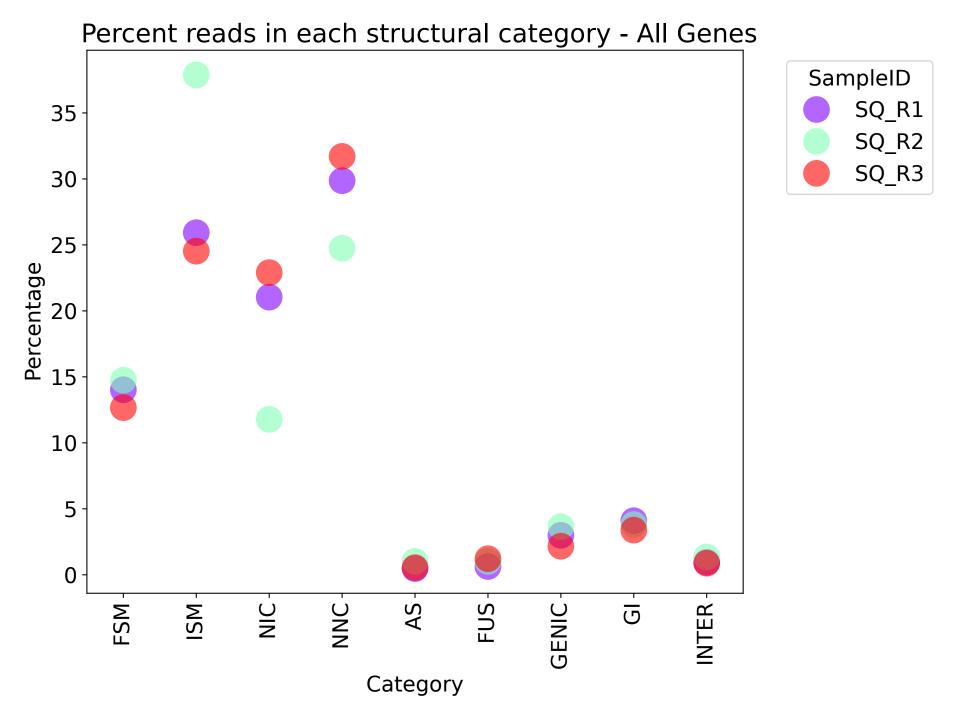
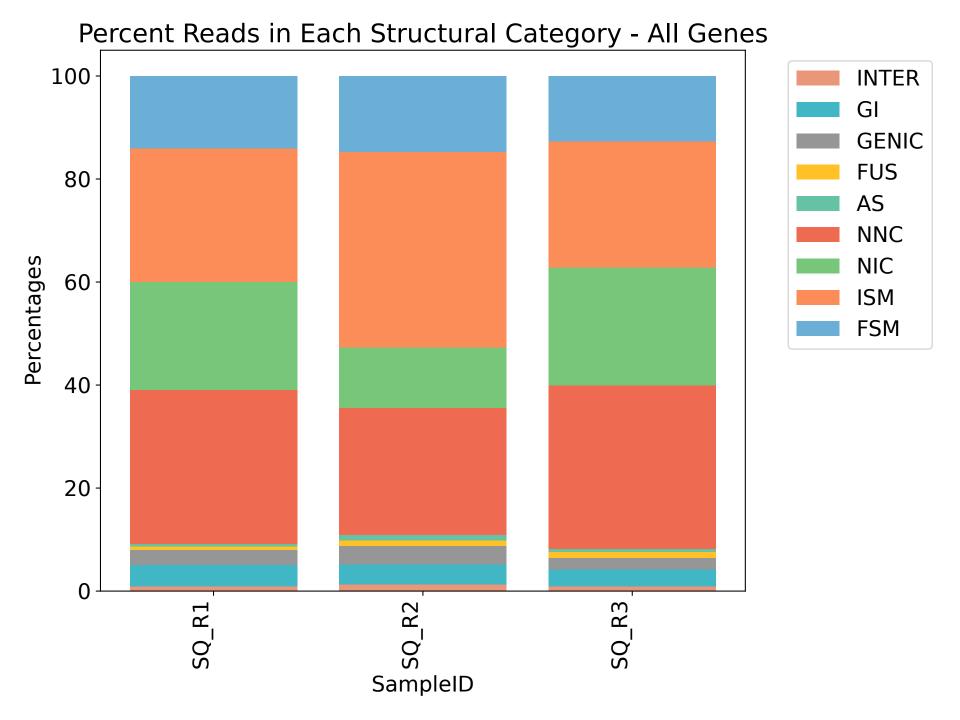
**SQANTI-reads** report

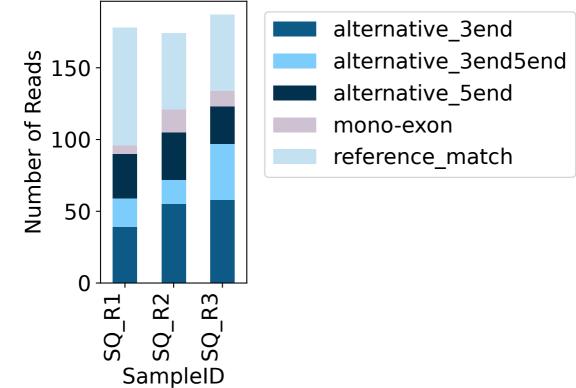


Percent reads in each structural category - Annotated Genes SampleID 40 SQ\_R1 SQ\_R2 SQ\_R3 30 Percentage 10 0 GENIC INTER FSM ISM <u>G</u> AS Category

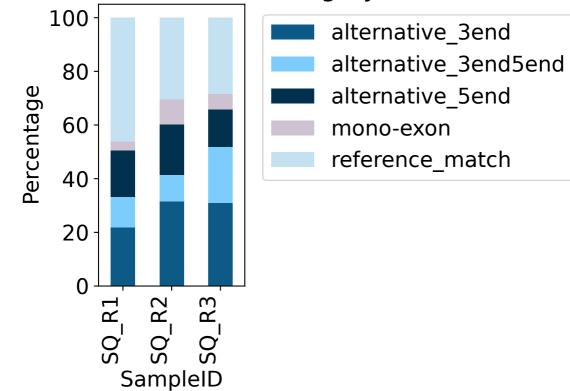


ads in Each Structural Category - Annotated Ger 100 GI **GENIC** 80 Percentages **NNC** 60 NIC **ISM** 40 **FSM** 20 SQ R1 SQ\_R2 SQ\_R3 SampleID

