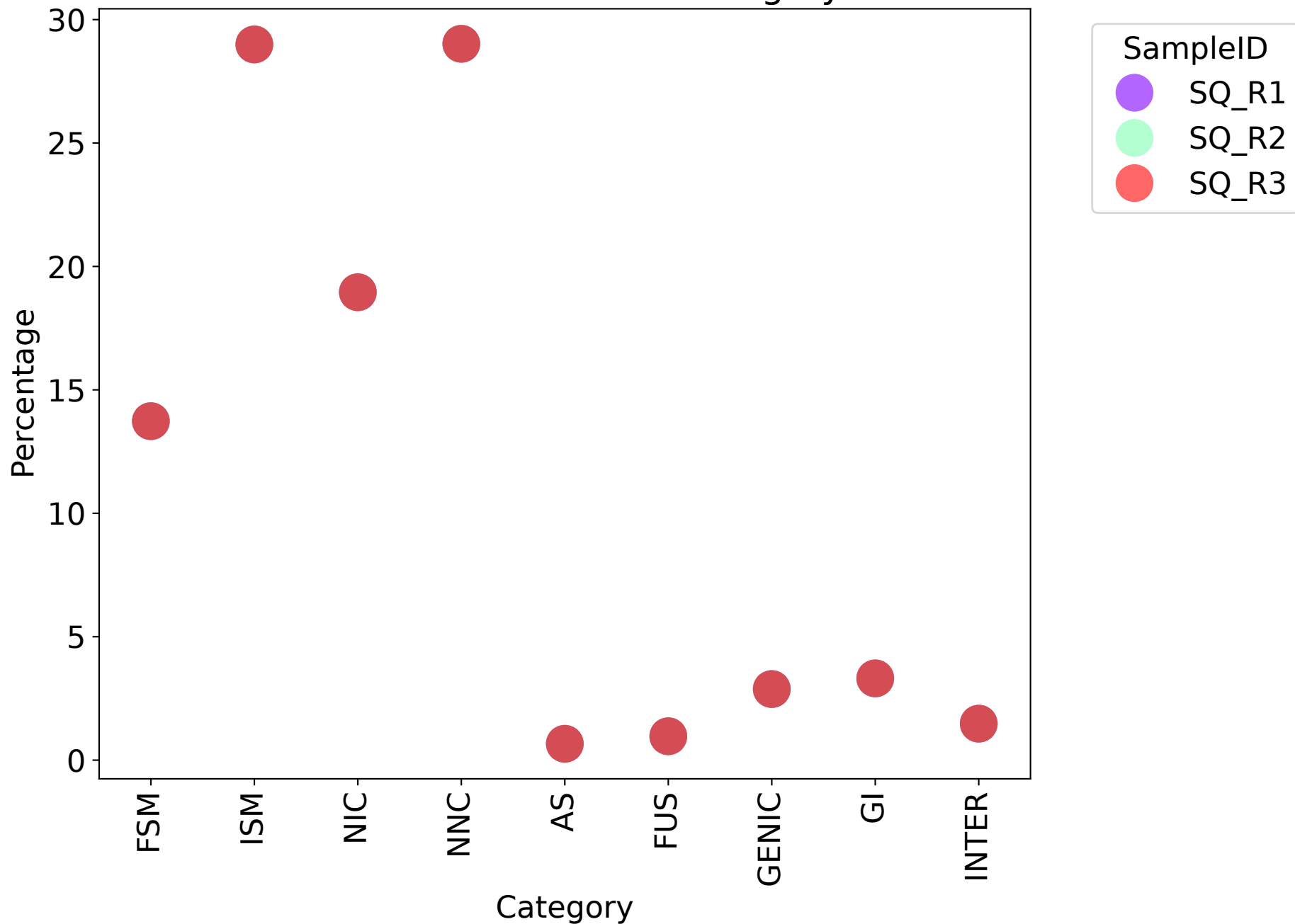
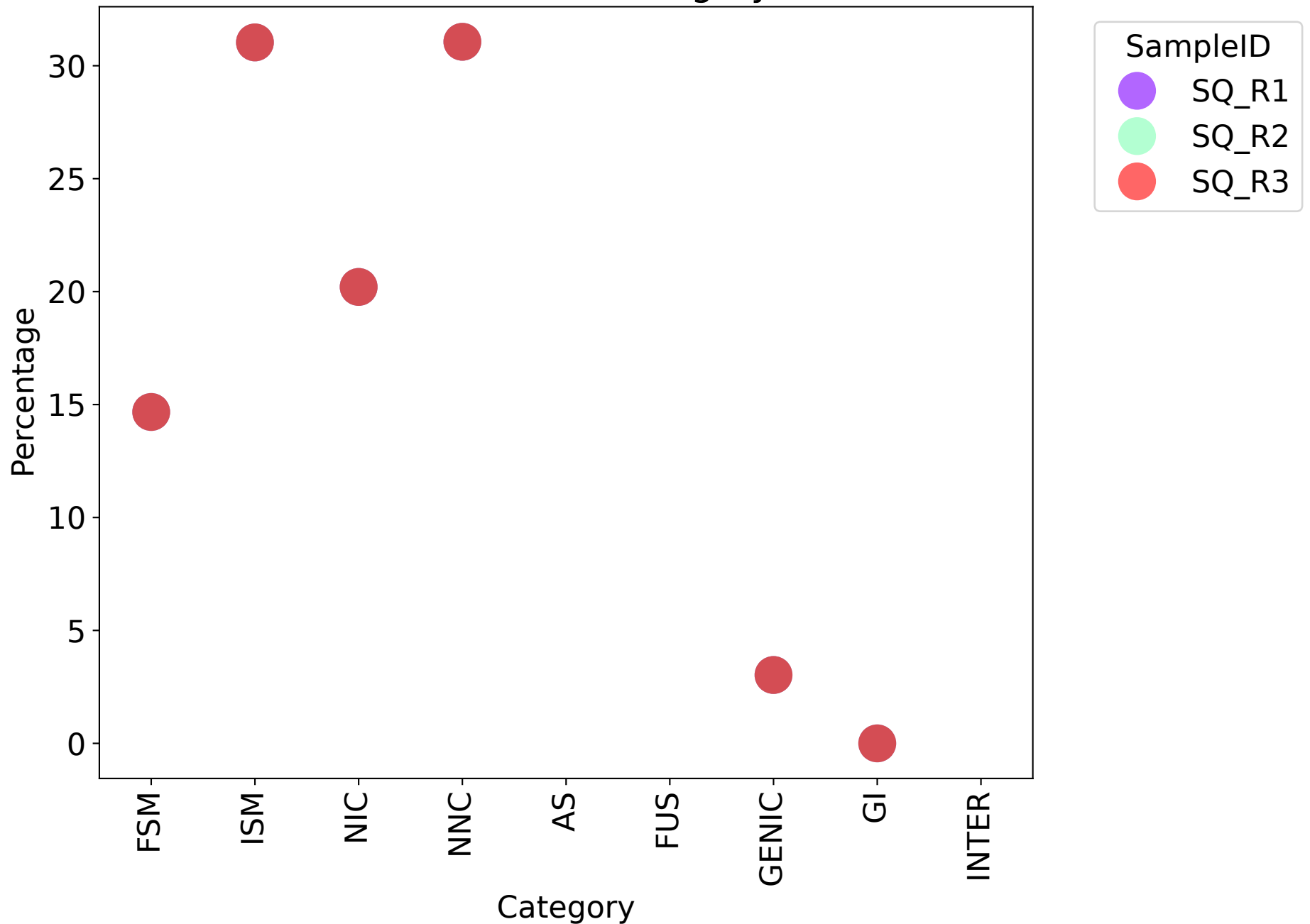


SQANTI-reads report

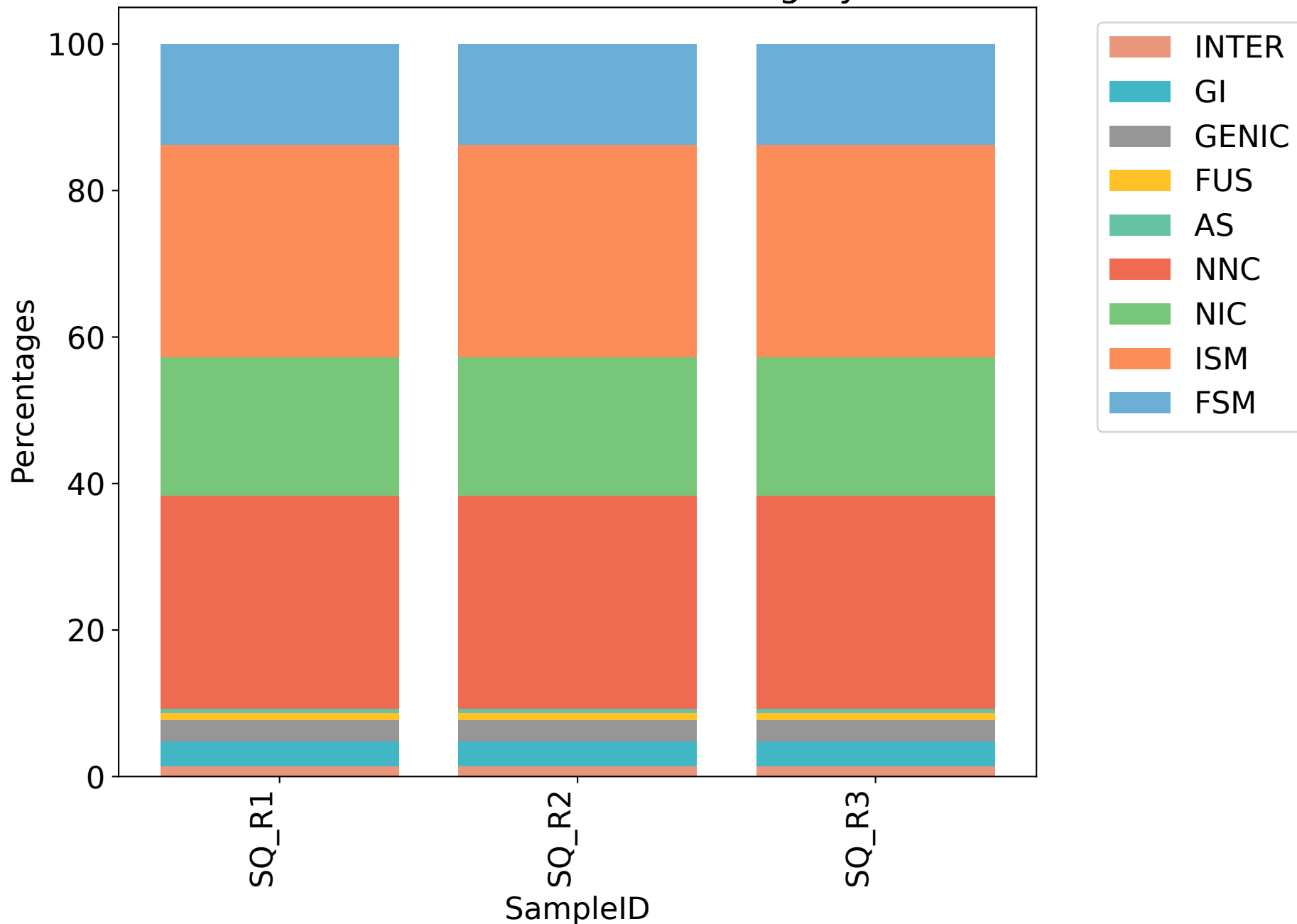
Percent reads in each structural category - All Genes



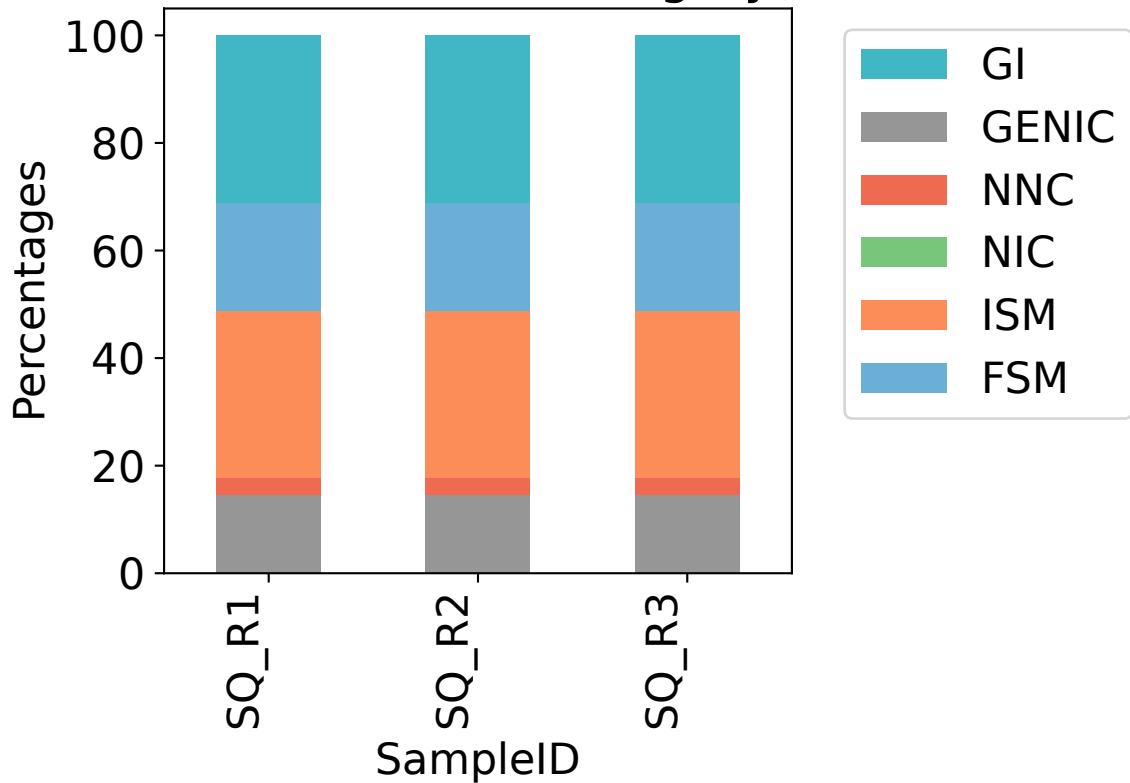
Percent reads in each structural category - Annotated Genes



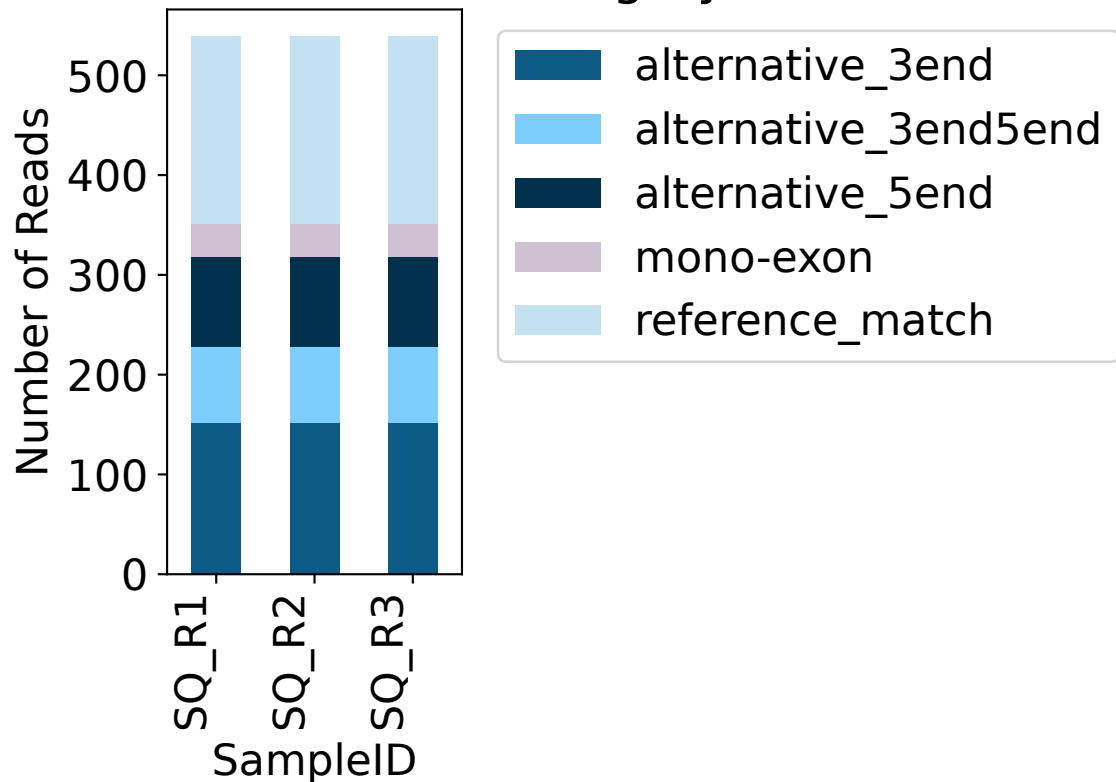
Percent Reads in Each Structural Category - All Genes



