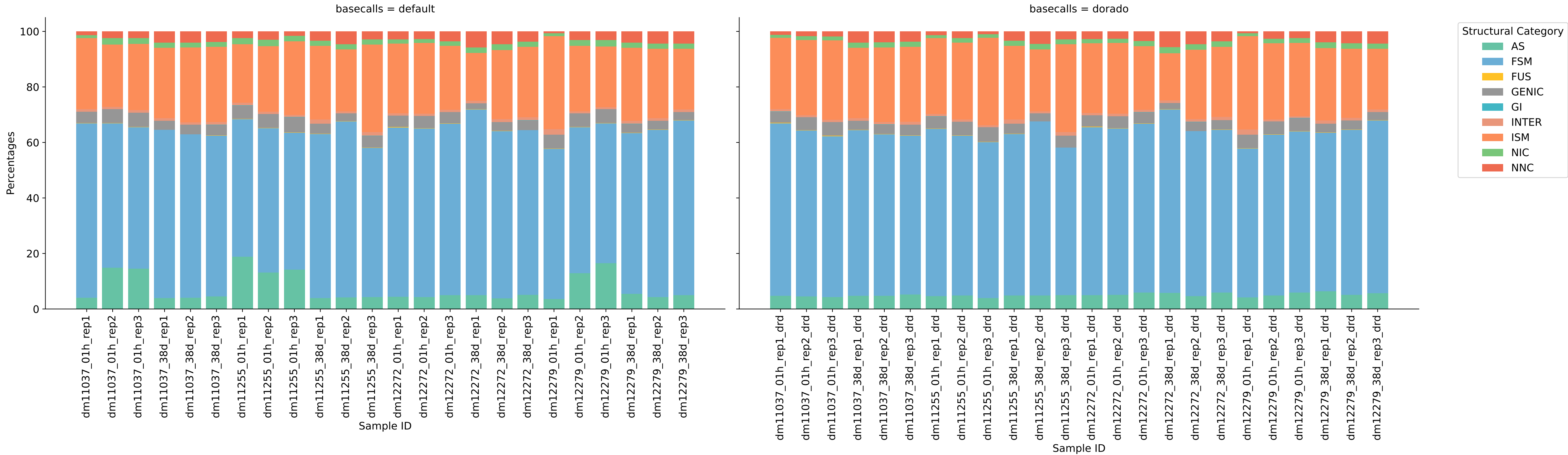
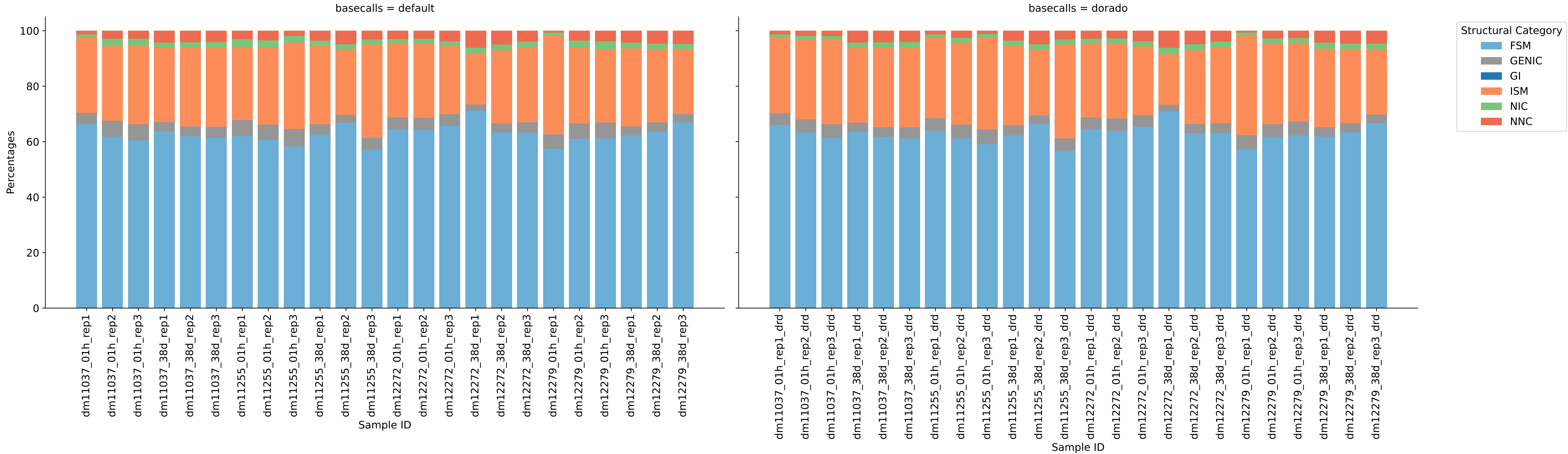


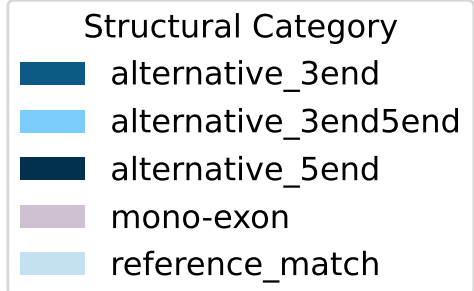