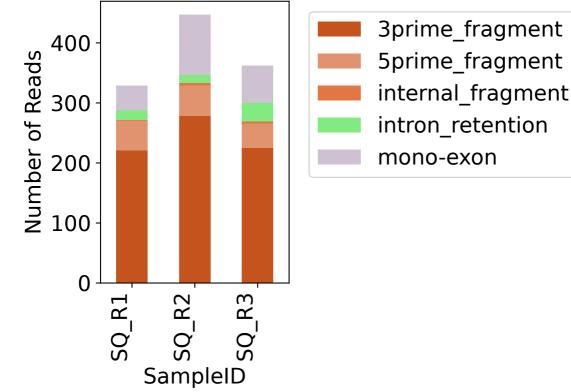
## of Reads in Each subcategory - FSM



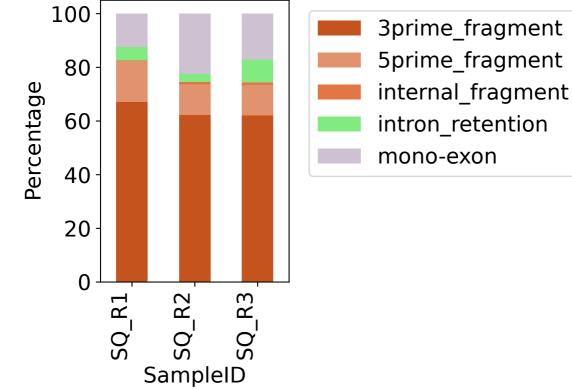
## of Reads in Each subcategory - FSM



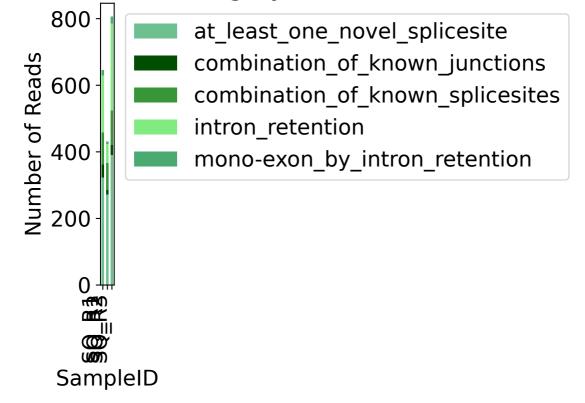
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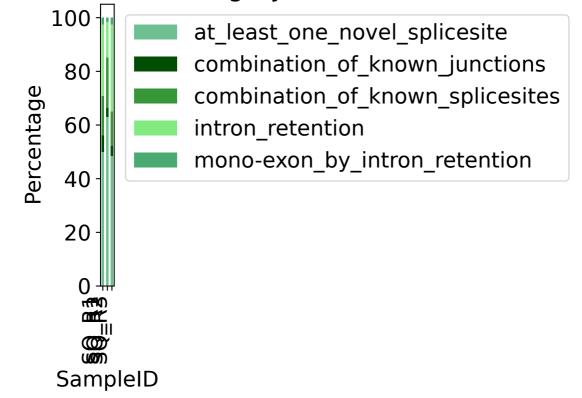
# er of Reads in Each subcategory - ISM

