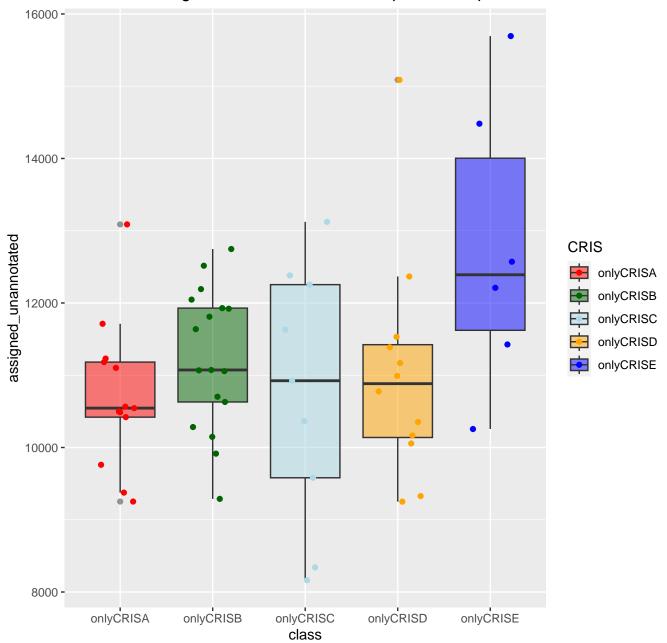
Number of assigned annotated transcripts for sample in each class 55000 -45000 **-CRIS** assigned_annotated onlyCRISA onlyCRISB 35000 onlyCRISC onlyCRISD onlyCRISE 25000 -



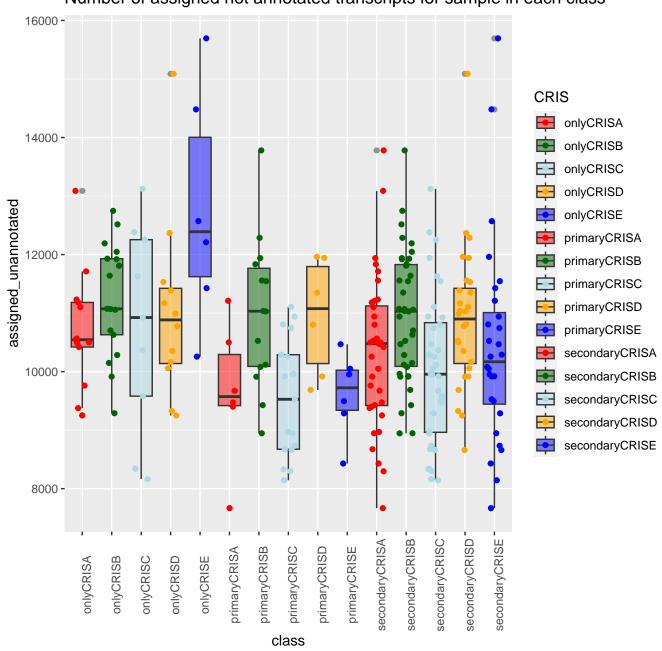
Number of assigned annotated transcripts for sample in each class



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 (total_transcripts - assigned_transcript)

Applies - assigned_transcript) **CRIS** onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE 2000 onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE class

Number of unassigned transcripts for sample in each class **CRIS** onlyCRISA onlyCRISB (total_transcripts - assigned_transcript) 6000 onlyCRISC onlyCRISD onlyCRISE primaryCRISA primaryCRISB primaryCRISC primaryCRISD 4000 primaryCRISE secondaryCRISA secondaryCRISB secondaryCRISC secondaryCRISD secondaryCRISE 2000 secondaryCRISB secondaryCRISC secondaryCRISA secondaryCRISD secondaryCRISE primaryCRISA primaryCRISC primaryCRISE primaryCRISB primaryCRISD onlyCRISC onlyCRISD onlyCRISE onlyCRISA onlyCRISB class

% of assigned not annotated transcripts for sample in each class 50 -((assigned_unannotated * 100)/assigned_transcript) **CRIS** onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE 20 onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE class