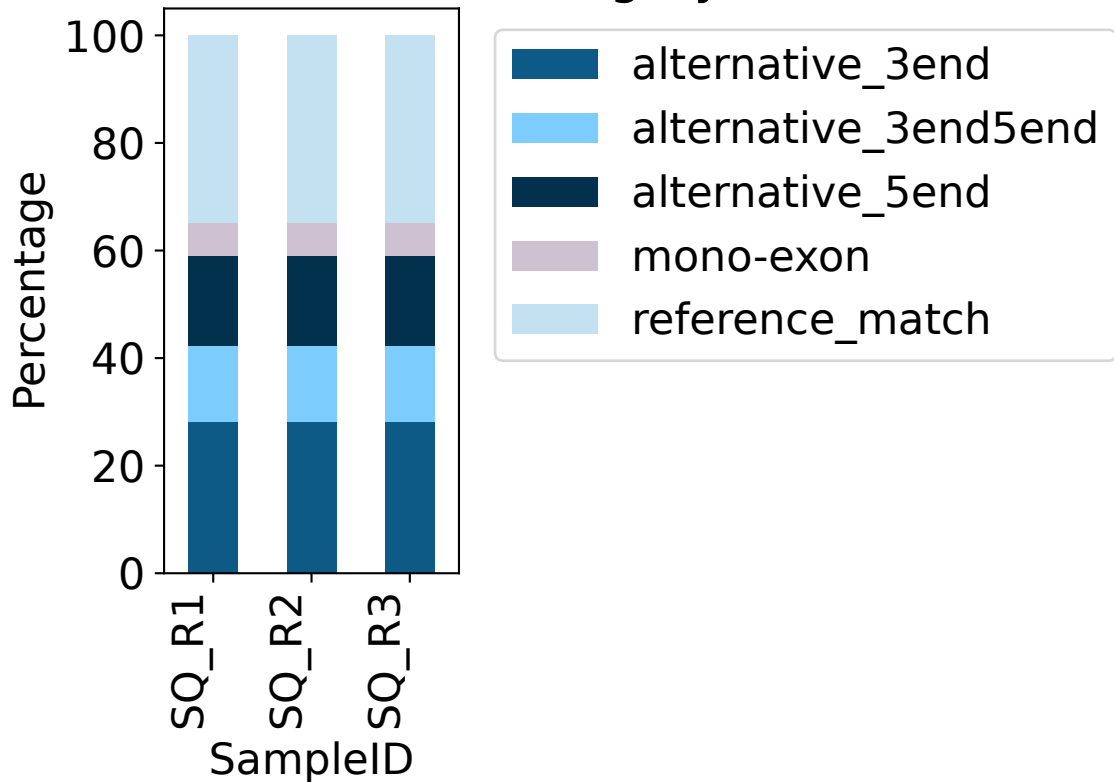
Reads in Each Structural Category - Annotated Gen



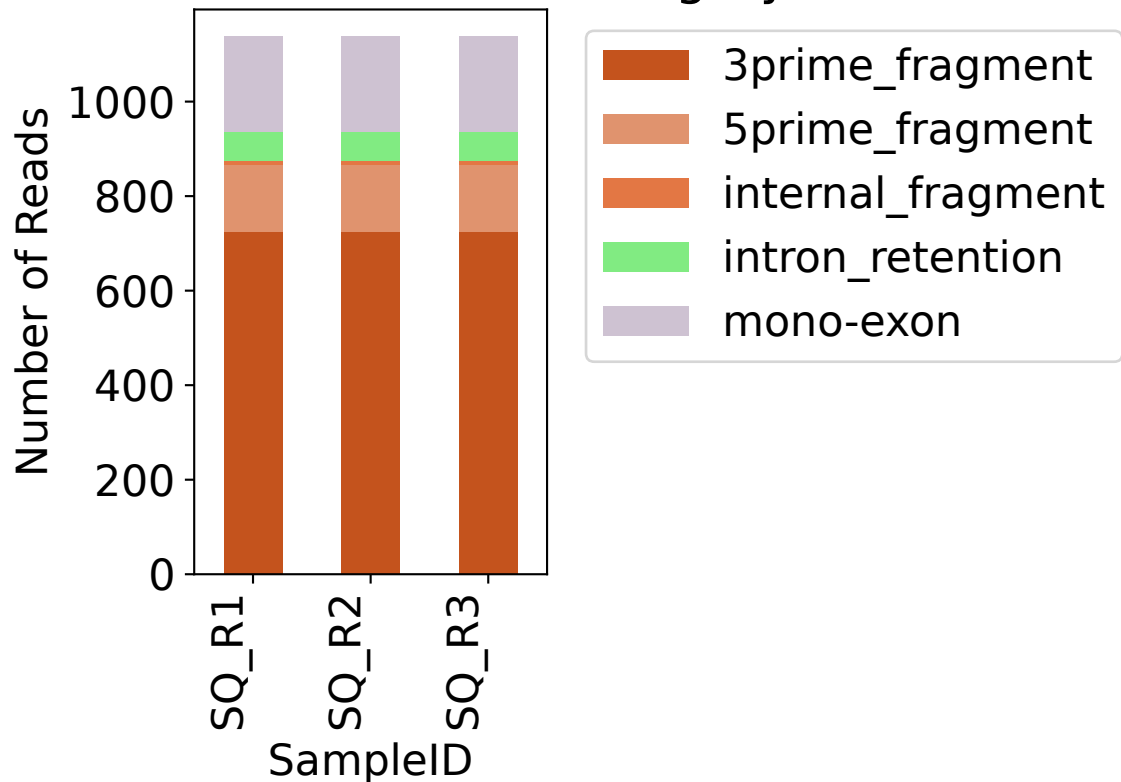
of Reads in Each subcategory - FSM



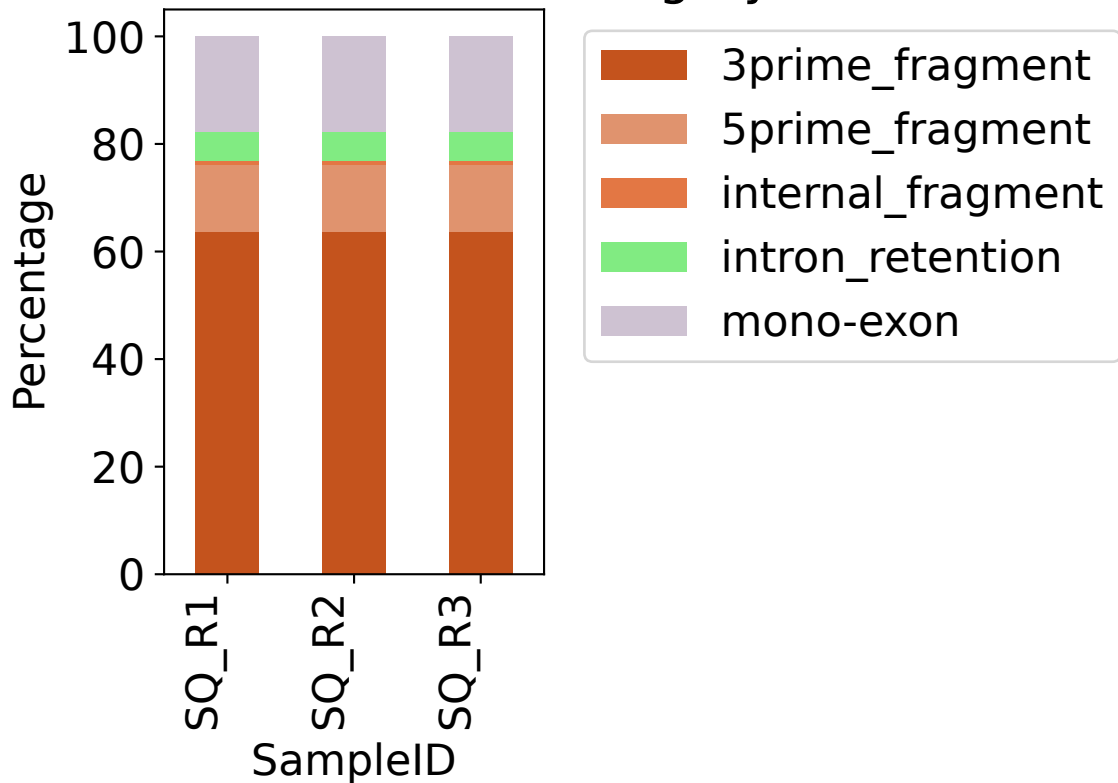
of Reads in Each subcategory - FSM



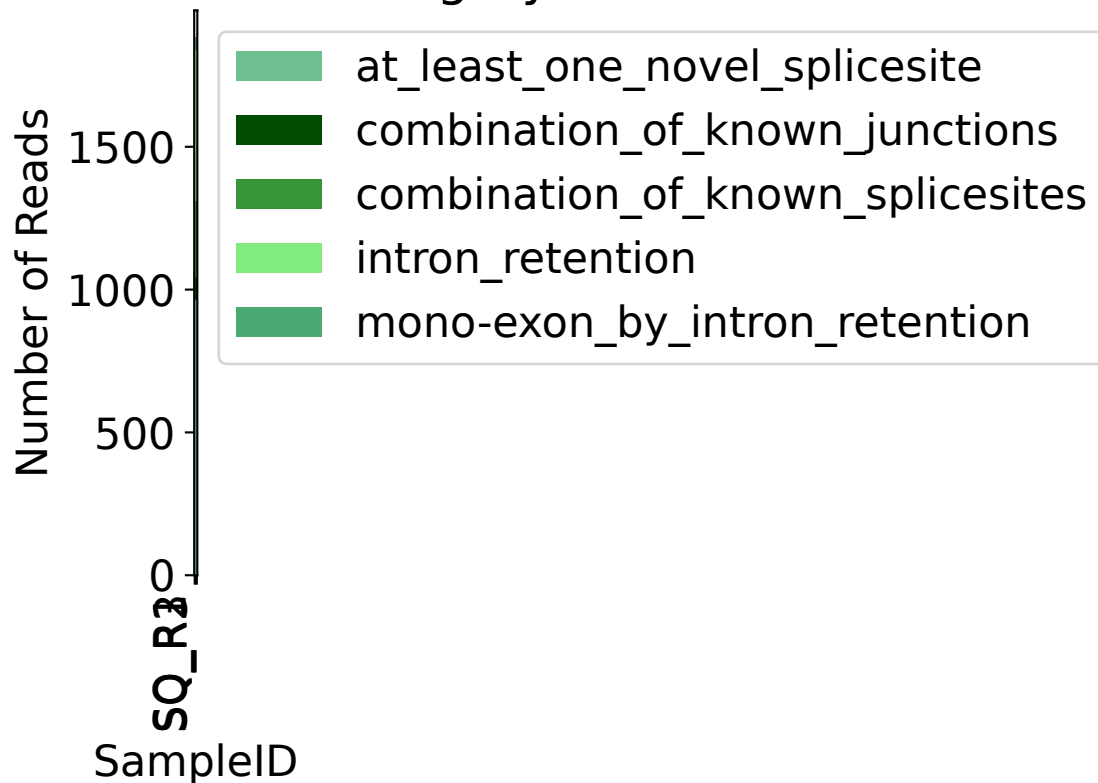
Number of Reads in Each subcategory - ISM