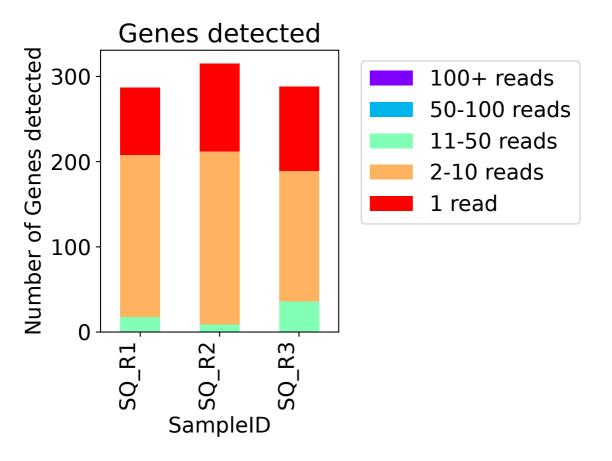


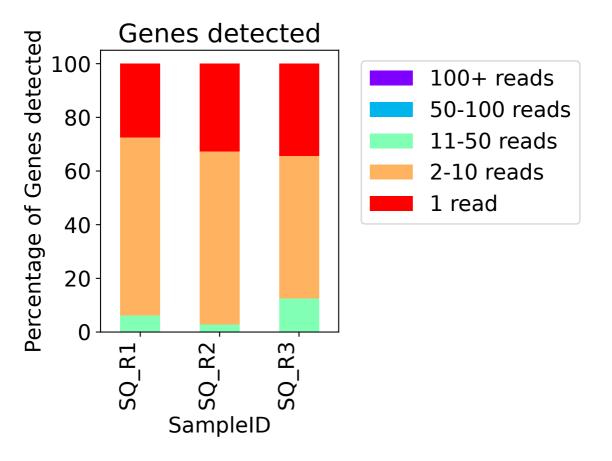
## s in Each subcategory - NIC/NNC

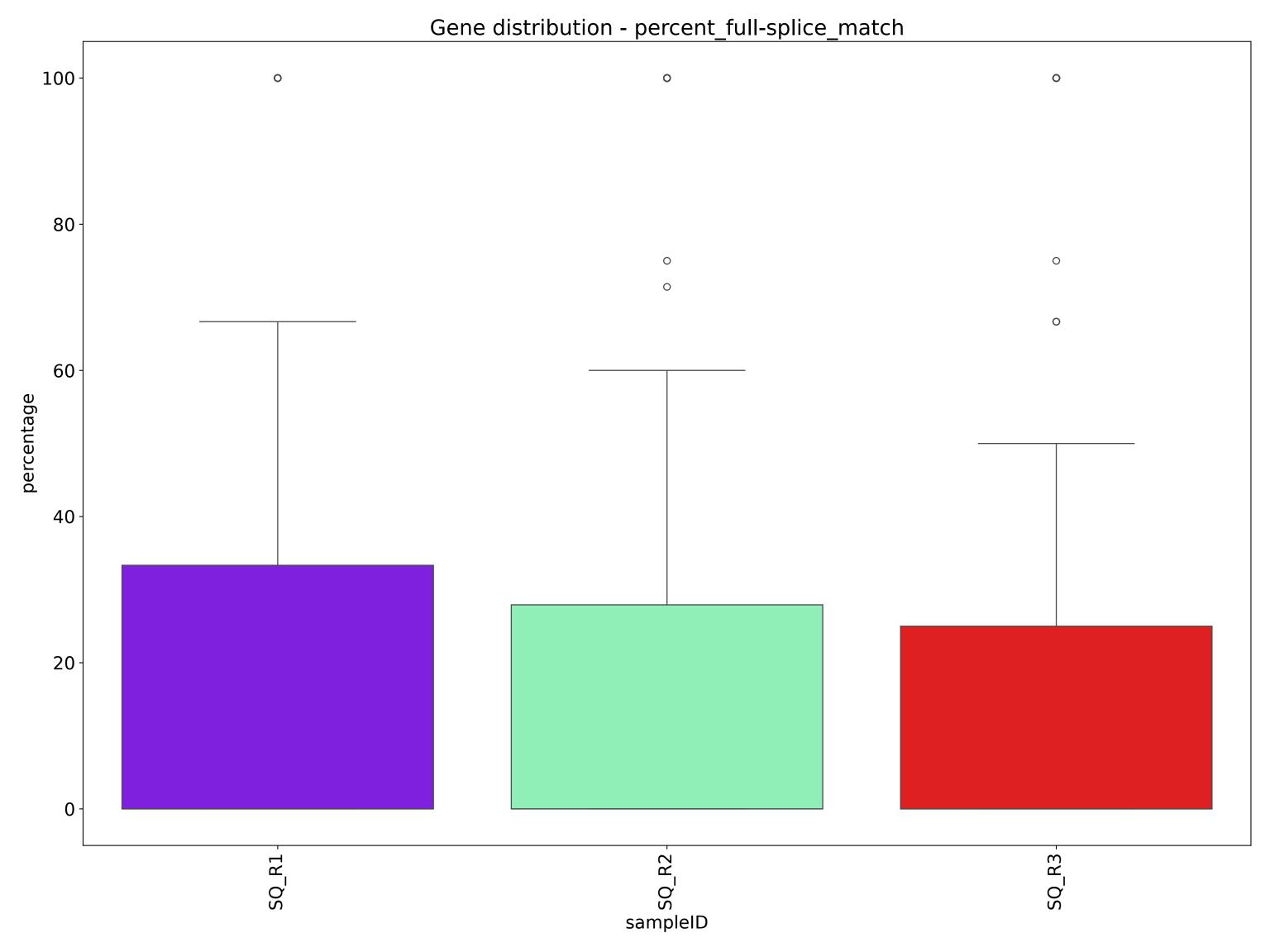


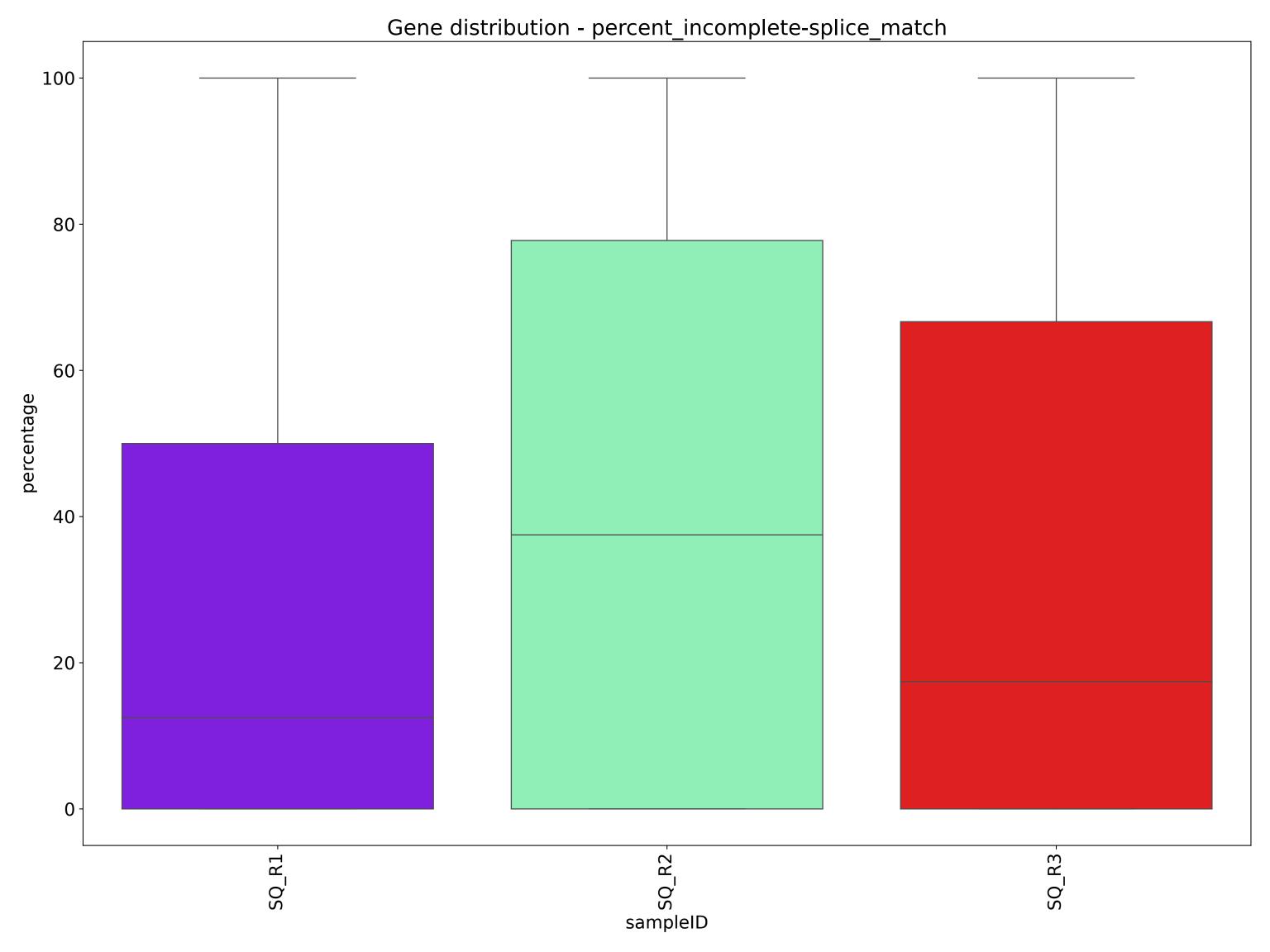
### s in Each subcategory - NIC/NNC

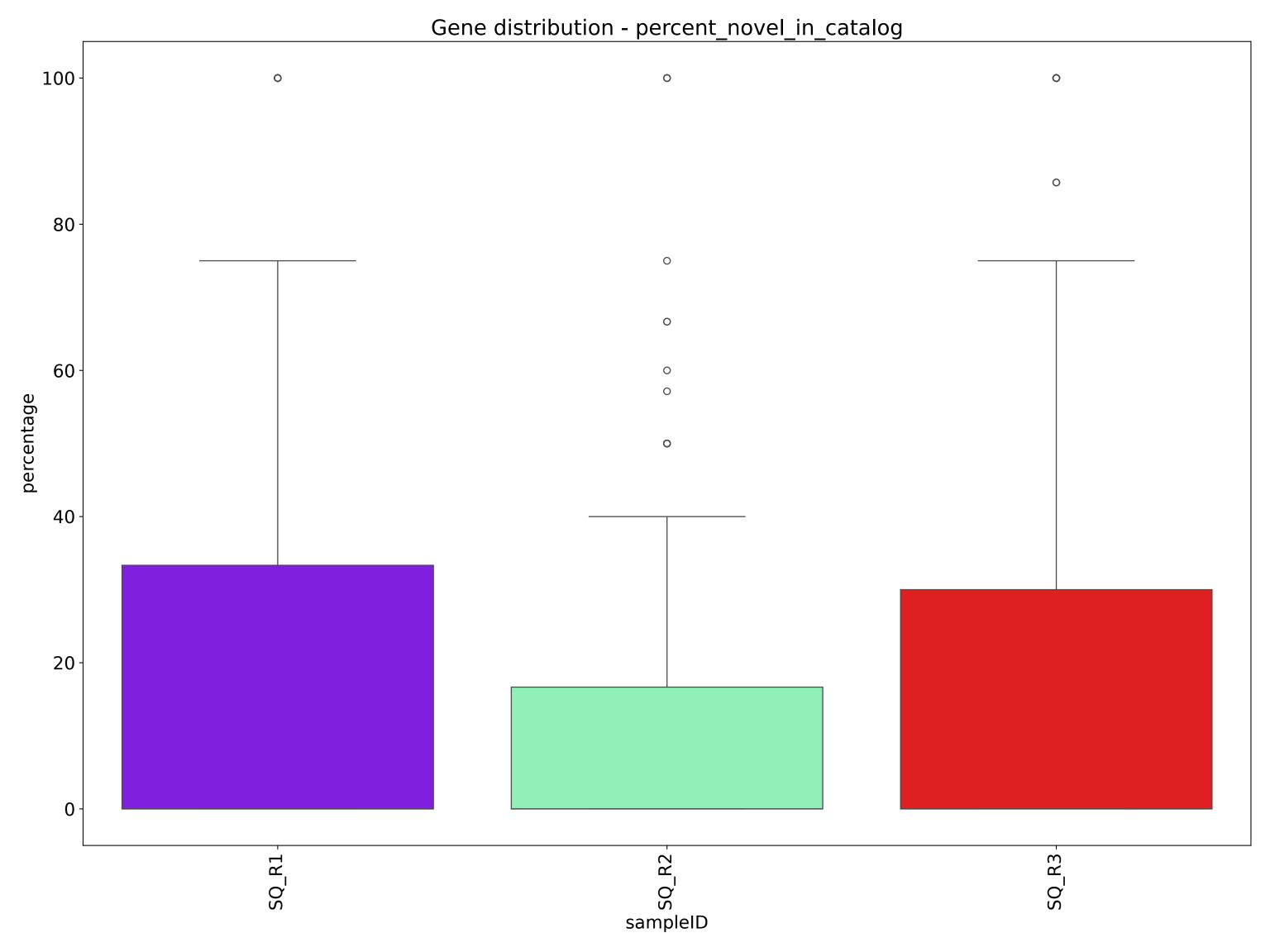