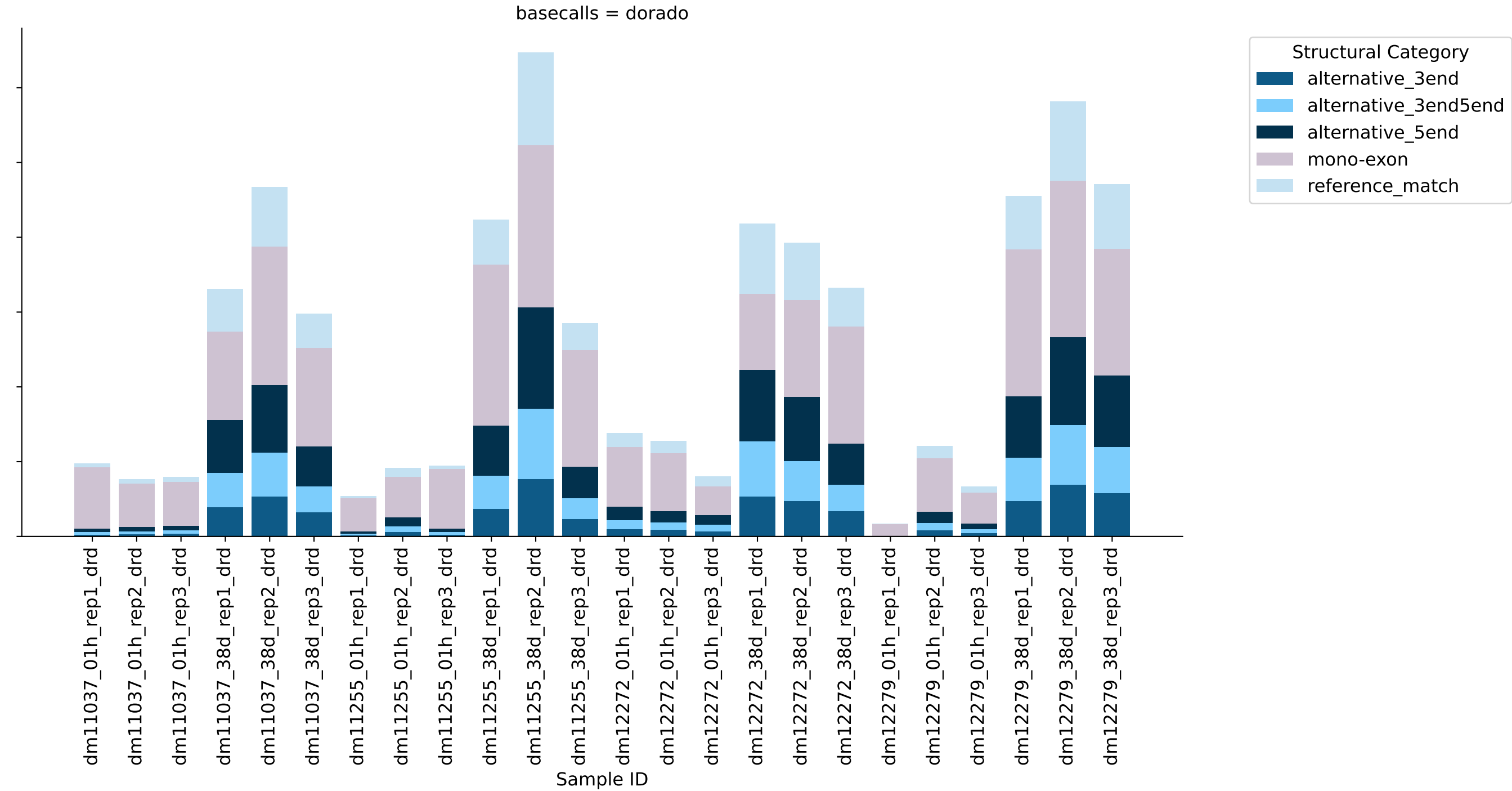
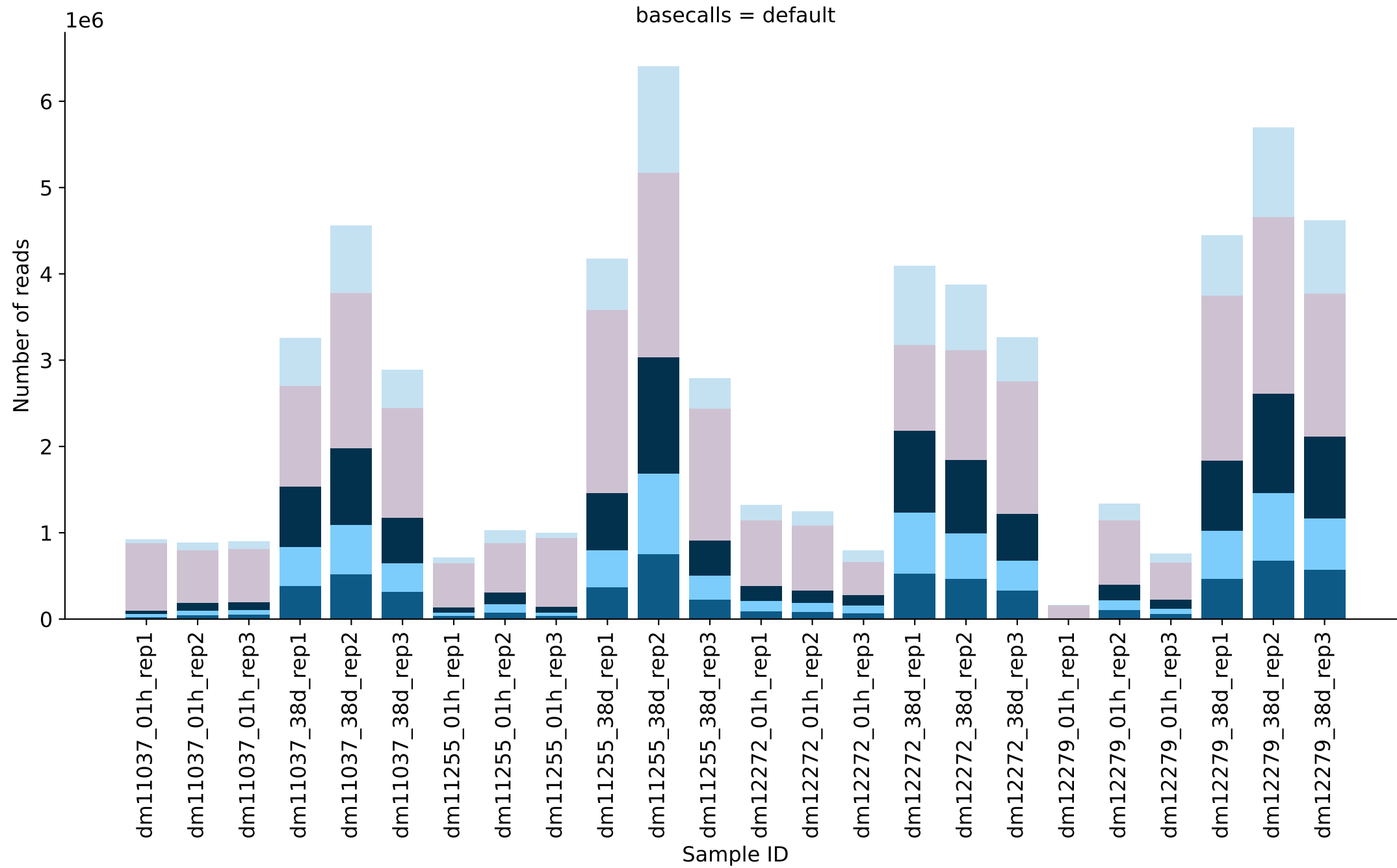
Percentage Reads in Each Structural Category - All Genes