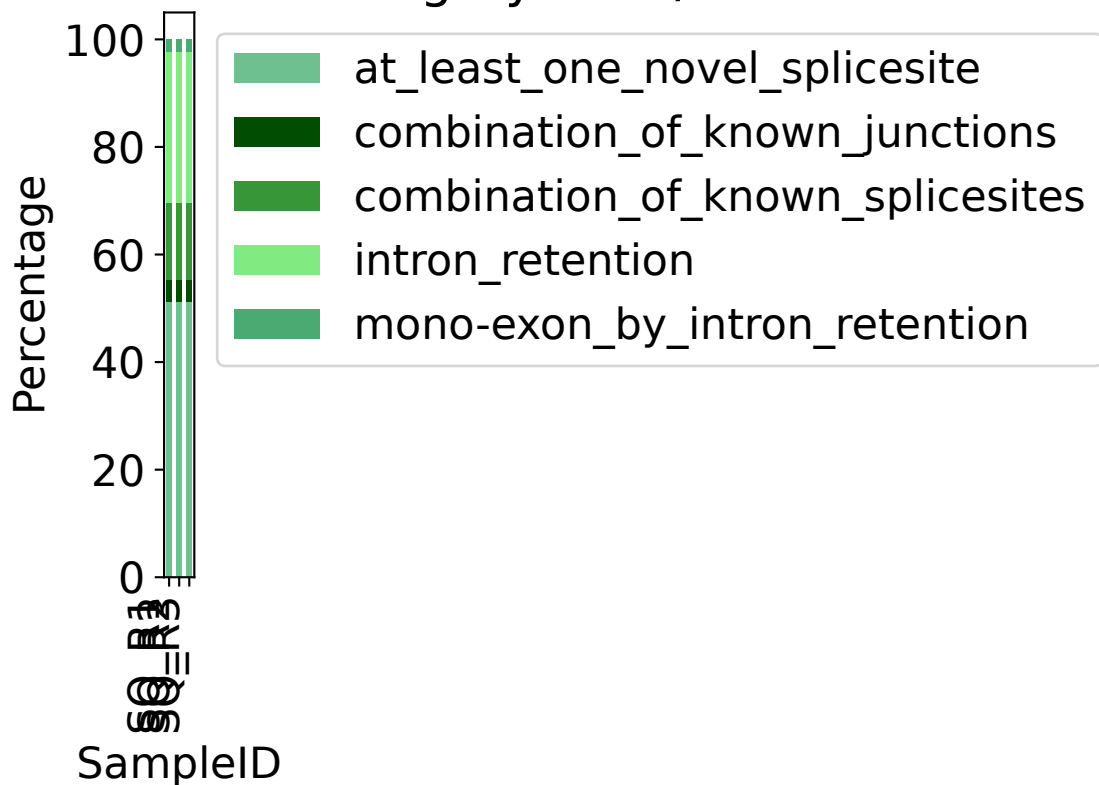
er of Reads in Each subcategory - ISM



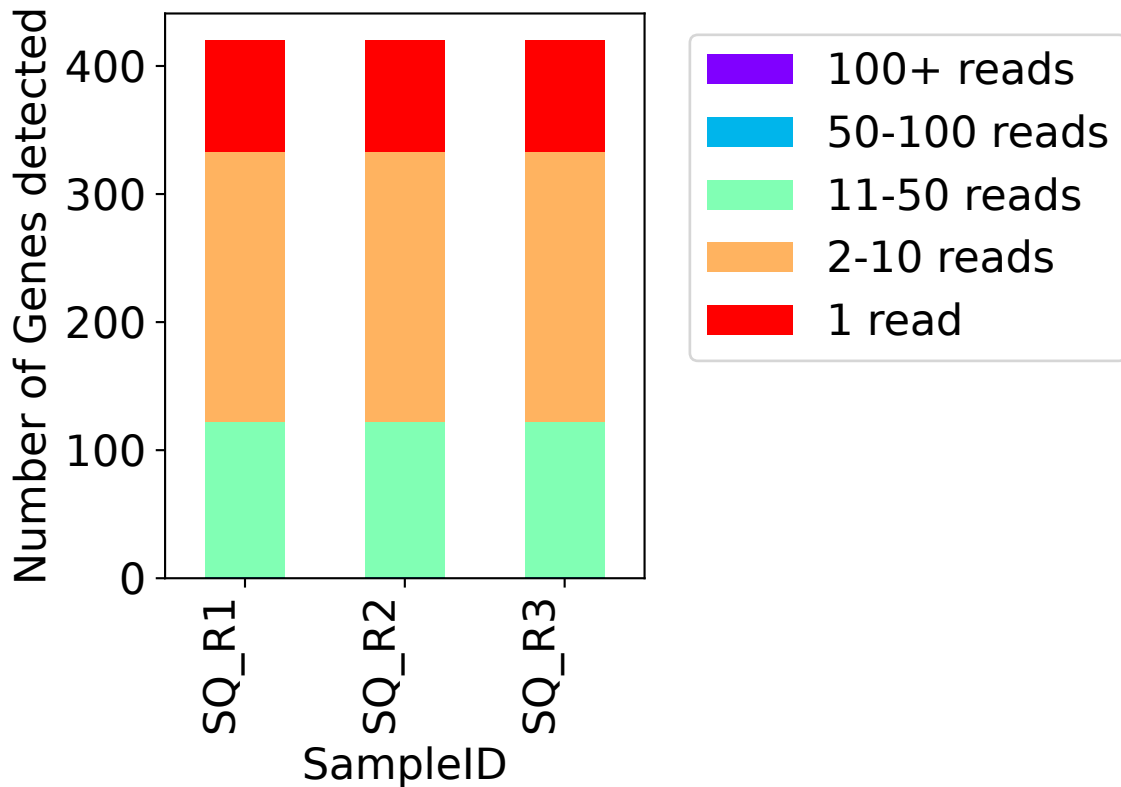
Reads in Each subcategory - NIC/NNC

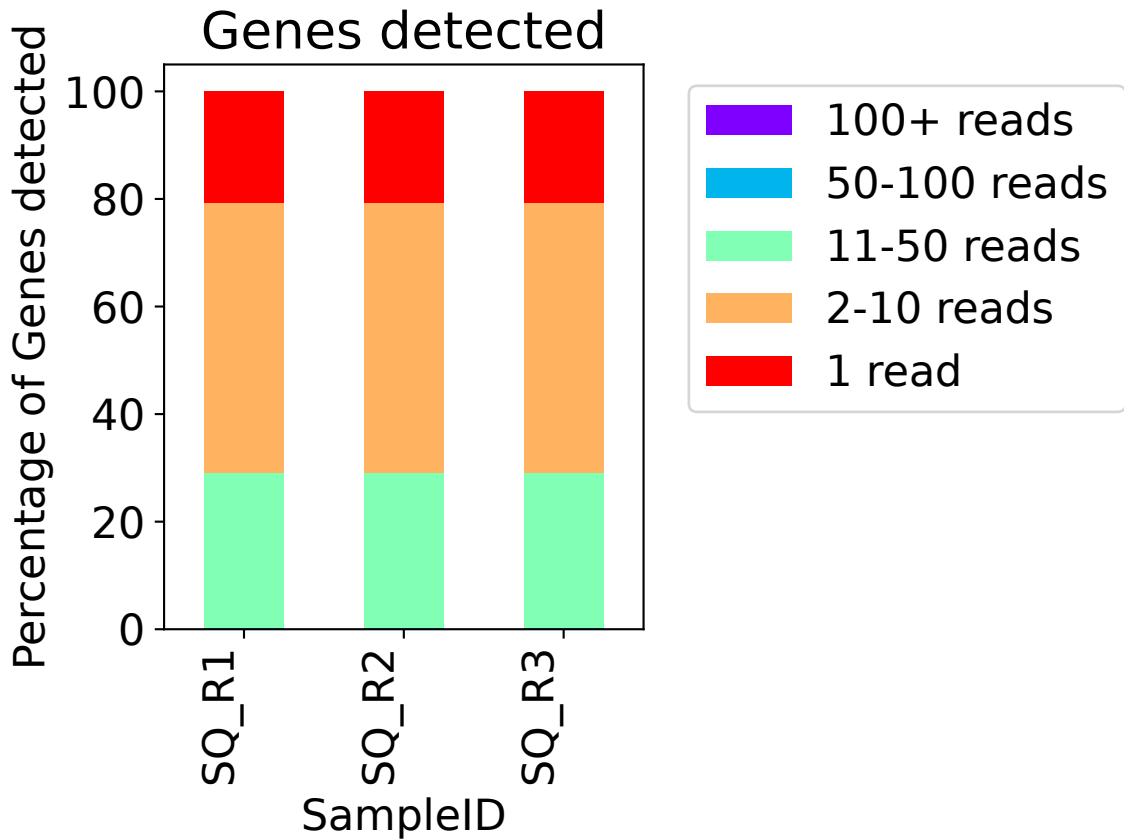


s in Each subcategory - NIC/NNC

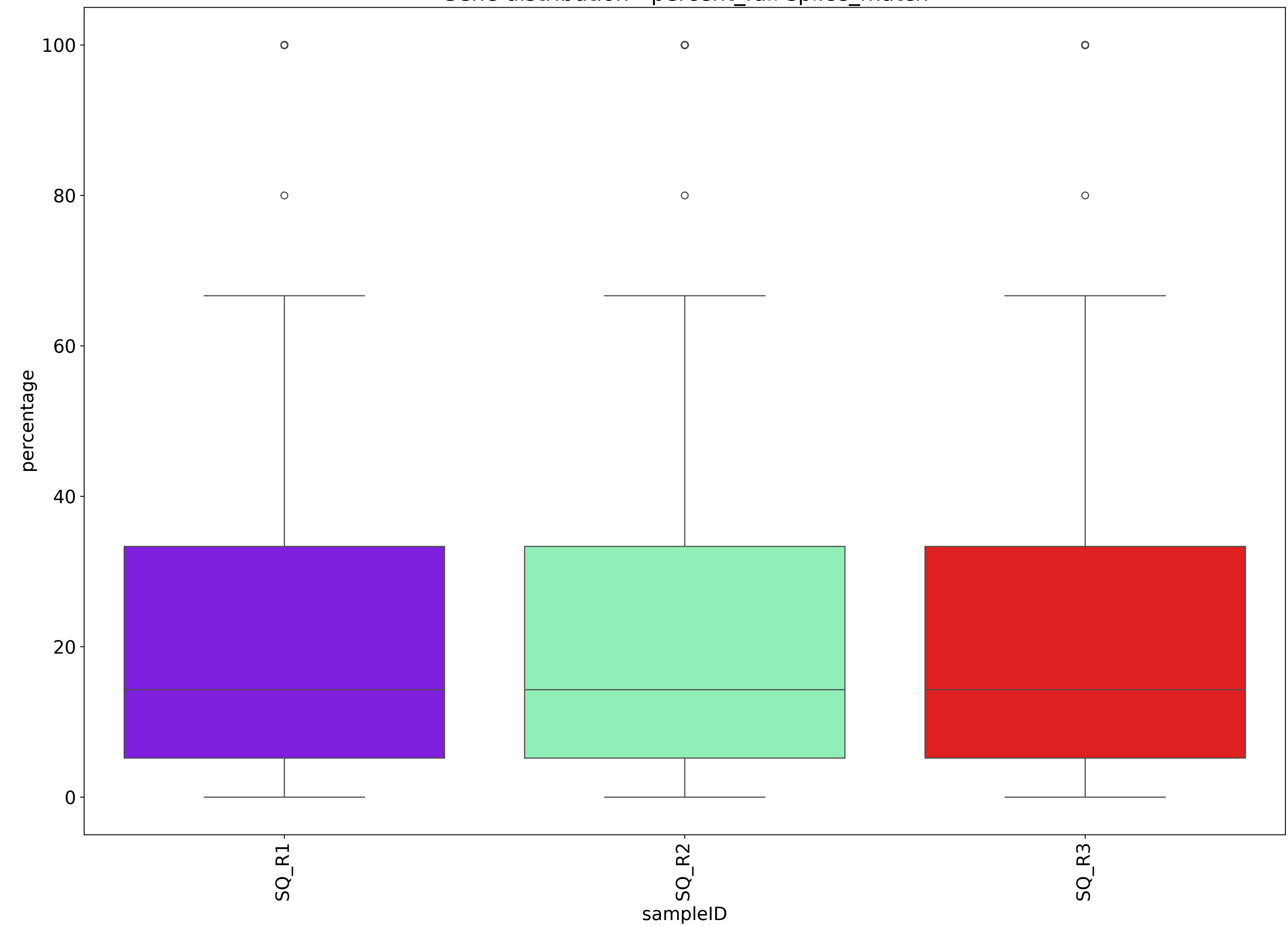


Genes detected

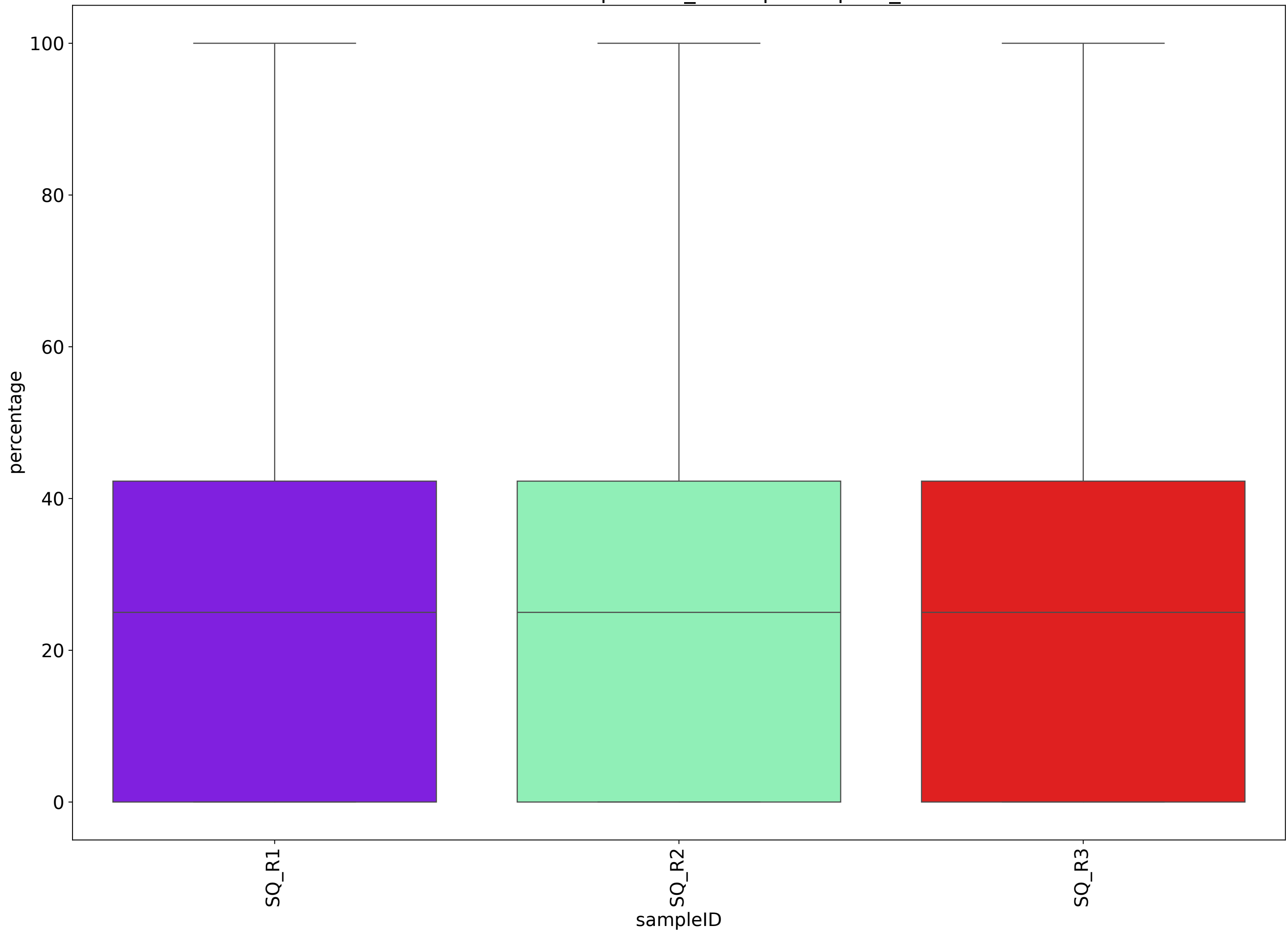




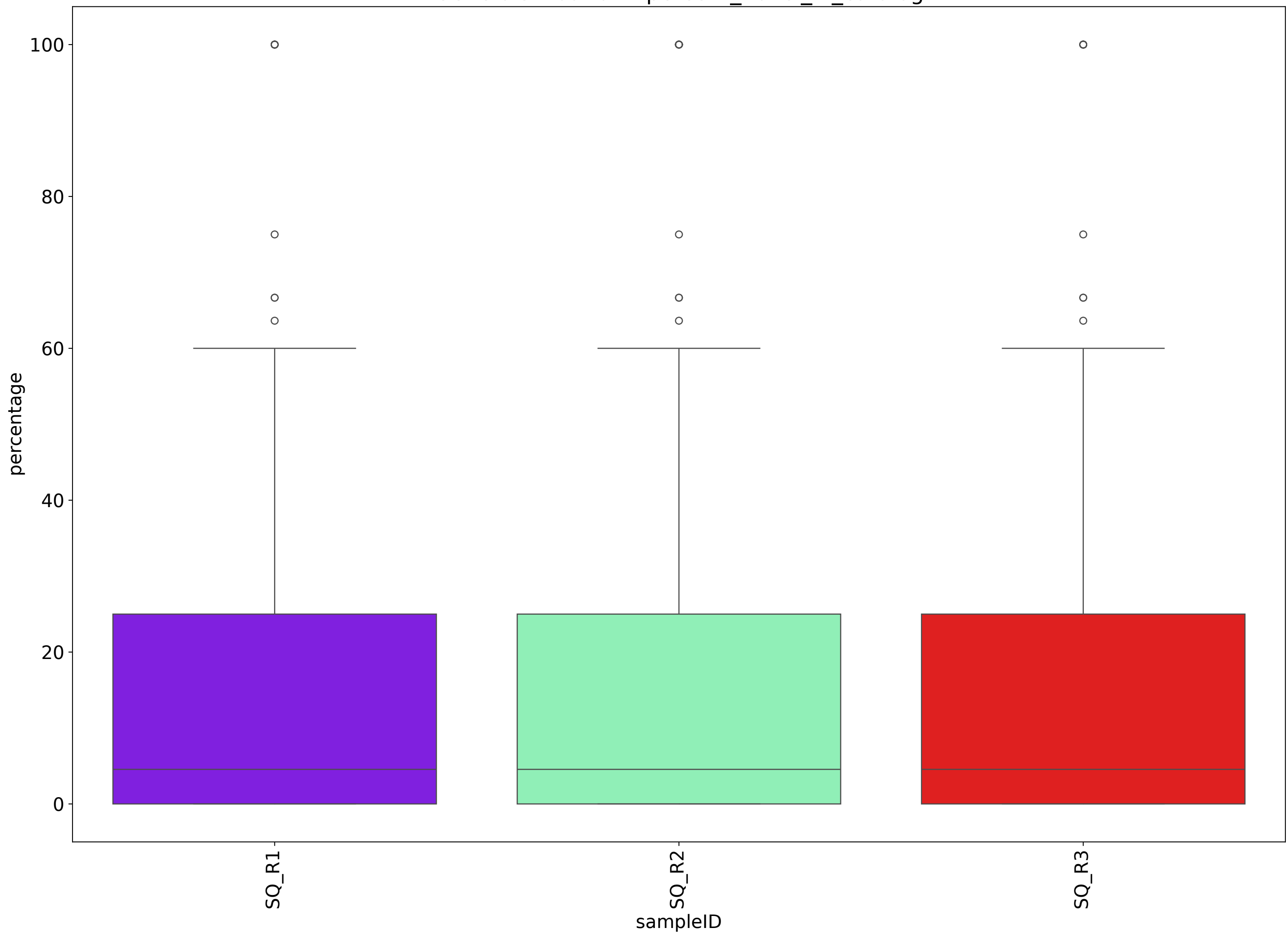
Gene distribution - percent_full-splice_match