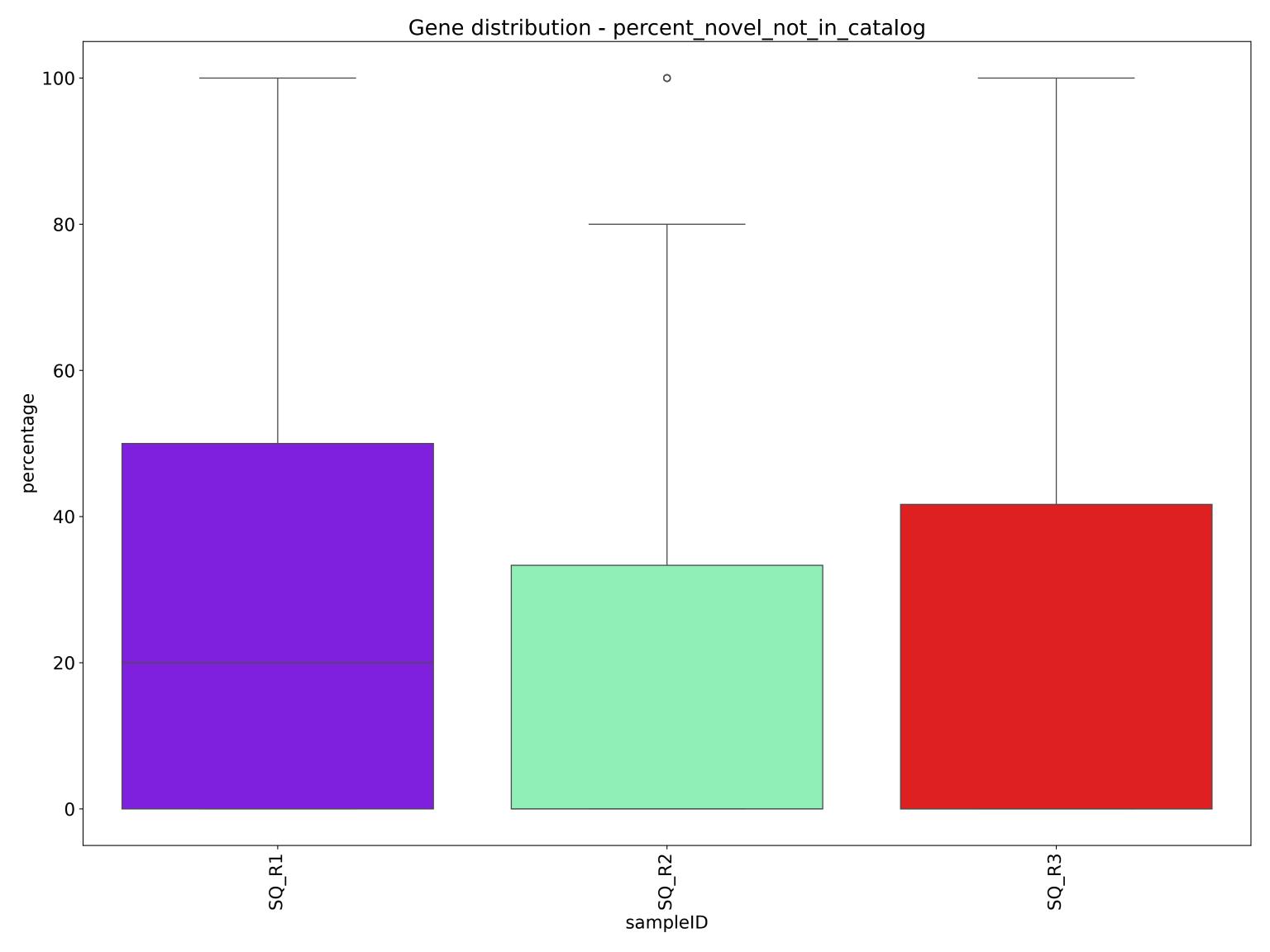


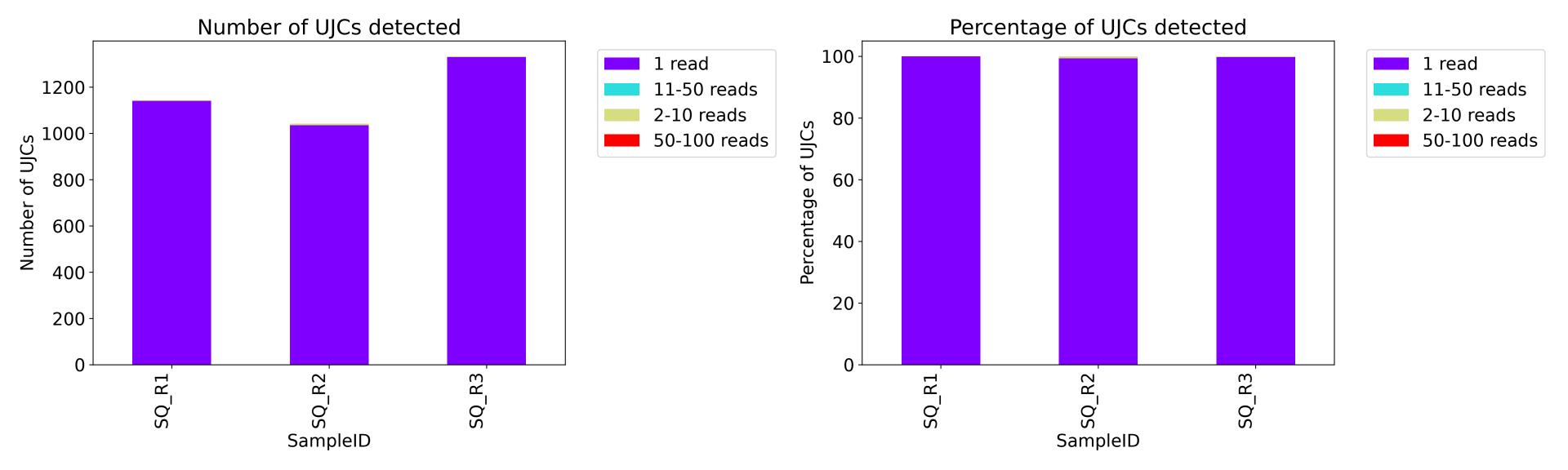


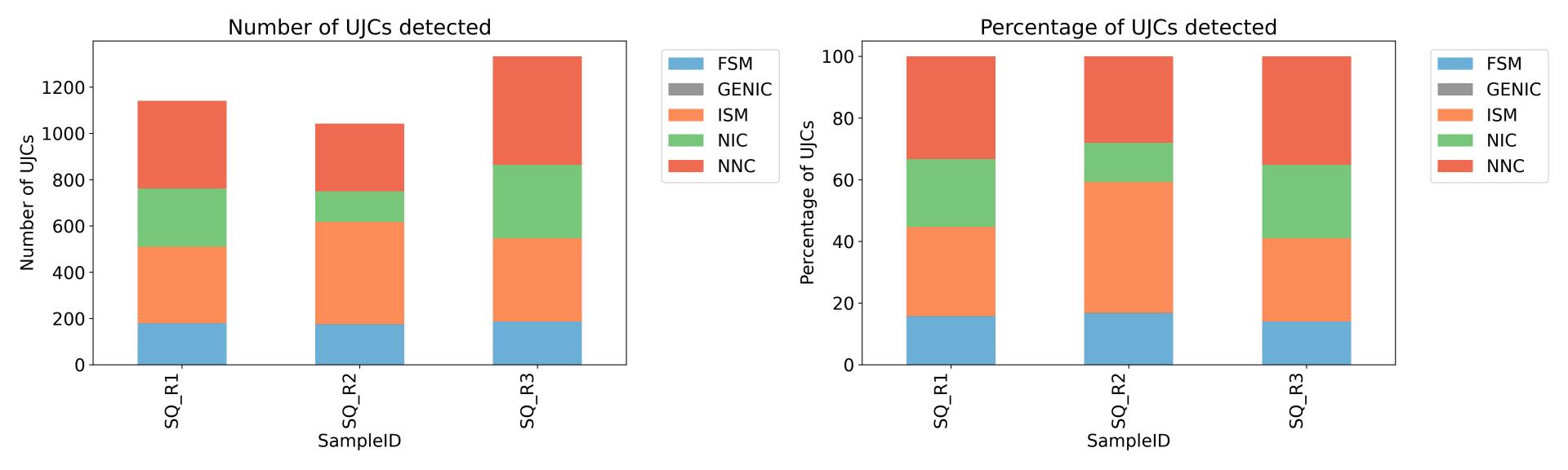


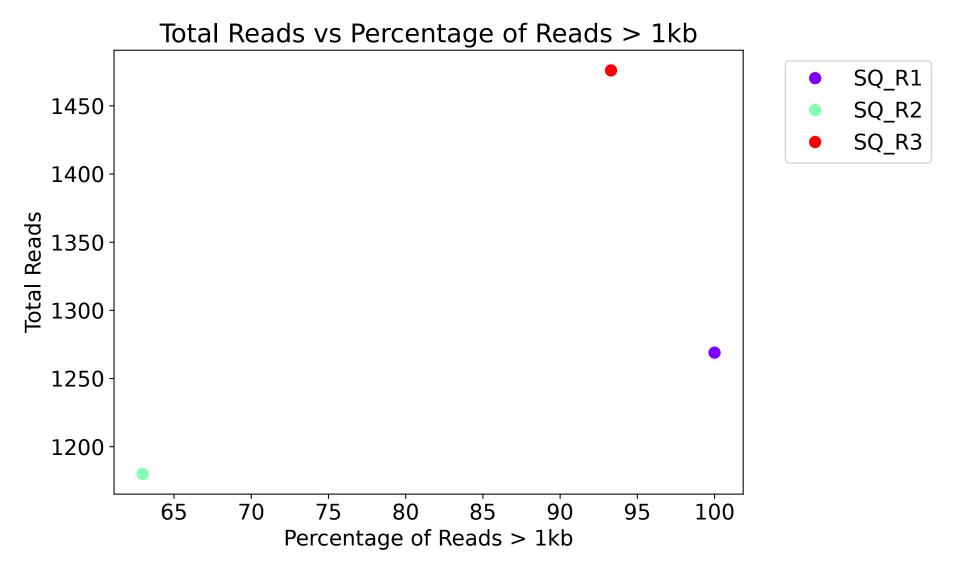




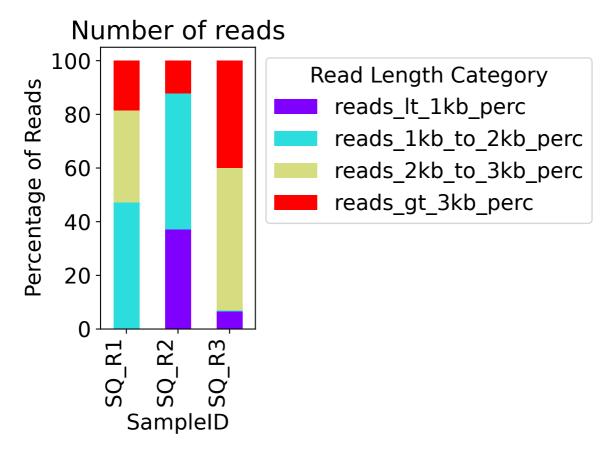