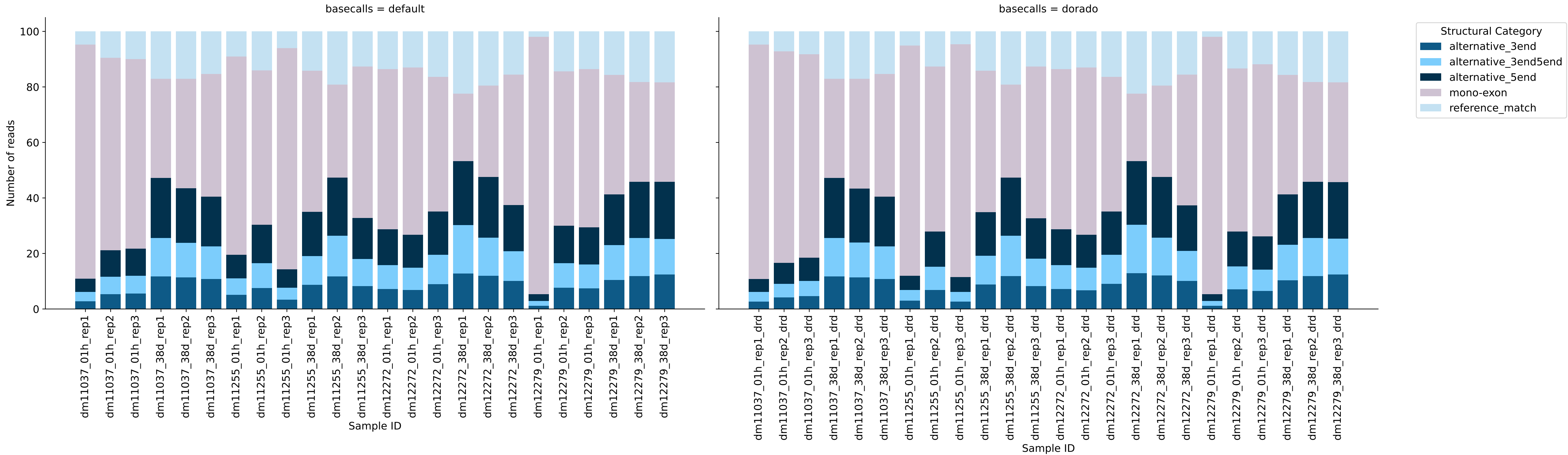
Percentage Reads in Each Structural Category - Annotated Genes



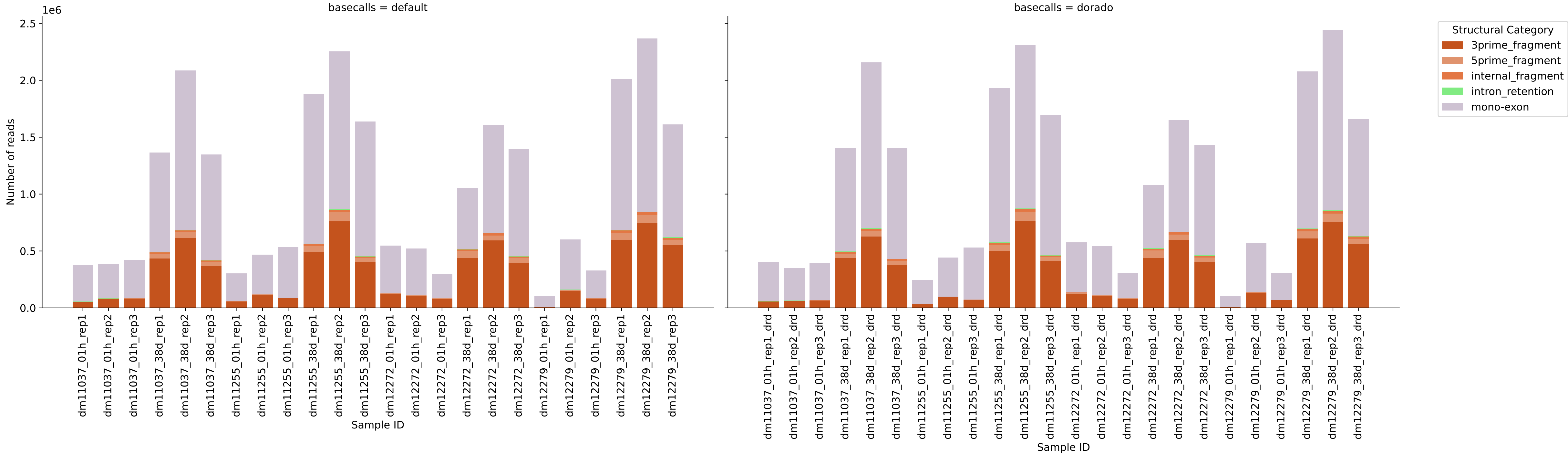