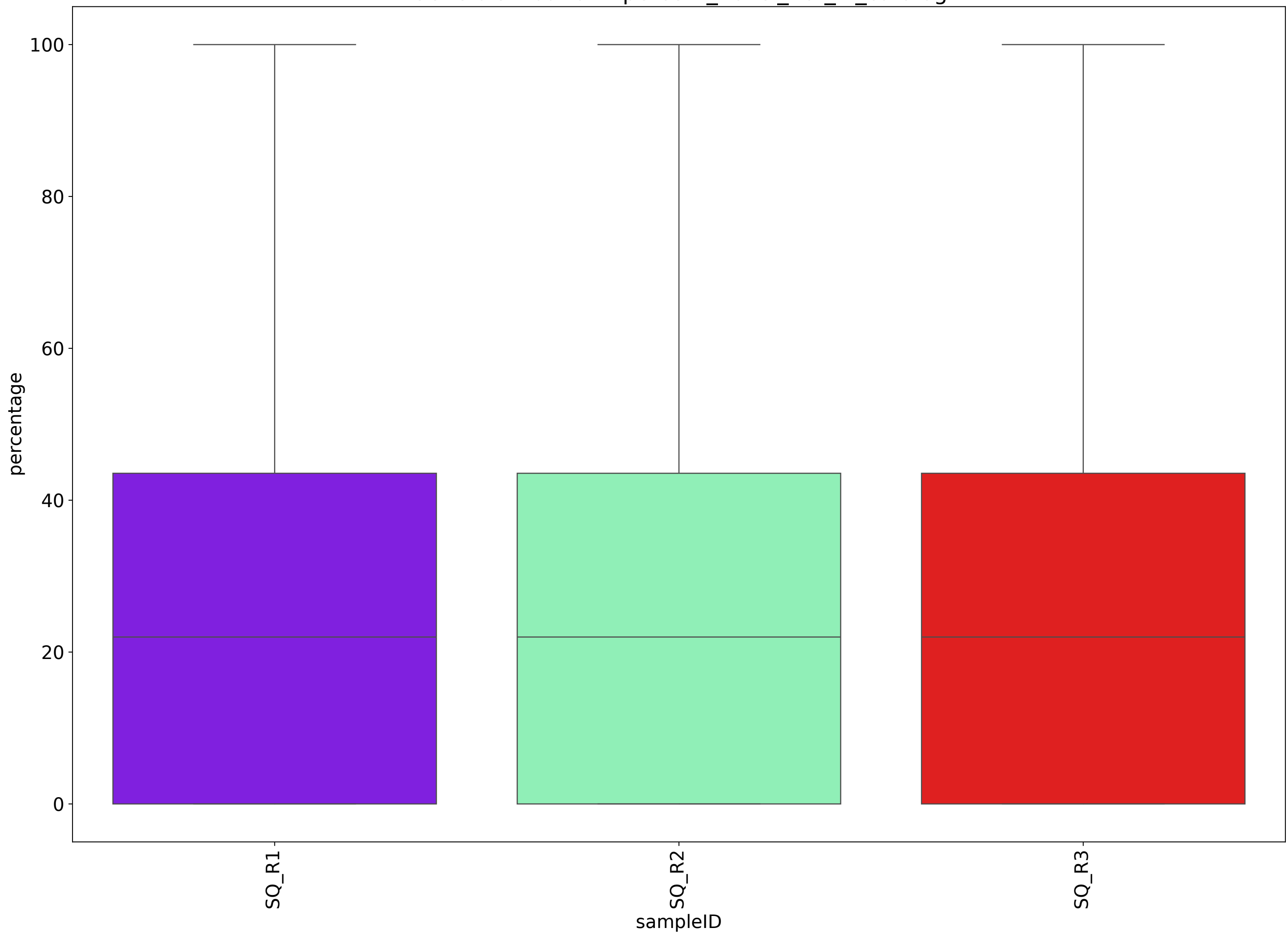
Gene distribution - percent_incomplete-splice_match



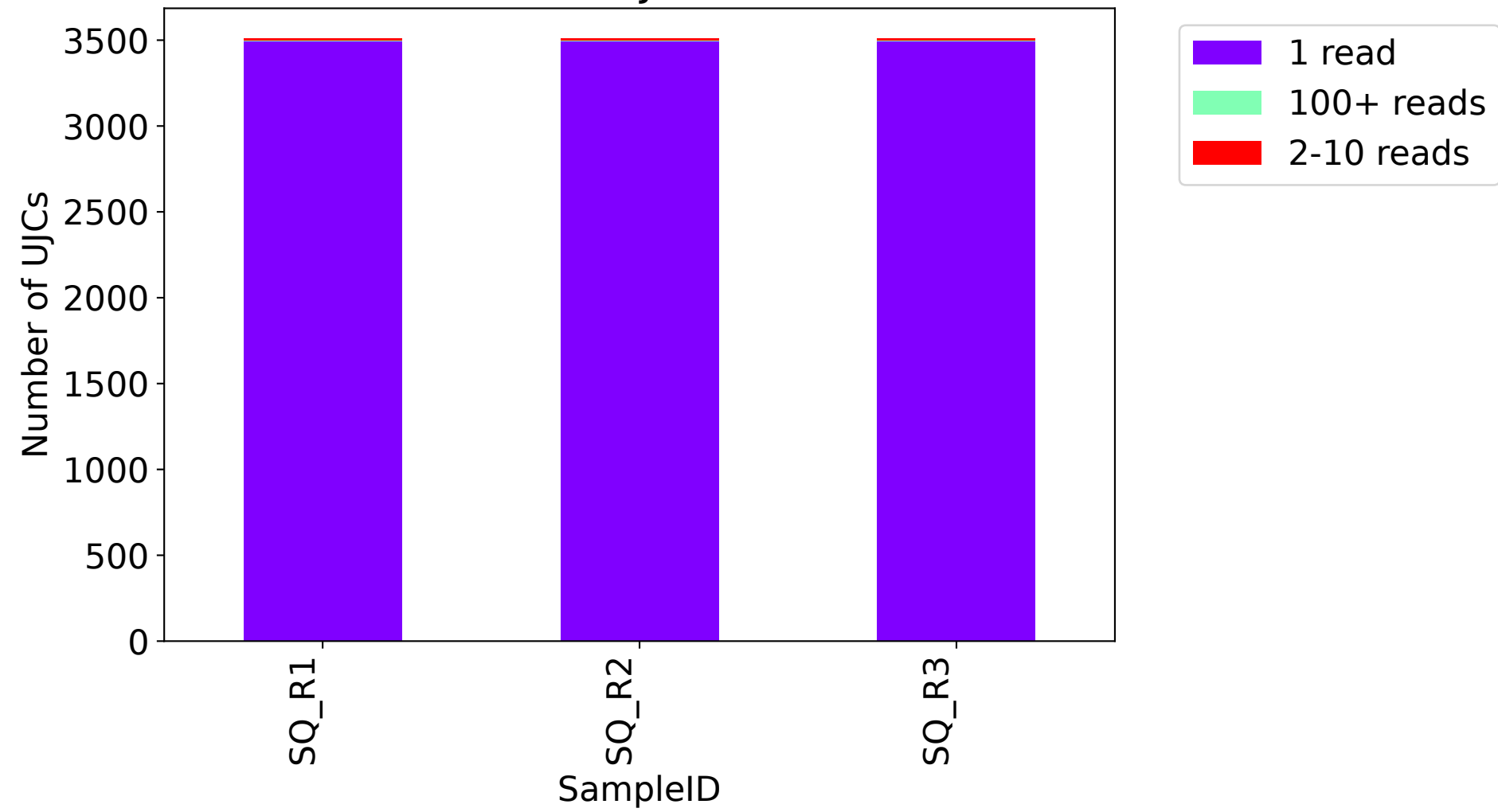
Gene distribution - percent_novel_in_catalog



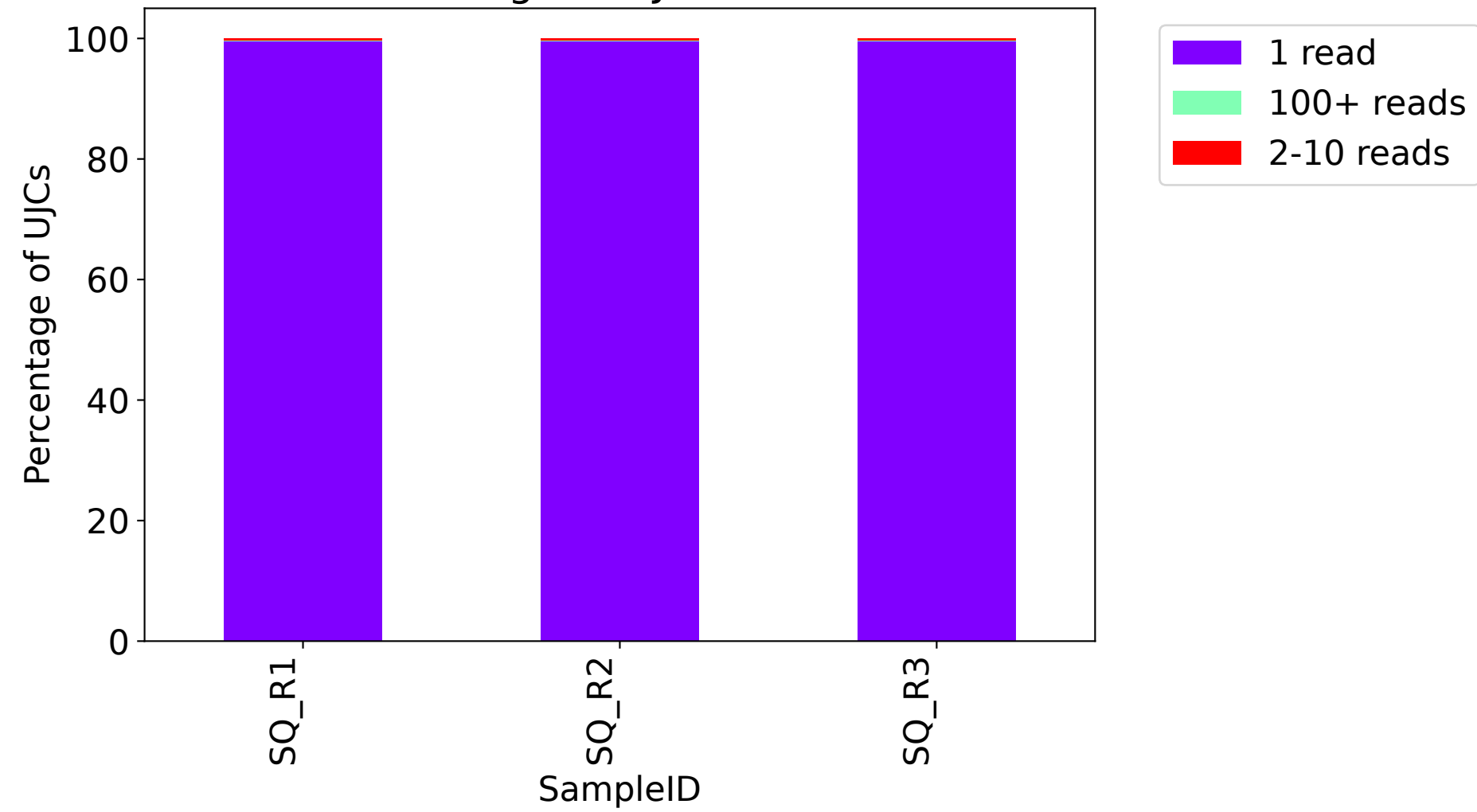
Gene distribution - percent_novel_not_in_catalog