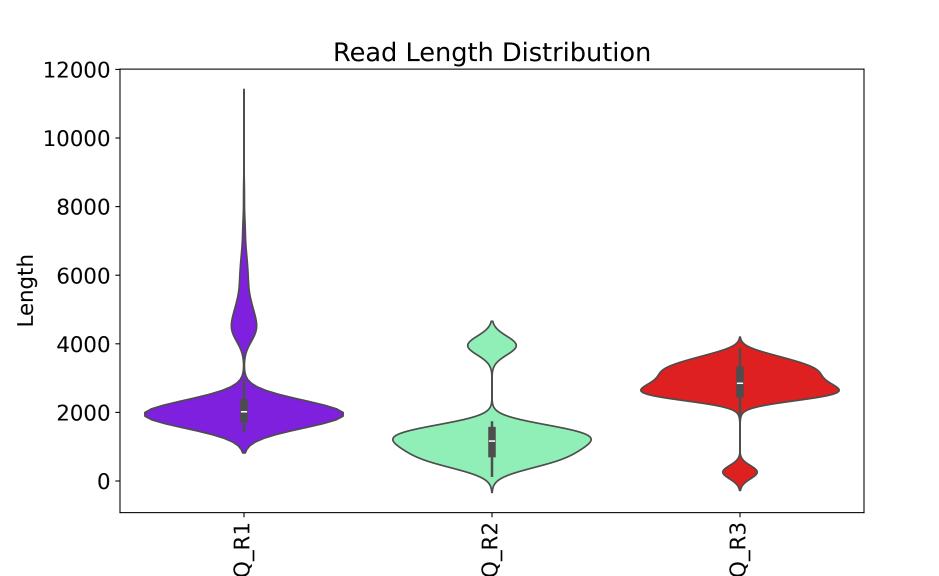


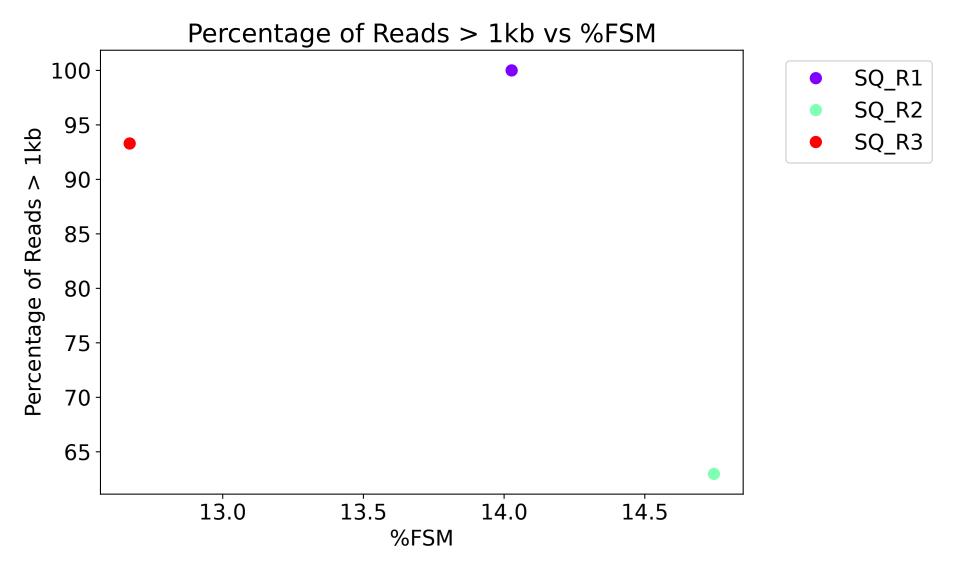


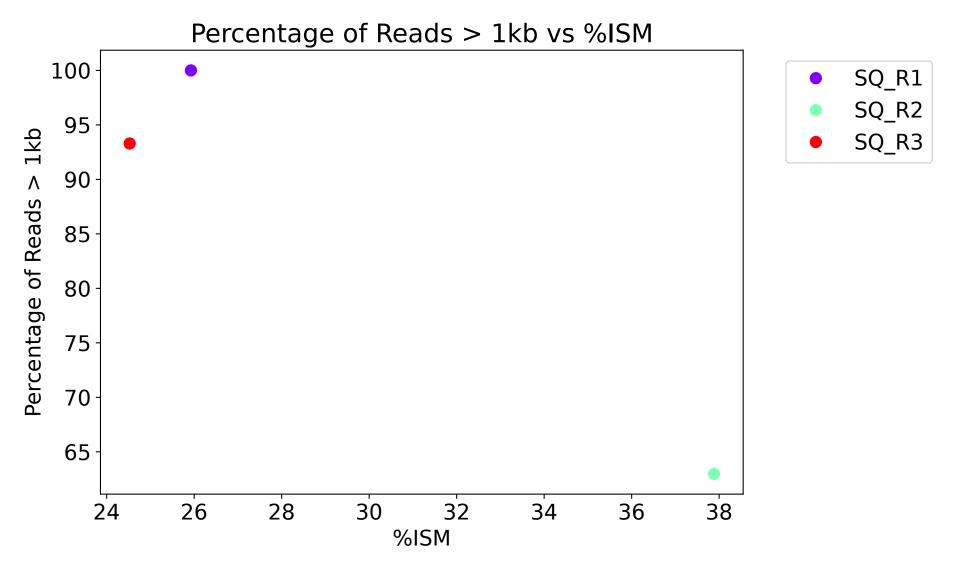


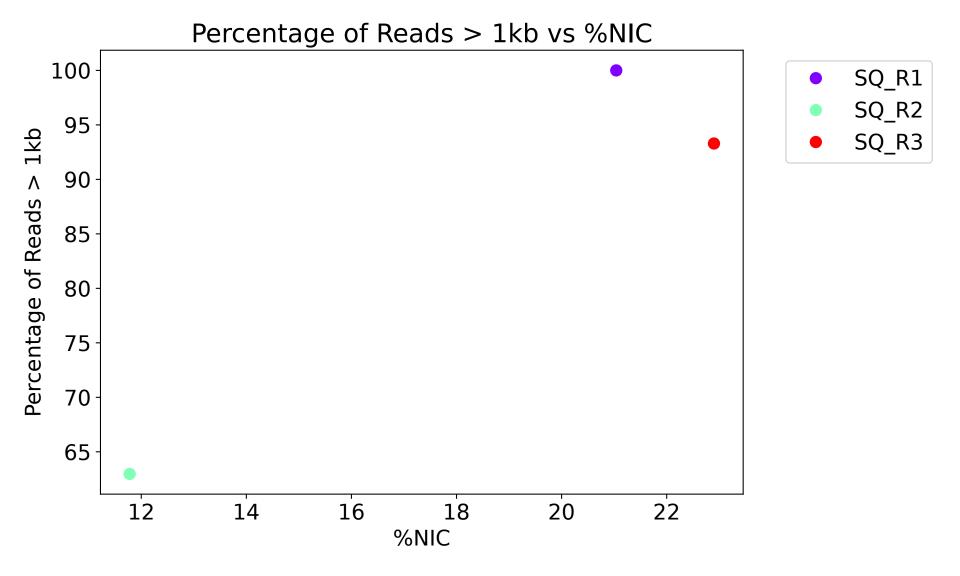


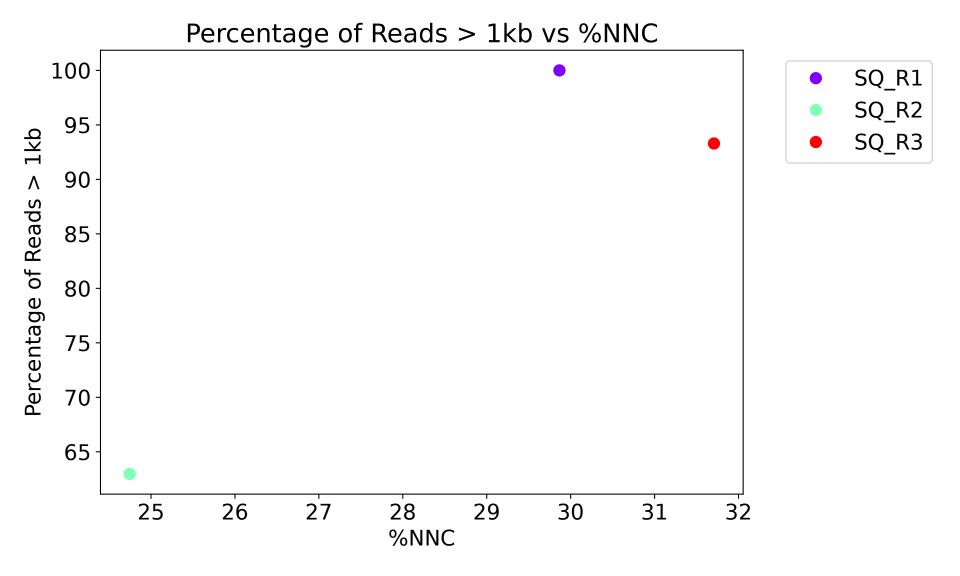


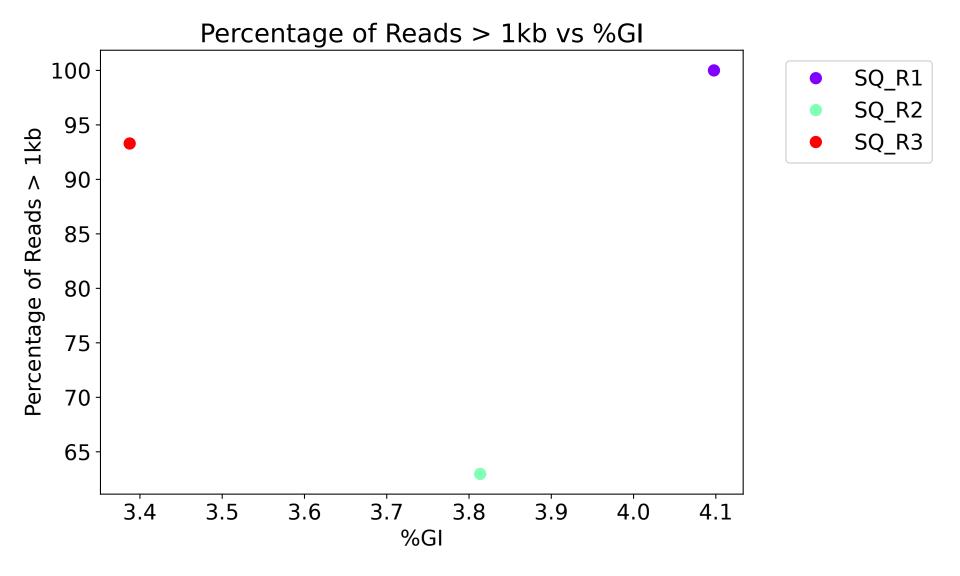