% of assigned not annotated transcripts for sample in each class 50 -**CRIS** ((assigned_unannotated * 100)/assigned_transcript) onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE primaryCRISA primaryCRISB primaryCRISC primaryCRISD primaryCRISE 30 secondaryCRISA 00 secondaryCRISB secondaryCRISC secondaryCRISD secondaryCRISE 20 secondaryCRISC secondaryCRISA secondaryCRISB secondaryCRISD secondaryCRISE primaryCRISB primaryCRISA primaryCRISC primaryCRISD primaryCRISE onlyCRISD onlyCRISA onlyCRISB onlyCRISC onlyCRISE

class

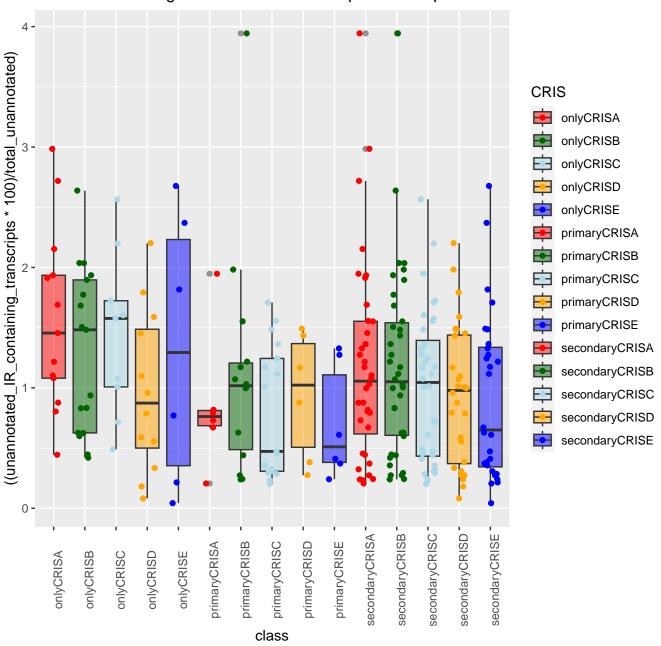
Rate of assignment for not annotated transcripts 87 -((assigned_unannotated * 100)/total_unannotated) **CRIS** onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE 78 onlyCRISD onlyCRISB onlyCRISC onlyCRISE onlyCRISA class

Rate of assignment for not annotated transcripts 90 -**CRIS** ((assigned_unannotated * 100)/total_unannotated) onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE primaryCRISA primaryCRISB 84 primaryCRISC primaryCRISD primaryCRISE secondaryCRISA secondaryCRISB secondaryCRISC secondaryCRISD secondaryCRISE 78 secondaryCRISA secondaryCRISD secondaryCRISB secondaryCRISC secondaryCRISE primaryCRISA primaryCRISB primaryCRISC primaryCRISD primaryCRISE onlyCRISD onlyCRISE onlyCRISC onlyCRISA onlyCRISB

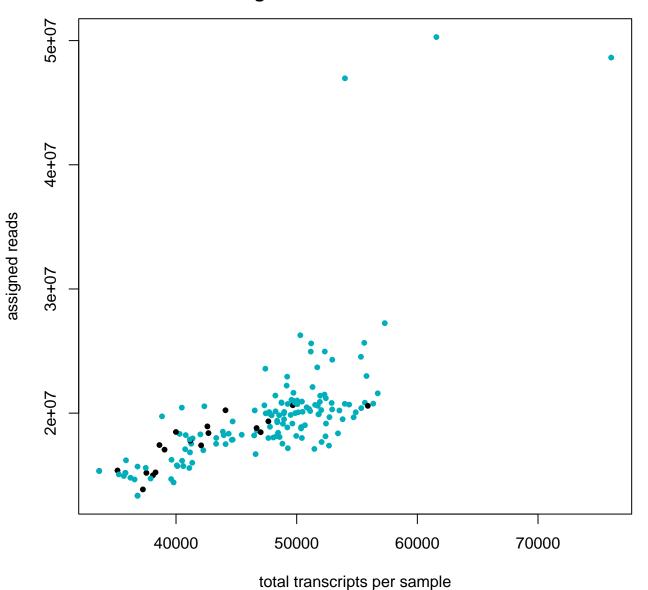
class

% IR containing not annotated transcripts for sample in each class 3 -((unannotated_IR_containing_transcripts * 100)/total_unannotated) **CRIS** onlyCRISA onlyCRISB onlyCRISC onlyCRISD onlyCRISE 0 onlyCRISA onlyCRISC onlyCRISB onlyCRISD onlyCRISE class

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



Pearson correlation between transcript number and assigned reads: 0.688022400952397



Distribution of number of isoforms per gene per sample