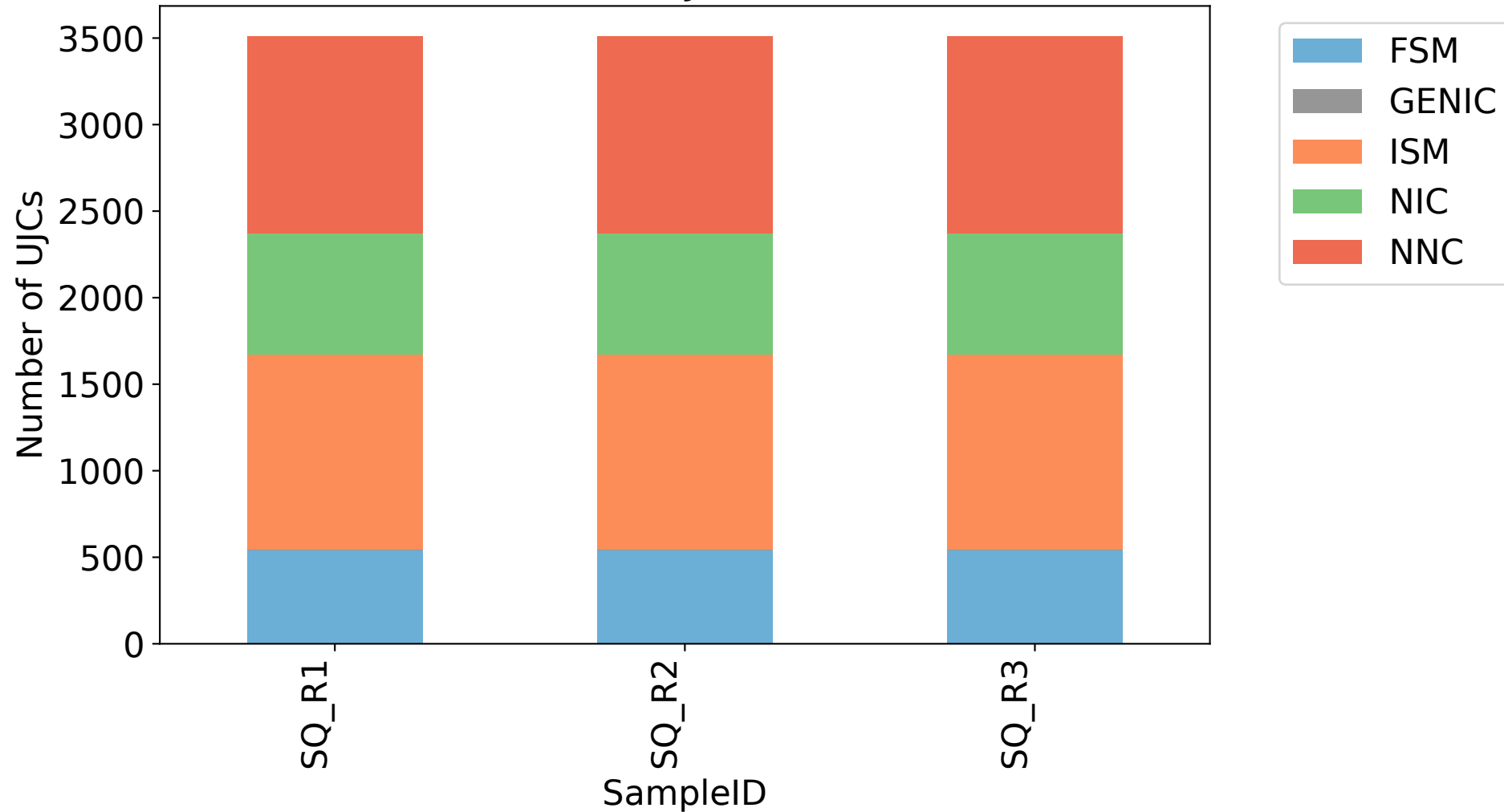
Number of UJCs detected



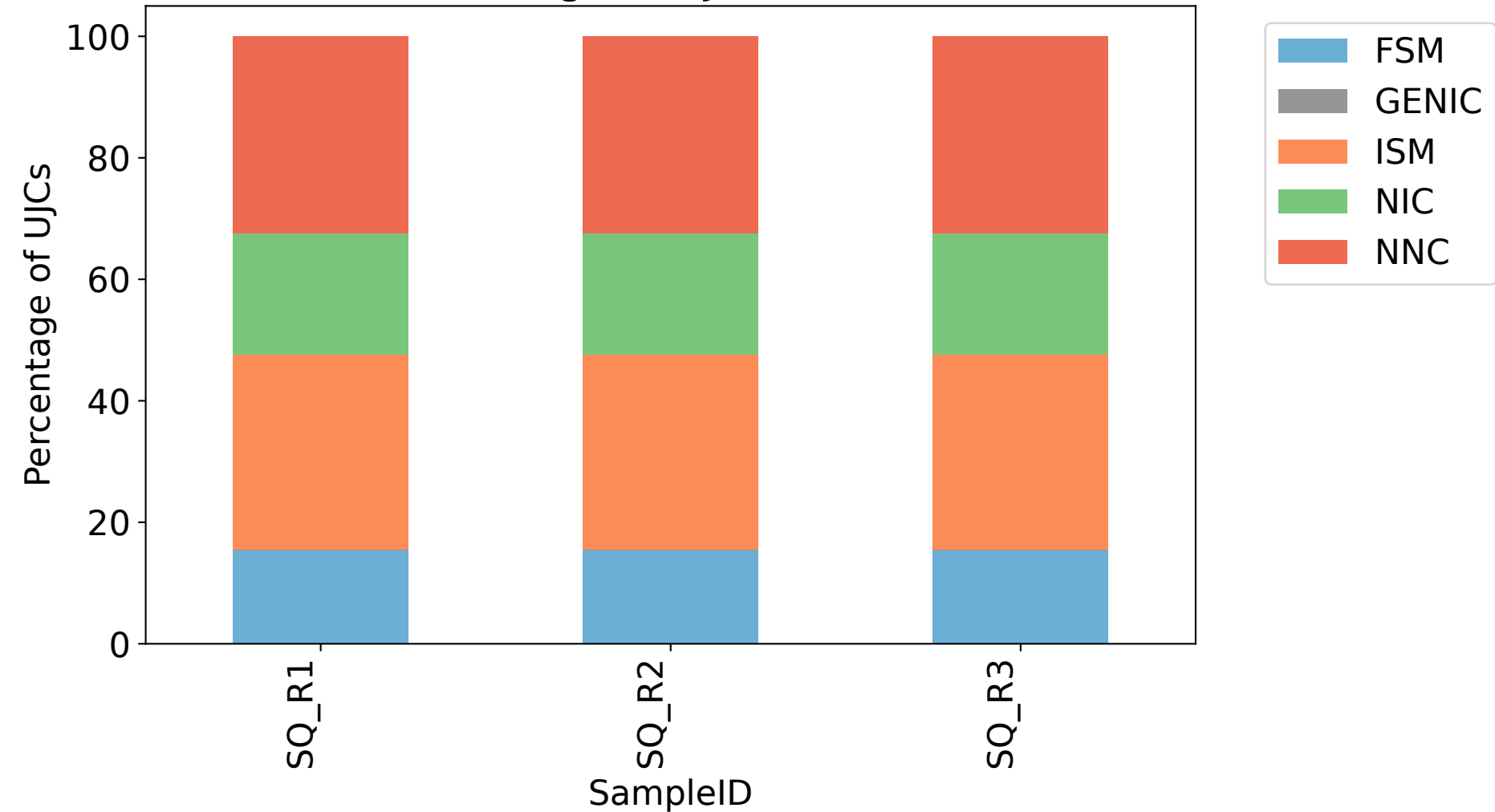
Percentage of UJCs detected



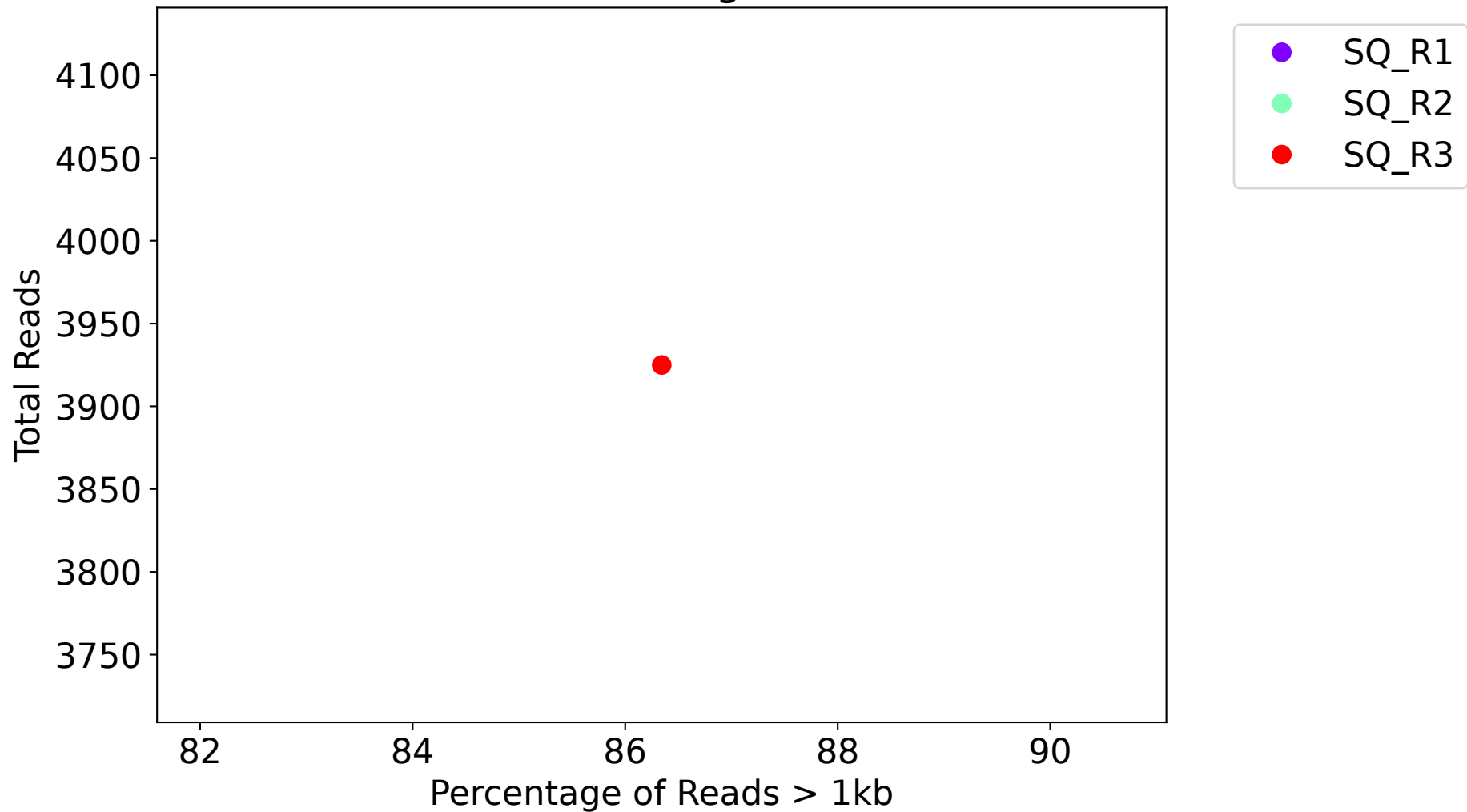
Number of UJCs detected

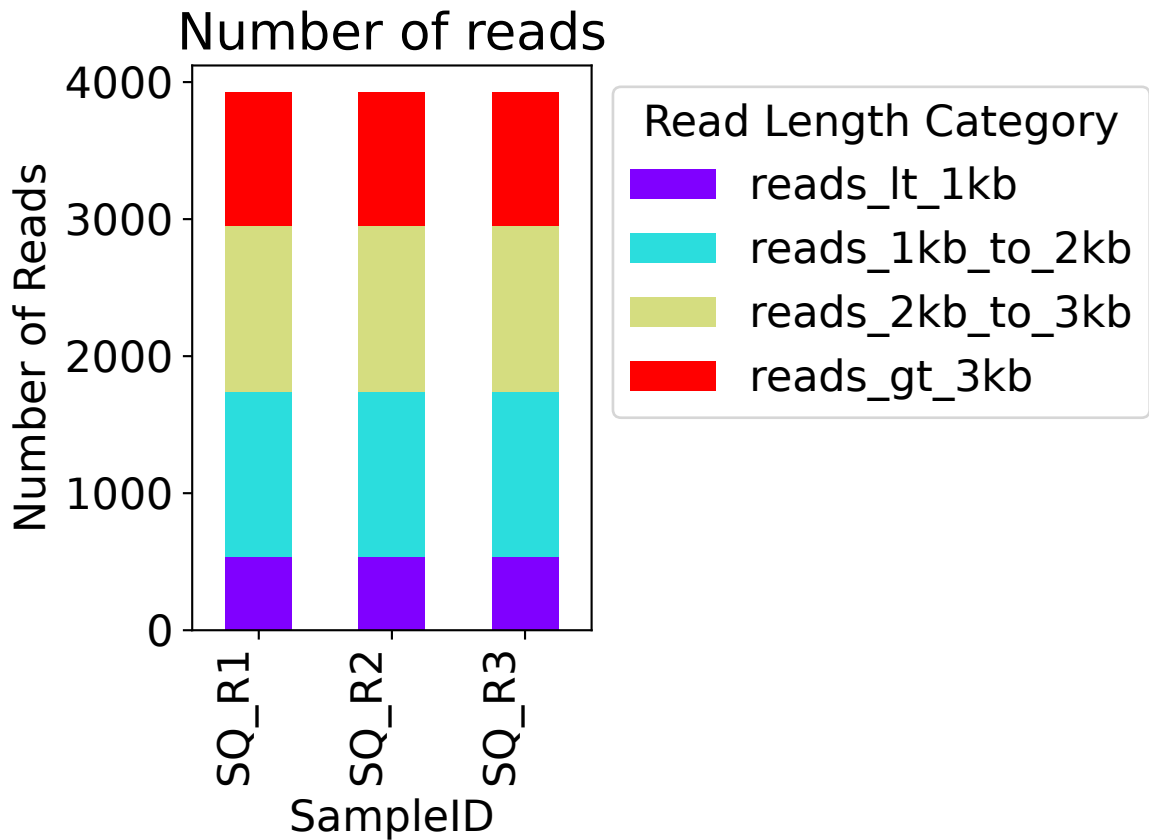


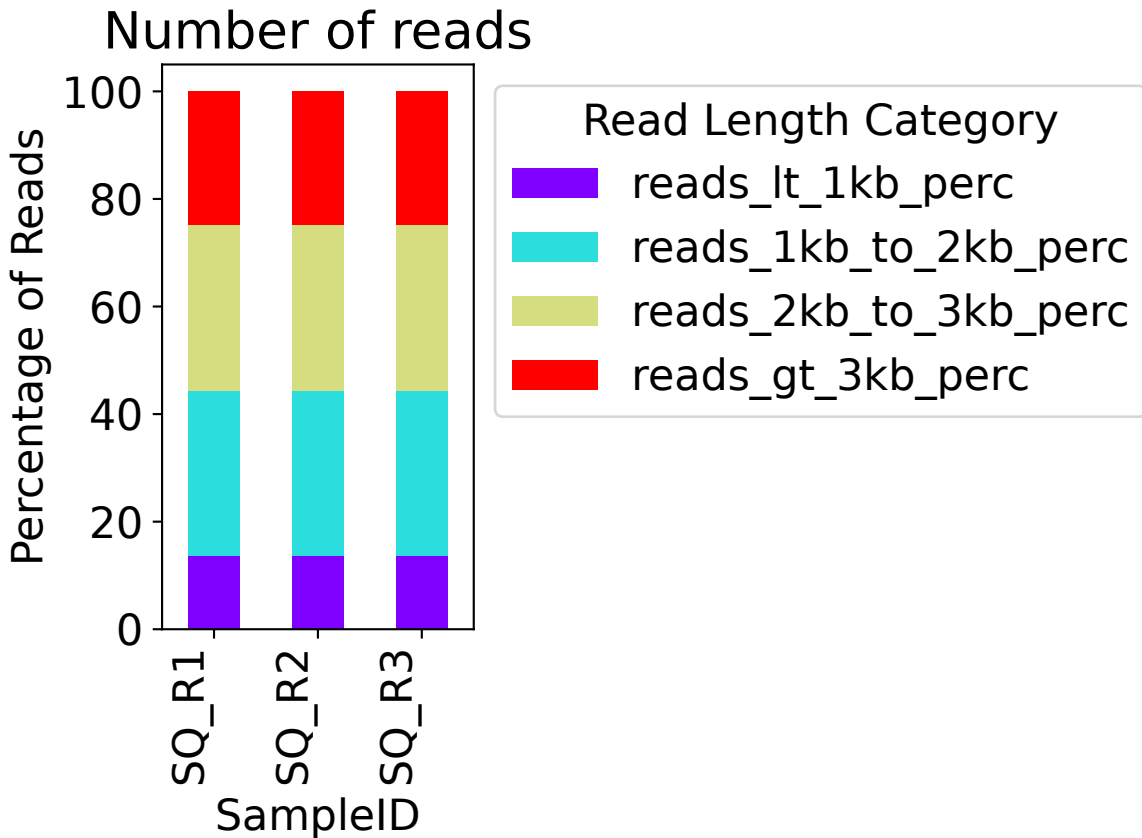
Percentage of UJCs detected



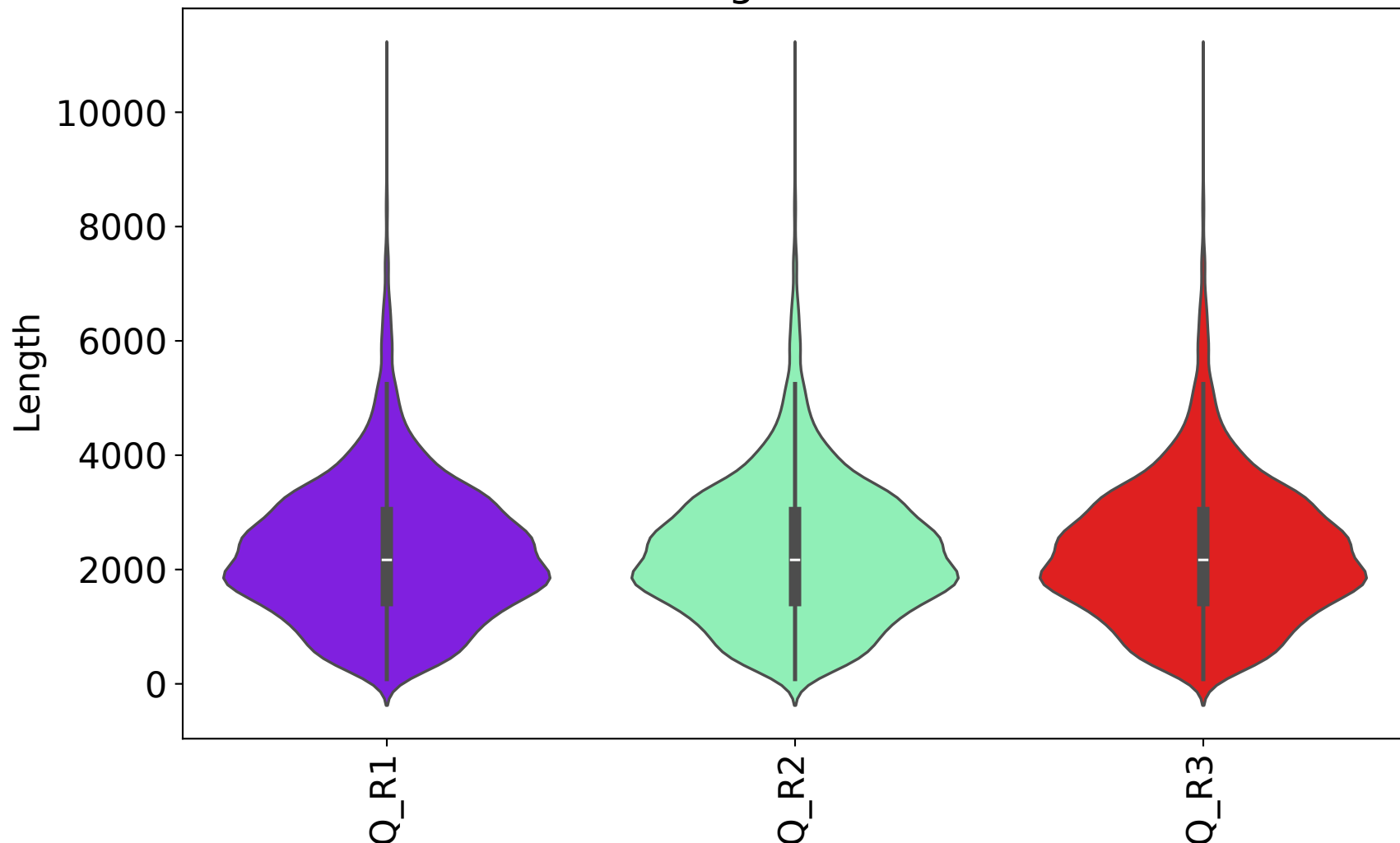
Total Reads vs Percentage of Reads > 1kb