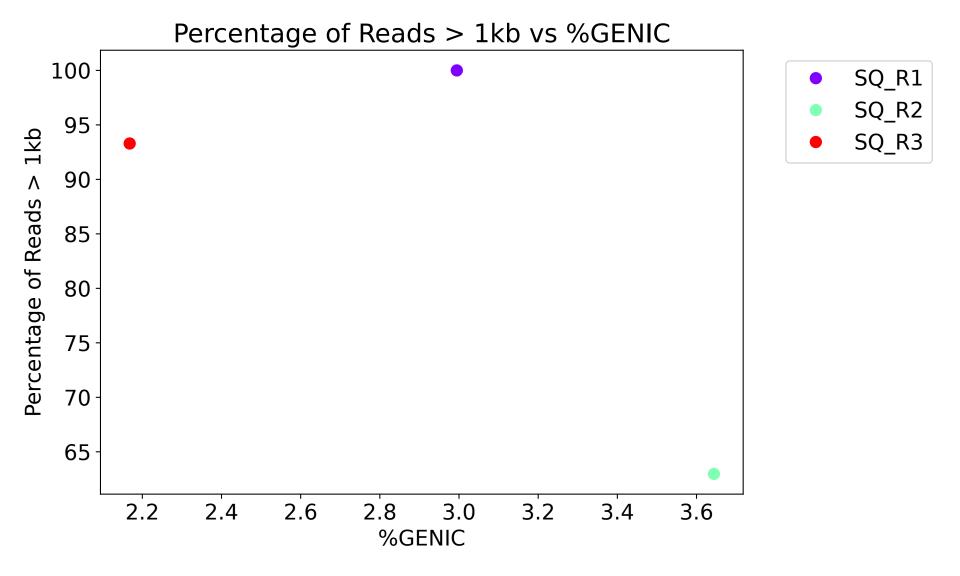




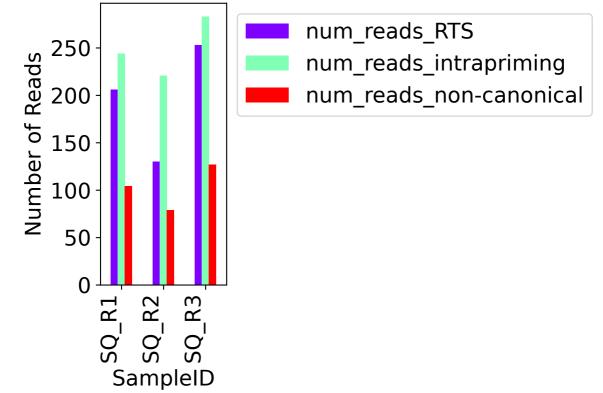








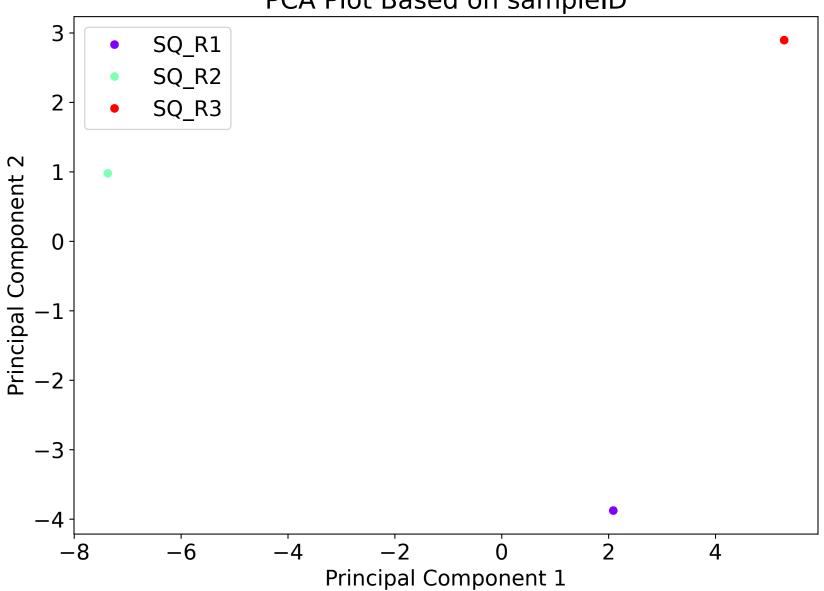
### Number of Artefact reads

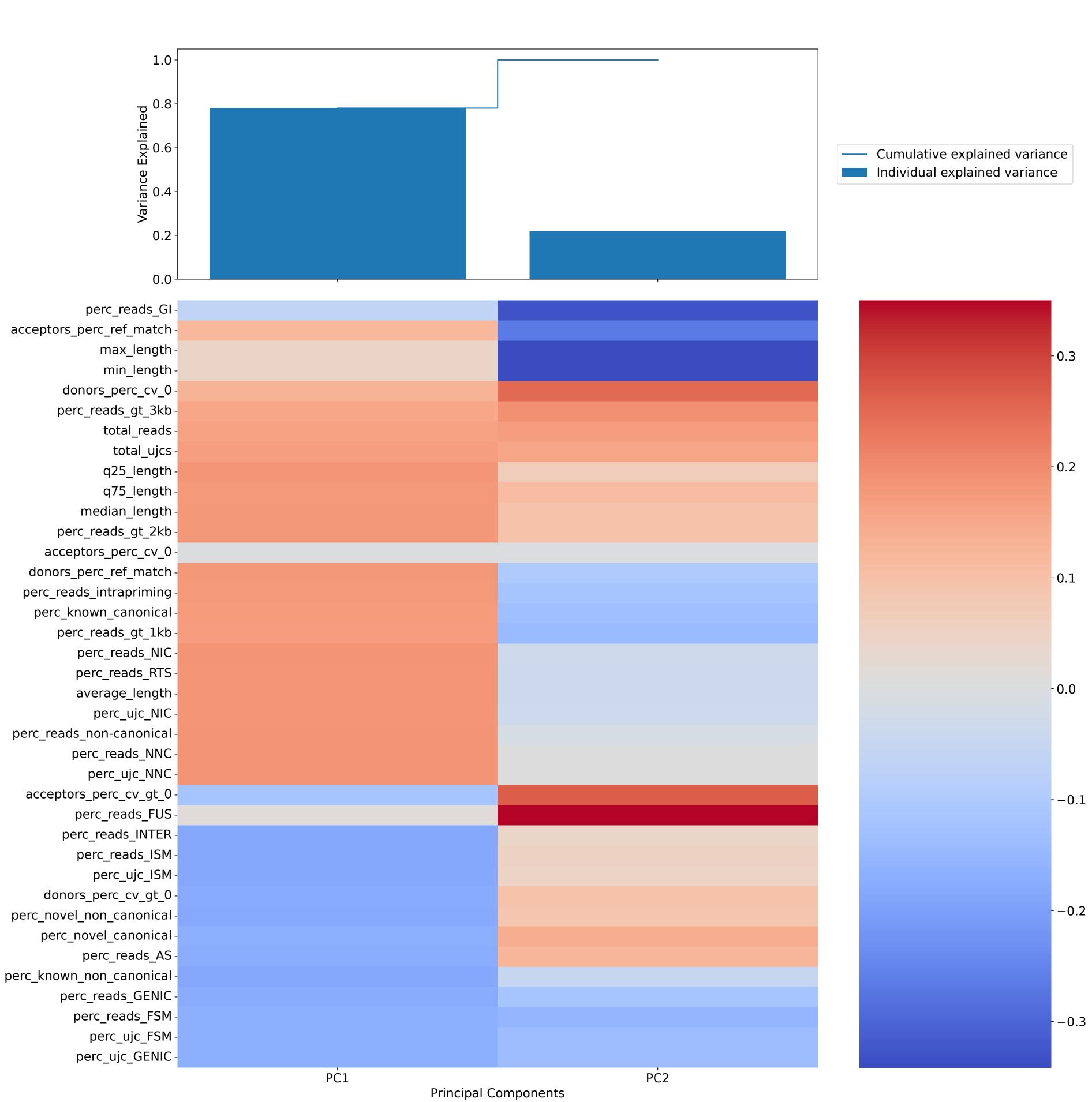


Percent Artefact reads 20 perc reads RTS