Number of Reads in Each Sub-Category - FSM



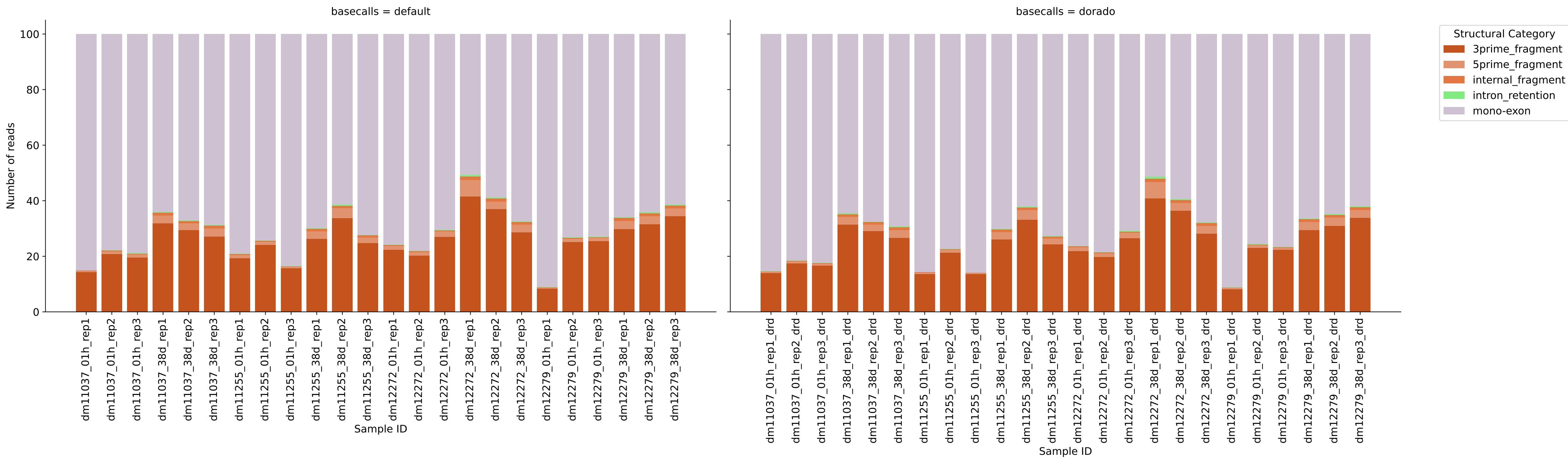
Percentage of FSM Reads in Each Sub-Category