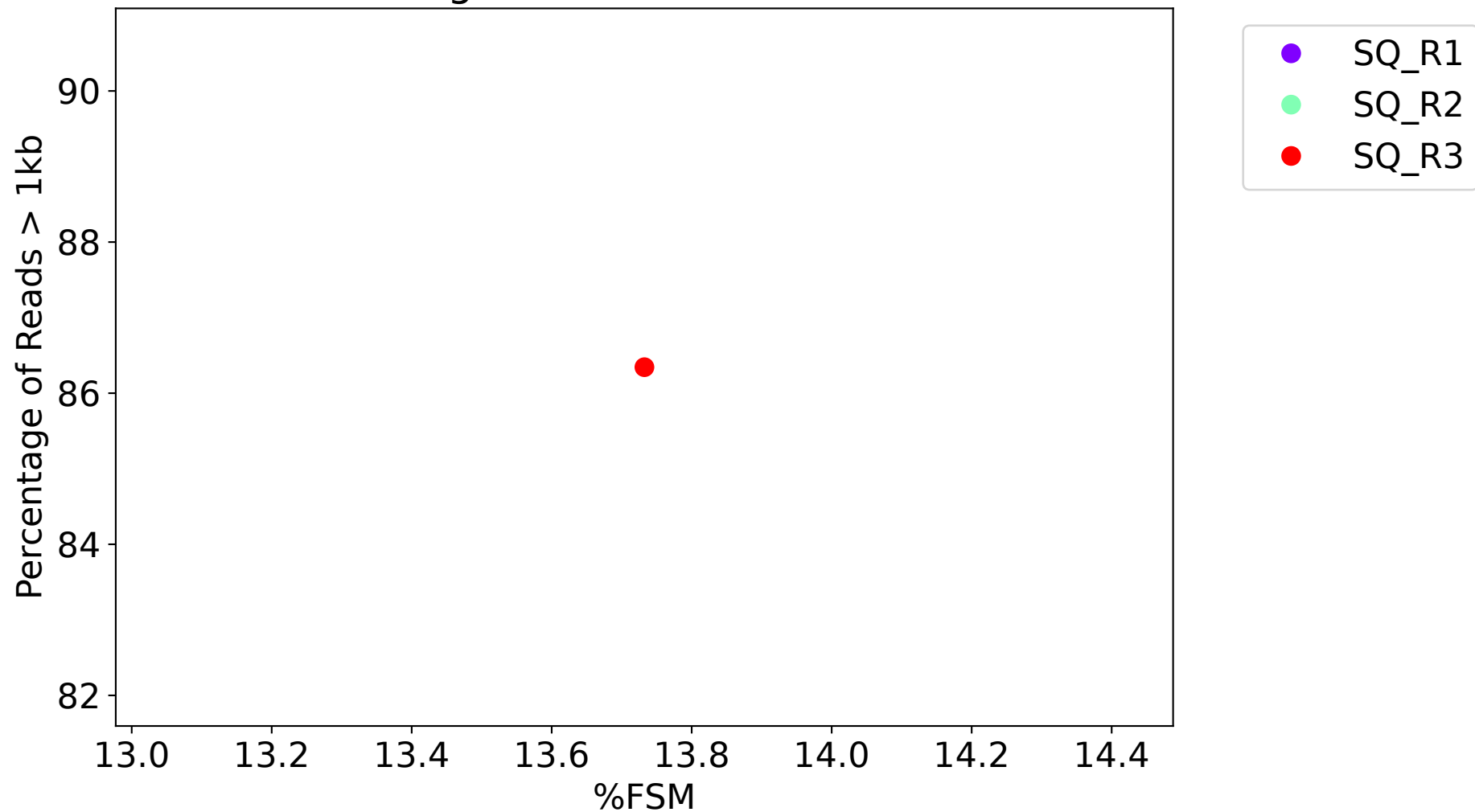




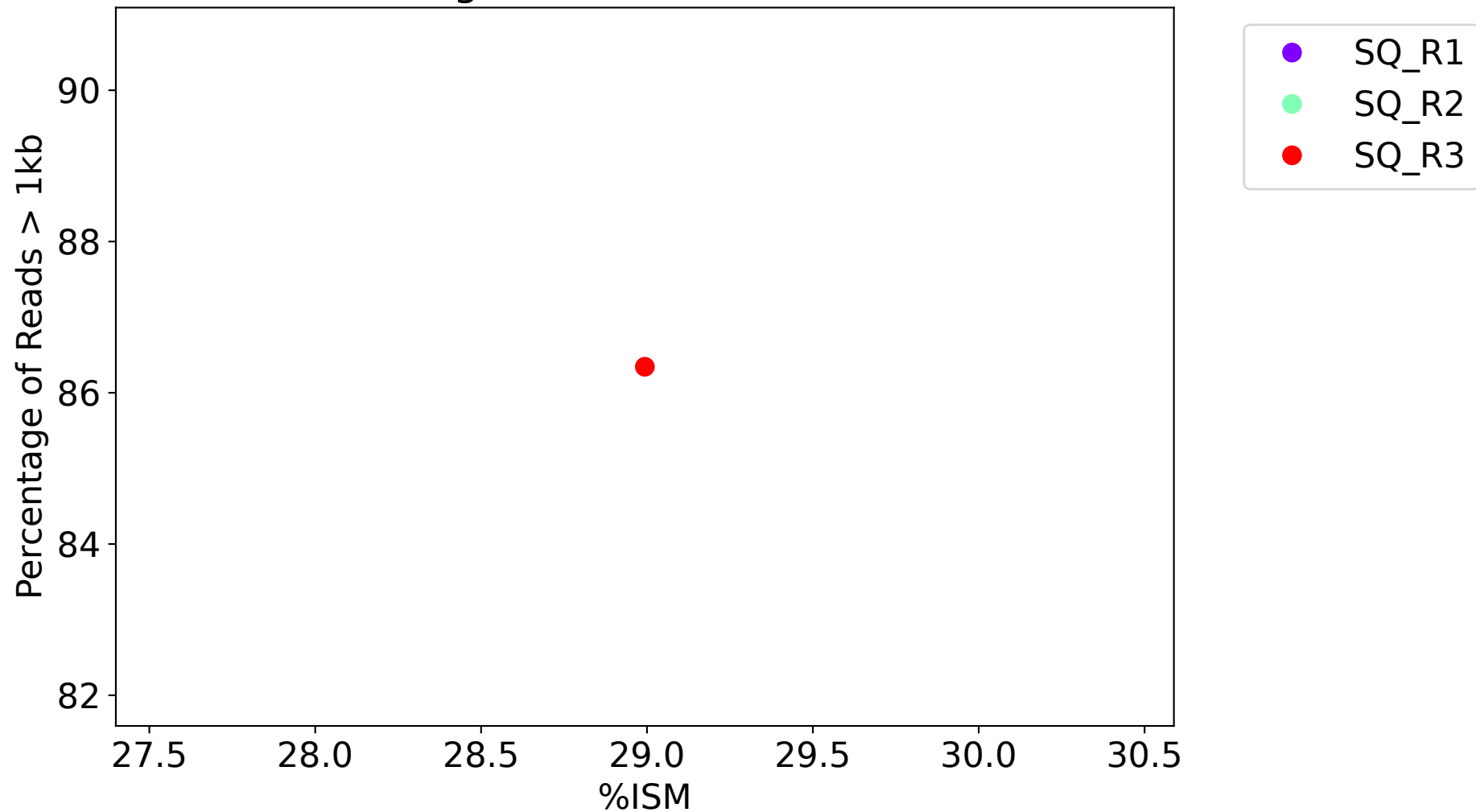
Read Length Distribution



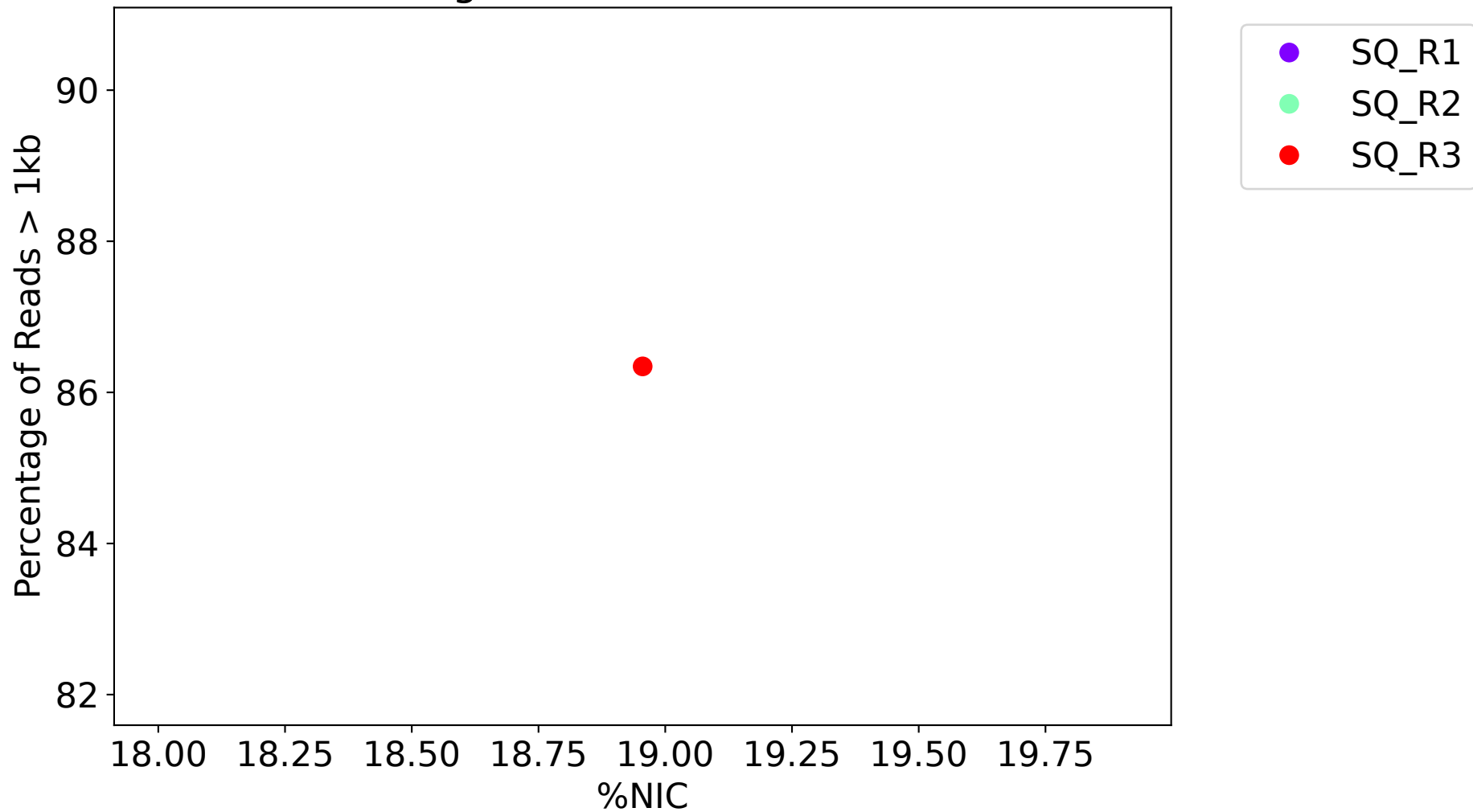
Percentage of Reads > 1kb vs %FSM



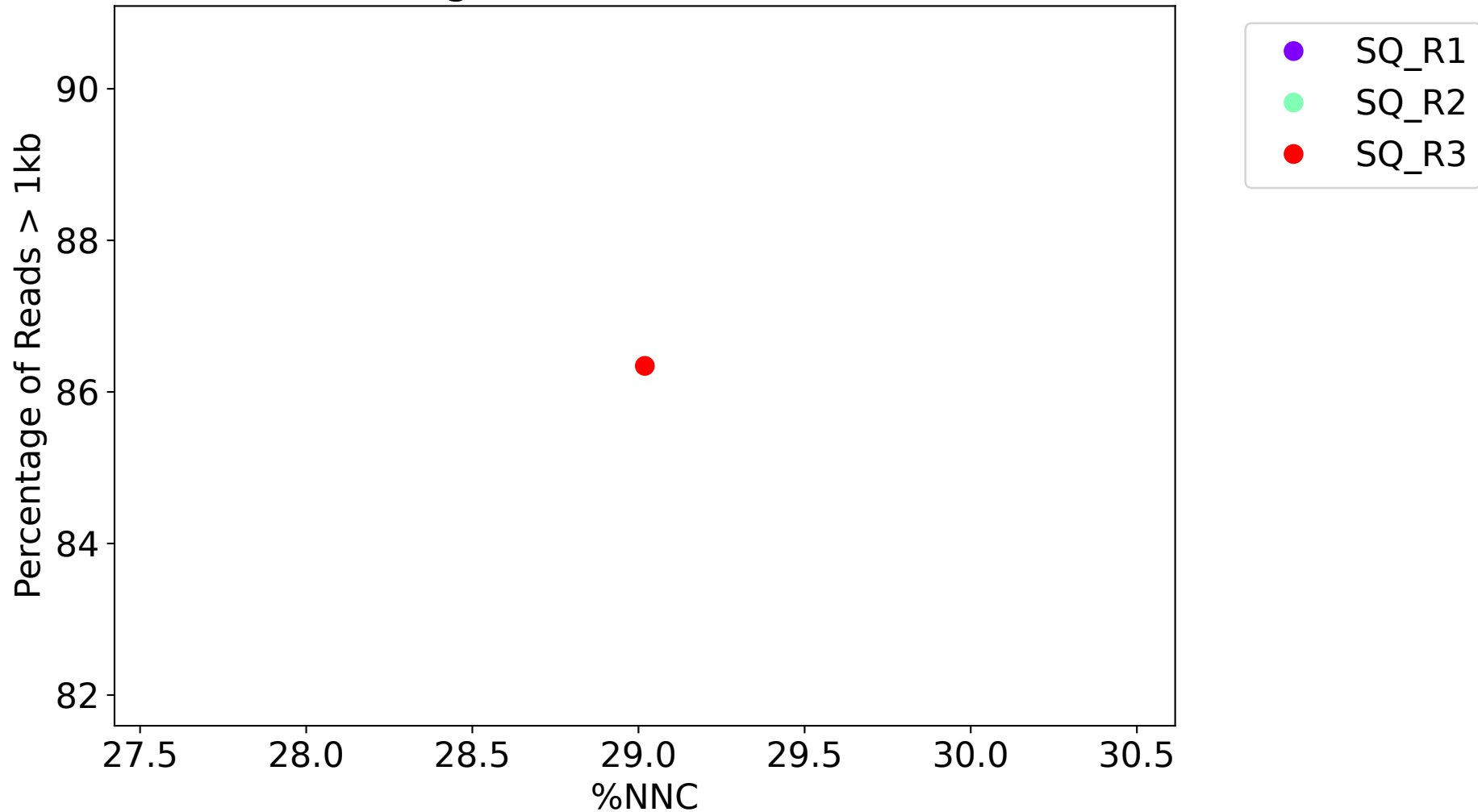
Percentage of Reads > 1kb vs %ISM



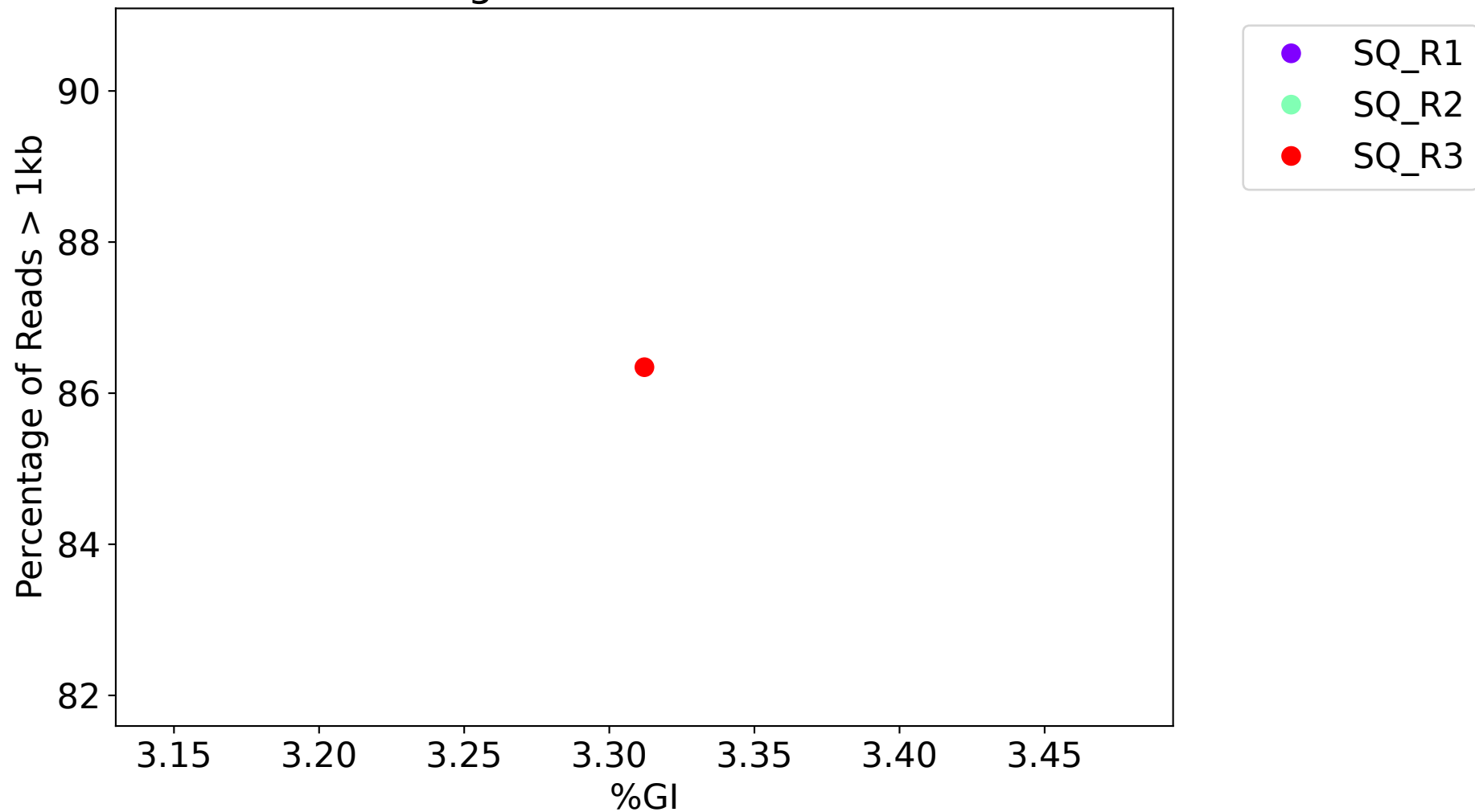
Percentage of Reads > 1kb vs %NIC