perc\_reads\_intrapriming 15 Percentage perc\_reads\_non-canonical 10

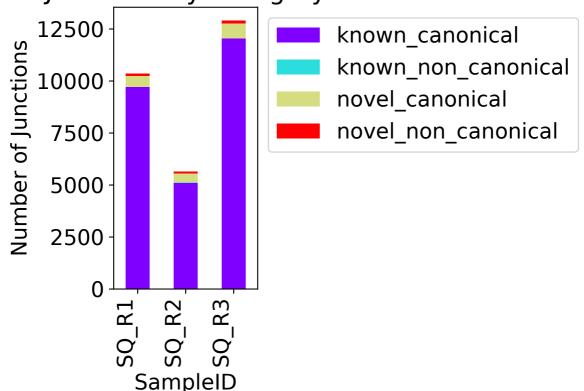
SampleID

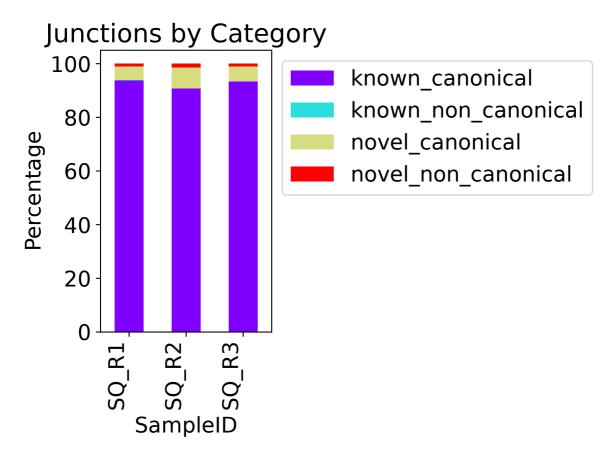
PCA Plot Based on sampleID

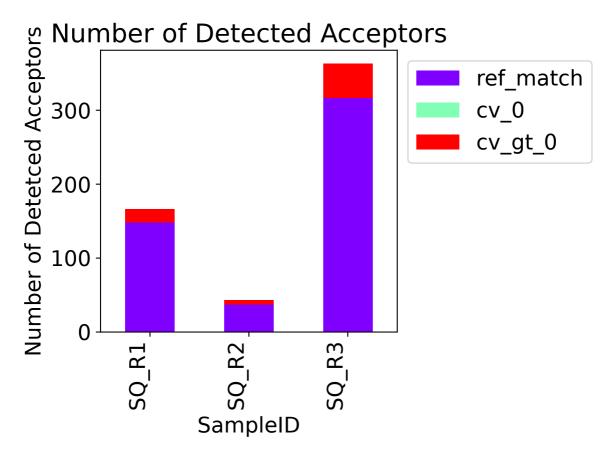