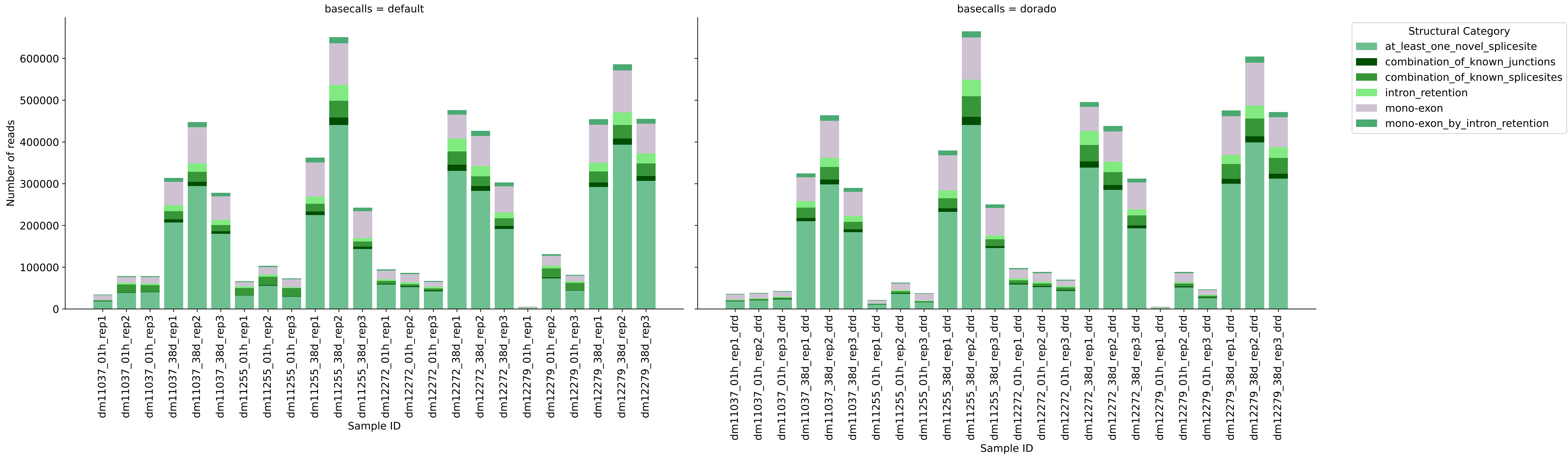
Number of Reads in Each Sub-Category - ISM



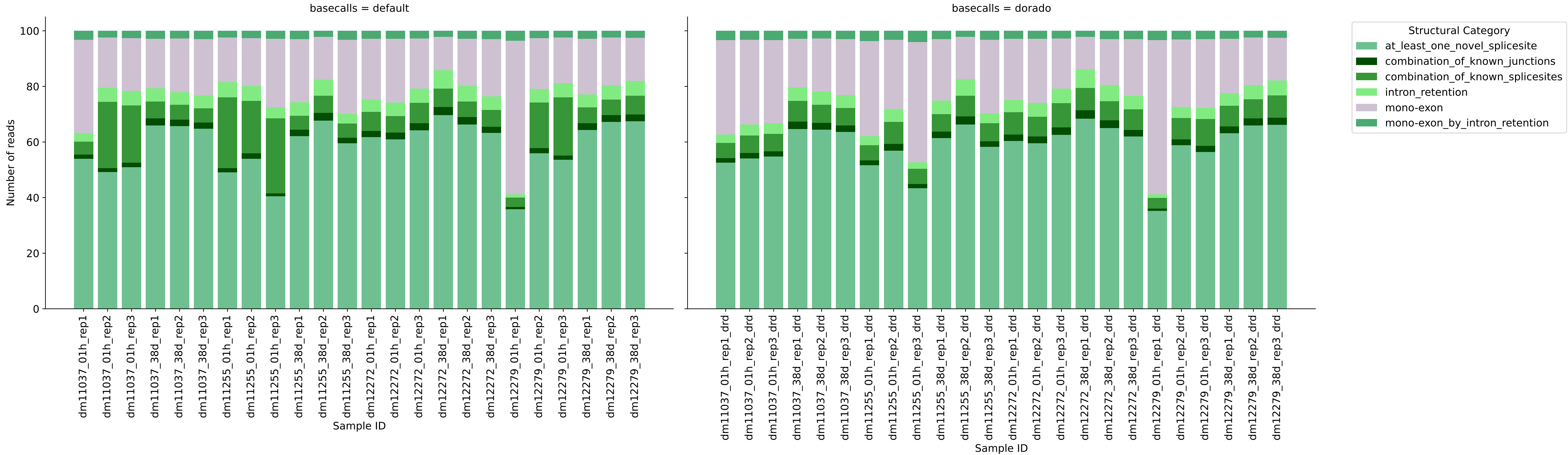