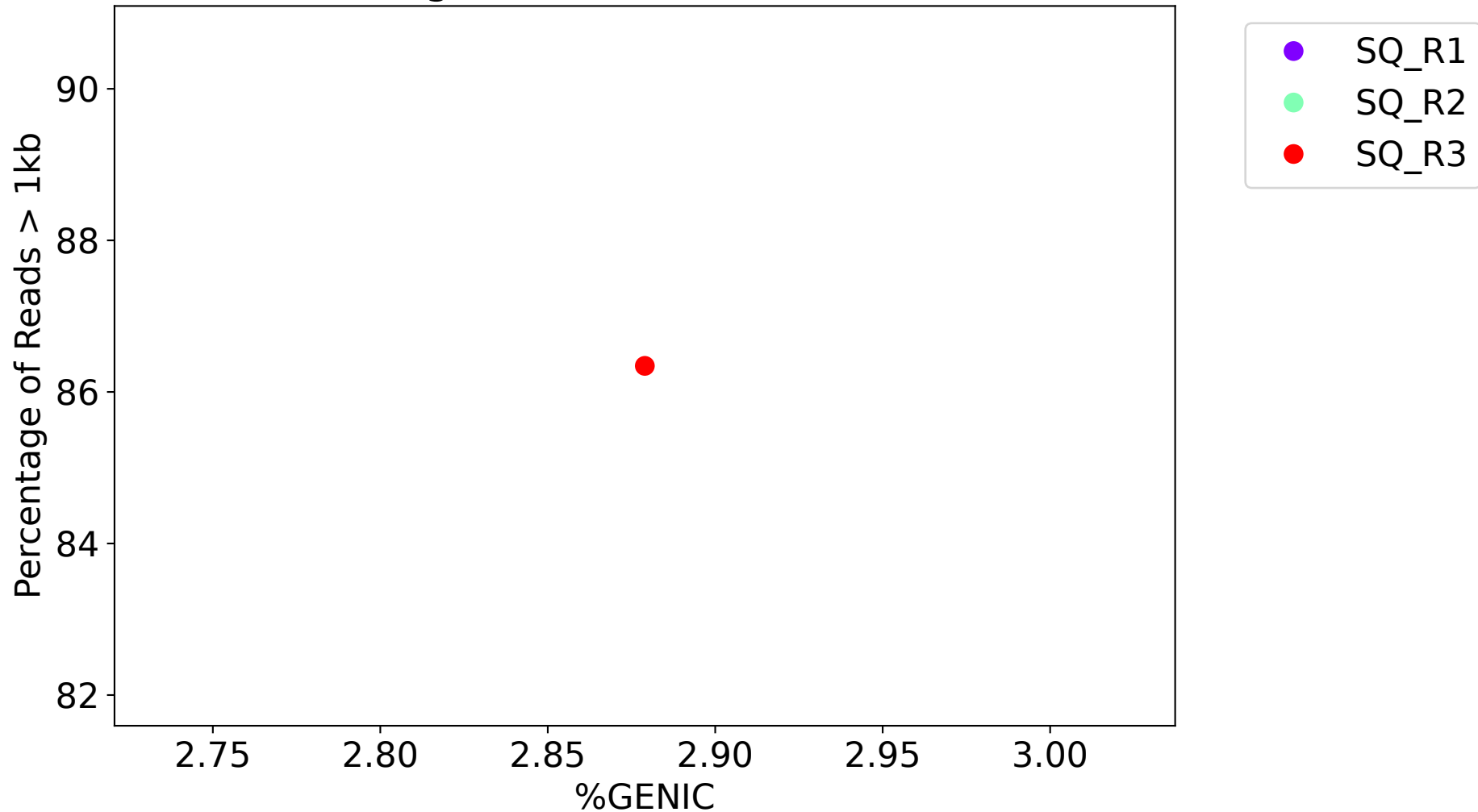
Percentage of Reads > 1kb vs %NNC



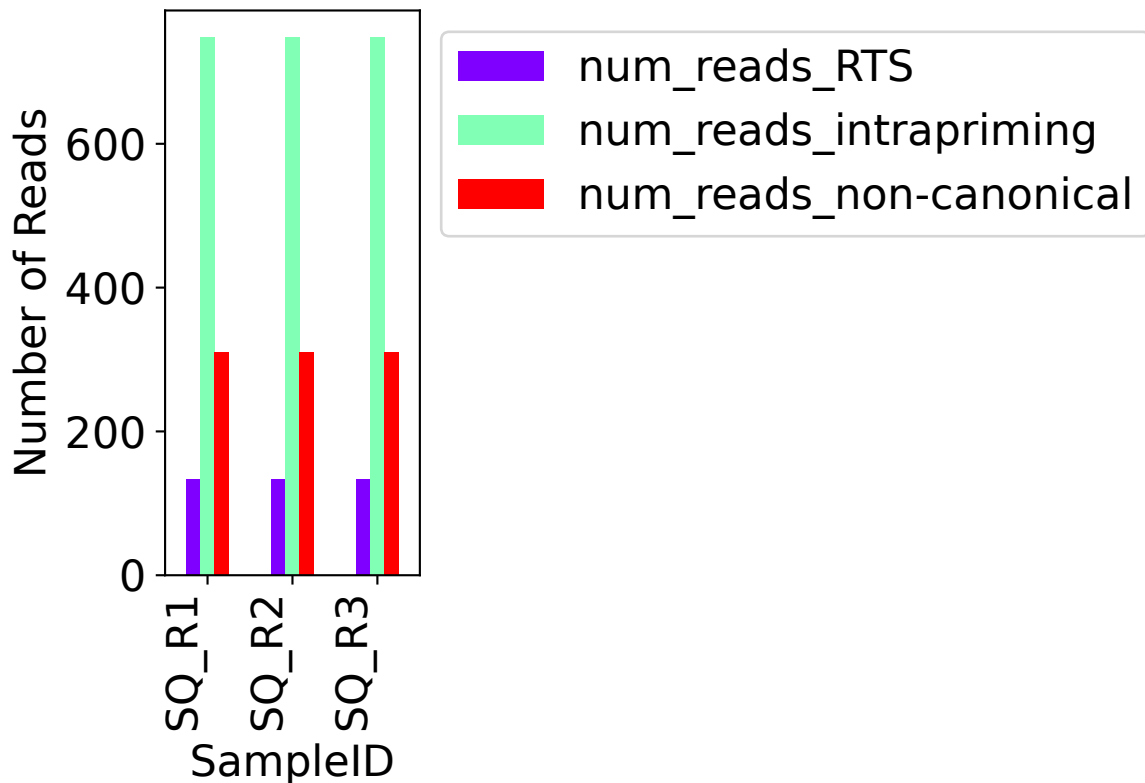
Percentage of Reads > 1kb vs %GI



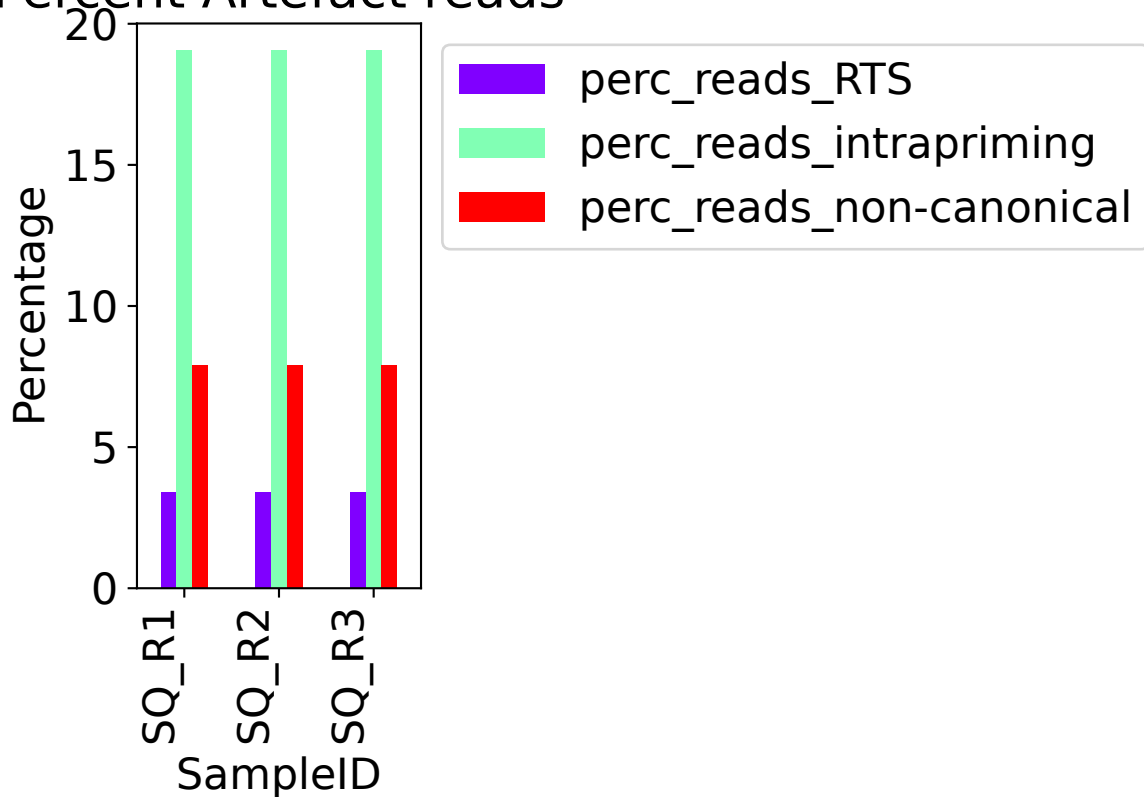
Percentage of Reads > 1kb vs %GENIC



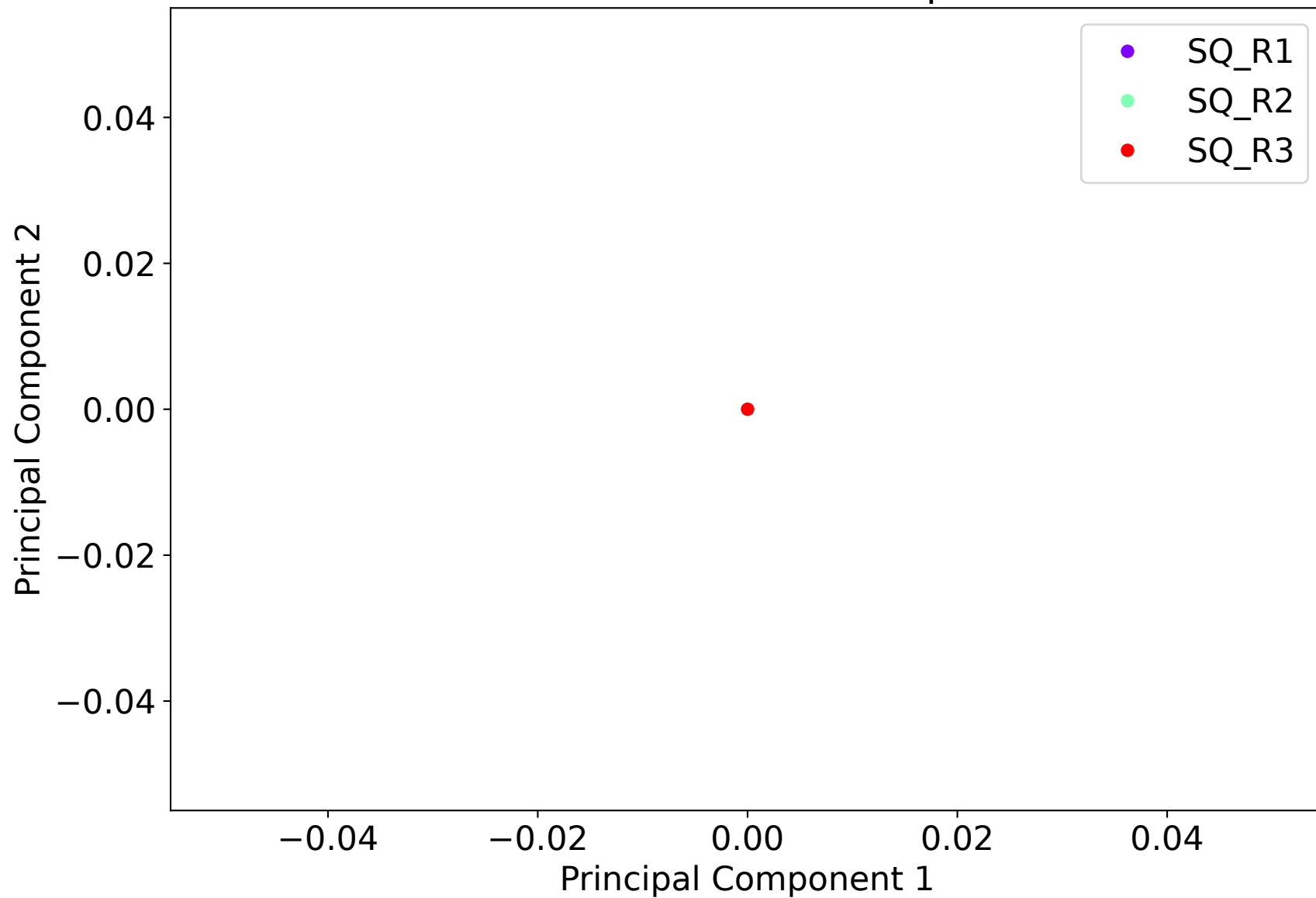
Number of Artefact reads



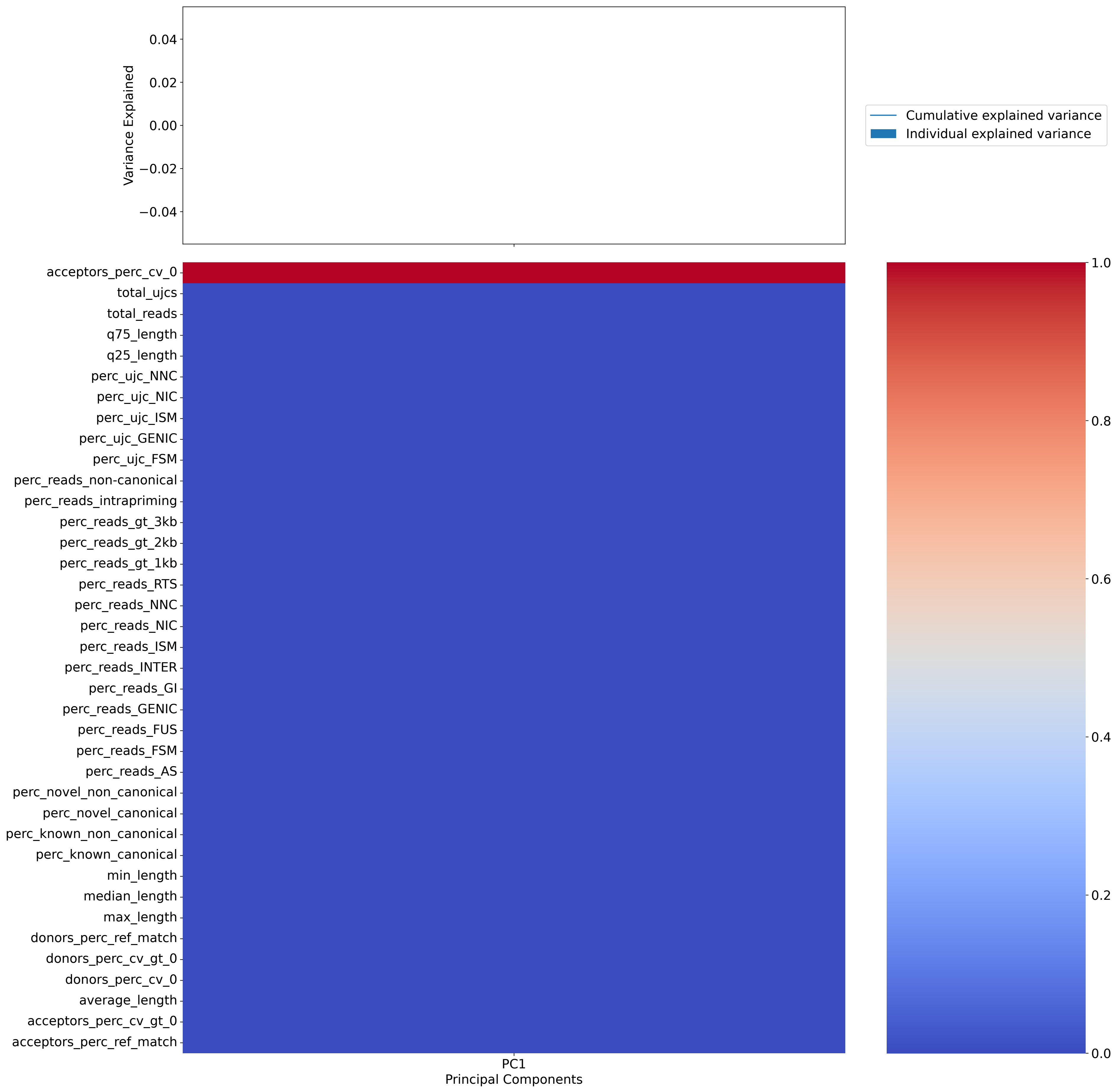
Percent Artefact reads