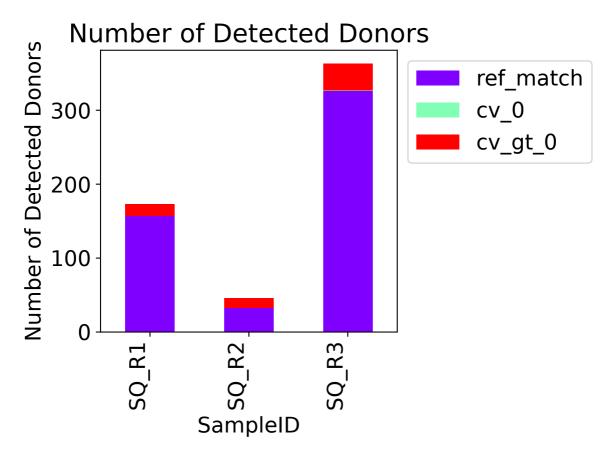


Junctions by Category

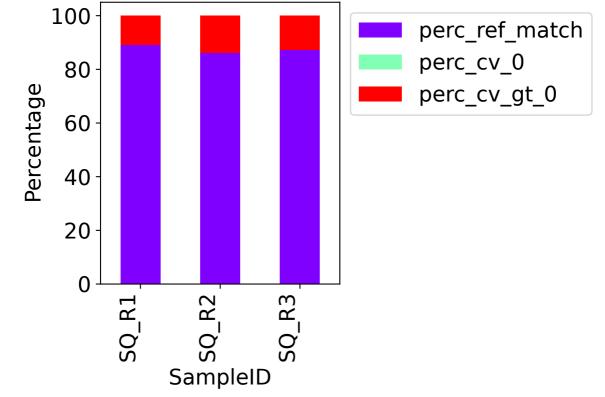








## Percentage of Detected Acceptors



# Number of Donors > 3 reads 100 perc ref match **Number of Donors** perc\_cv\_0 80 perc cv gt 0 60 40 20 SQ R1 SampleID