Percentage of ISM Reads in Each Sub-Category



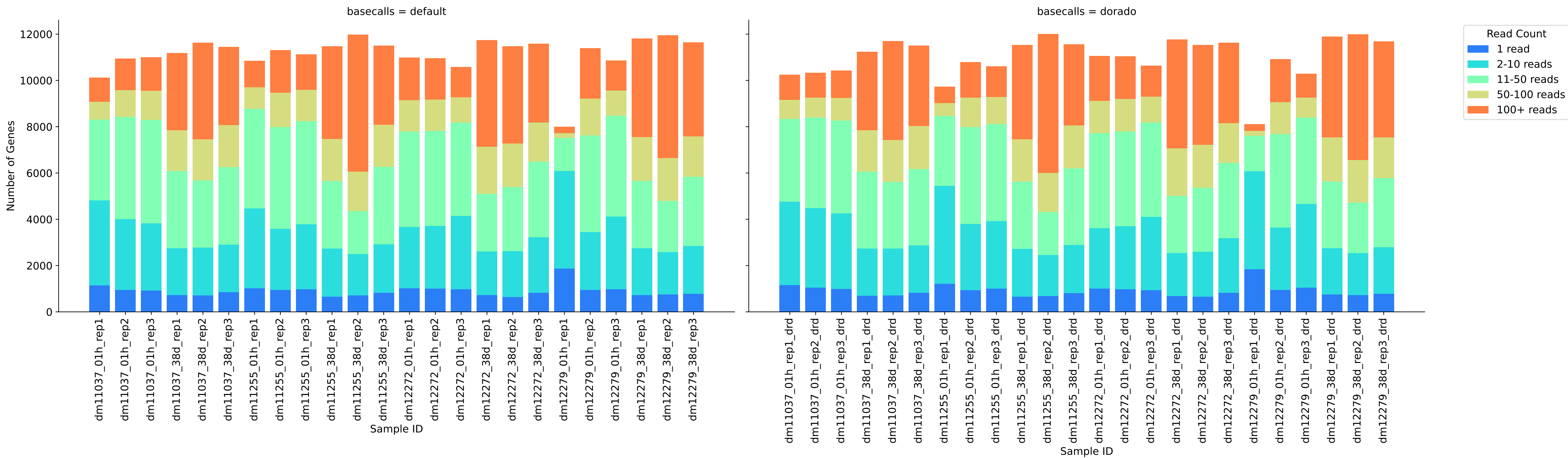
Number of Reads in Each Sub-Category - NIC and NNC