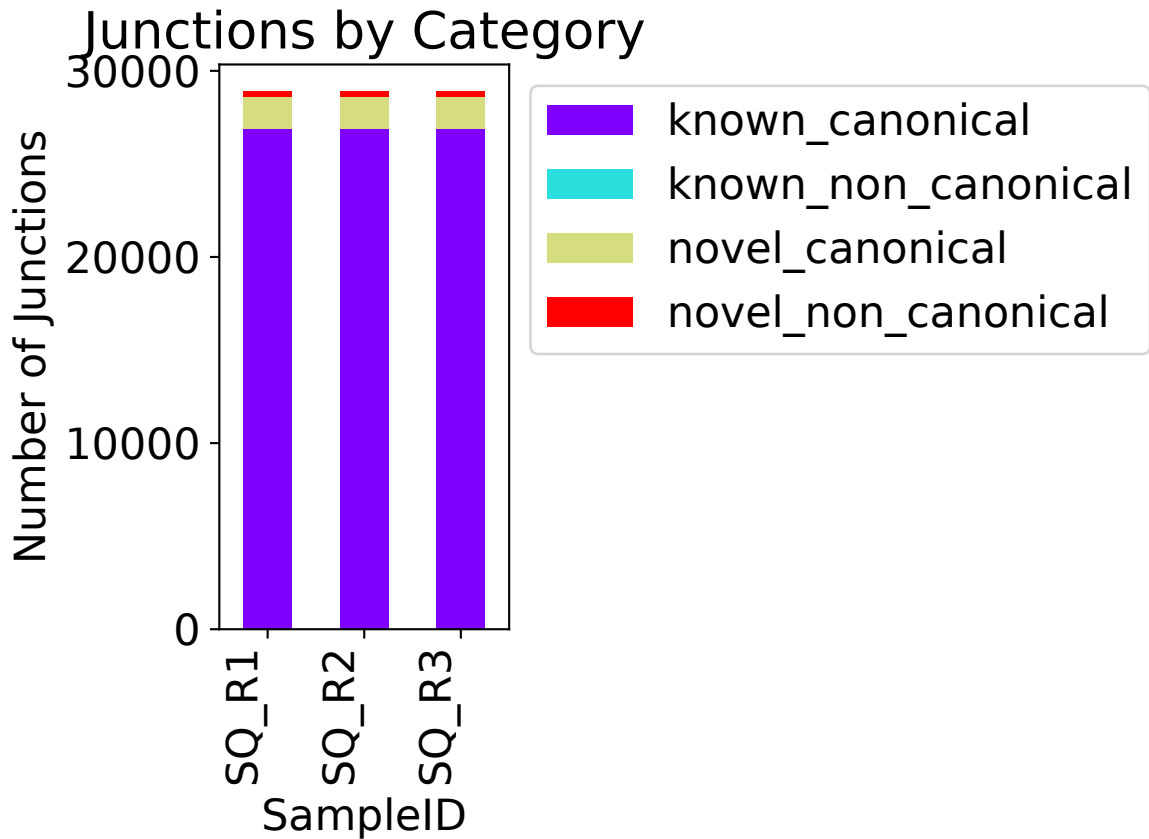


PCA Plot Based on sampleID

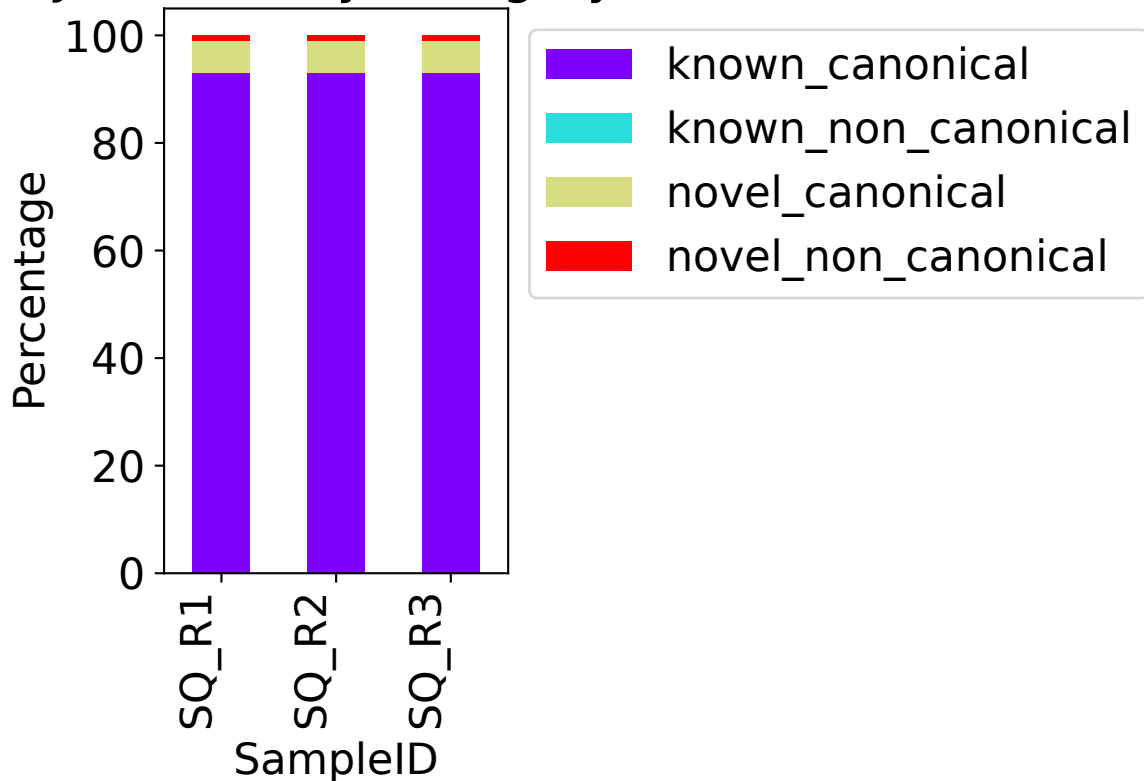


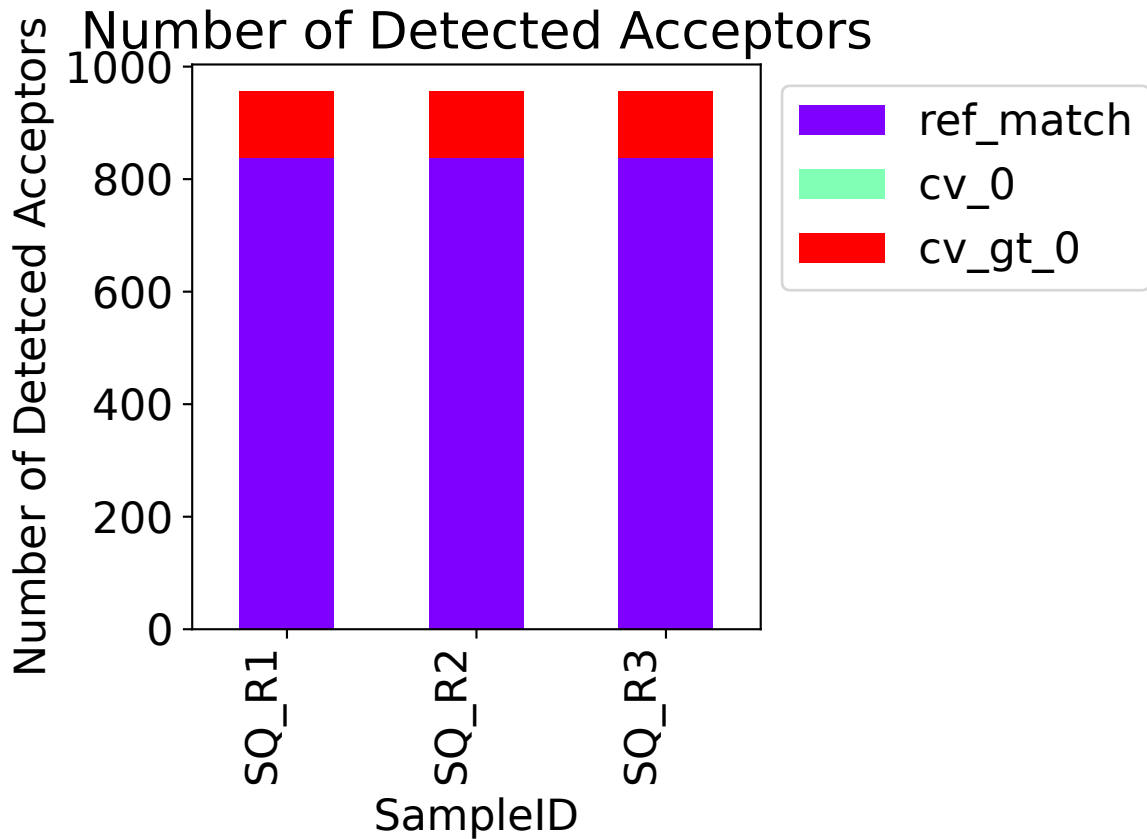
Variance and Heatmap of PC loadings

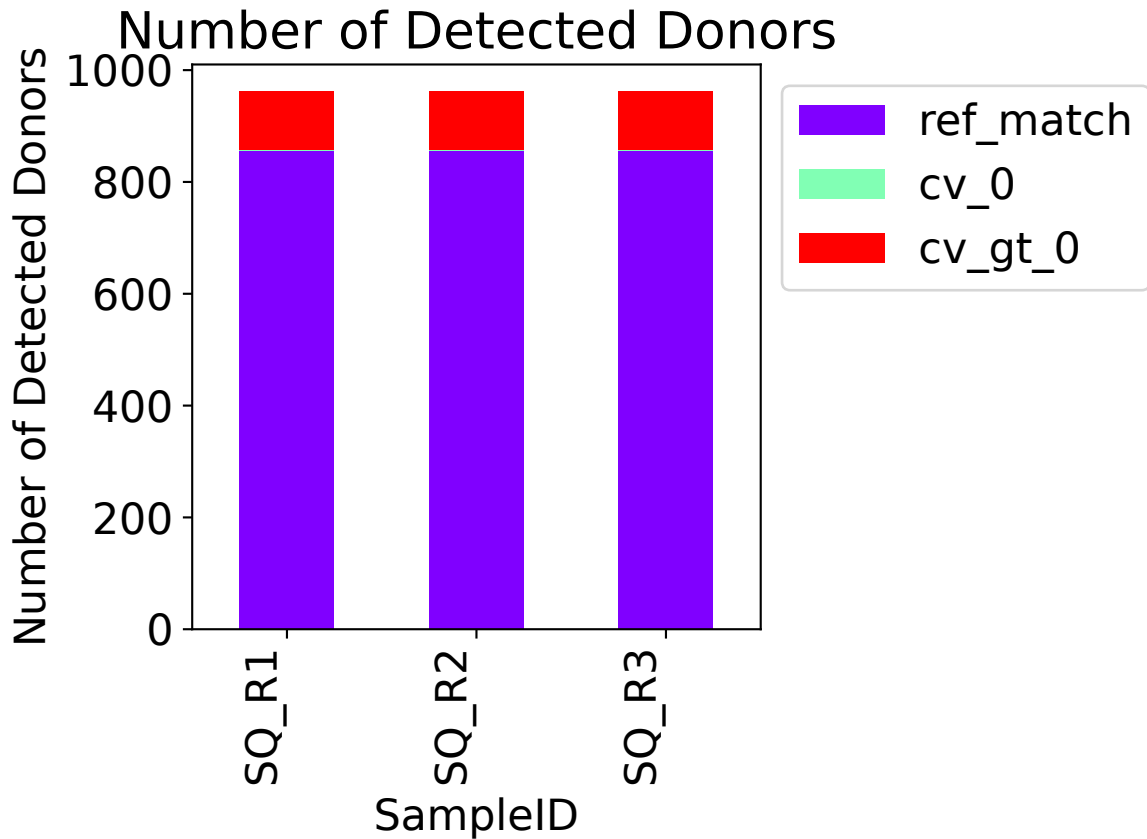




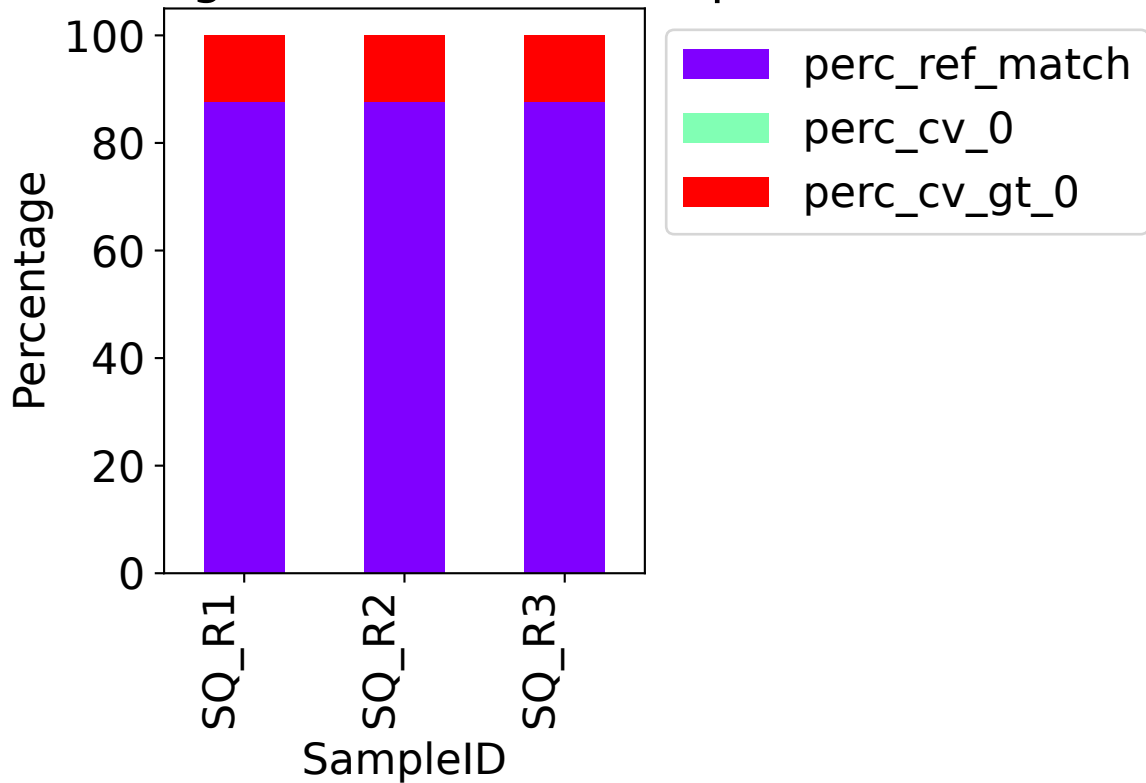
Junctions by Category







Percentage of Detected Acceptors



Number of Donors > 3 reads