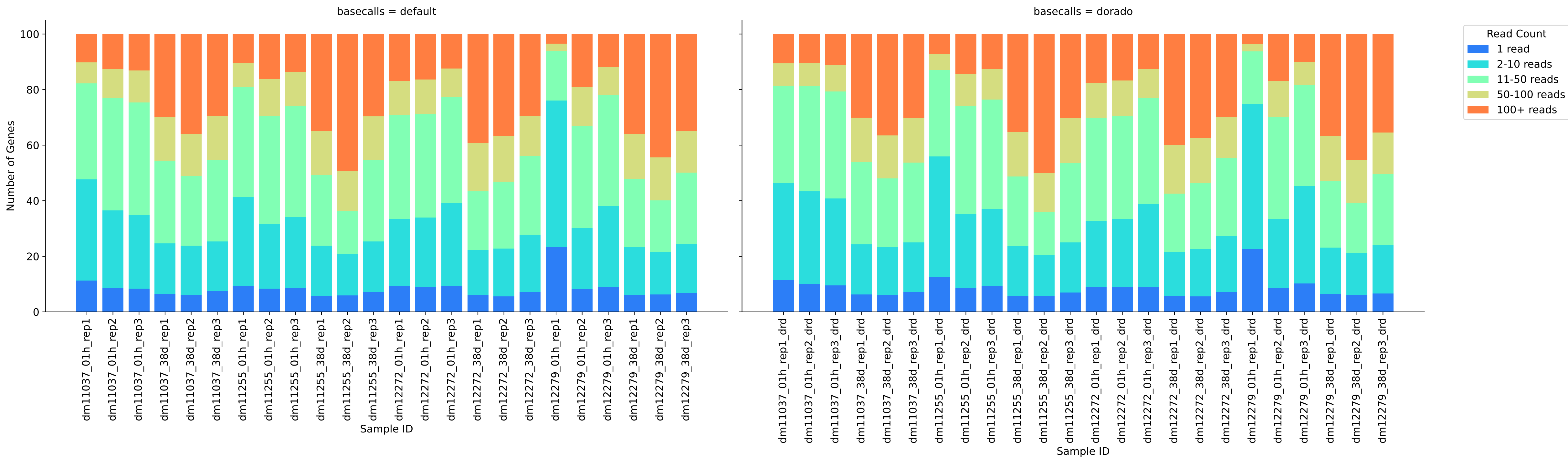
Percentage of NIC/NNC Reads in Each Sub-Category



Number of Genes Detected

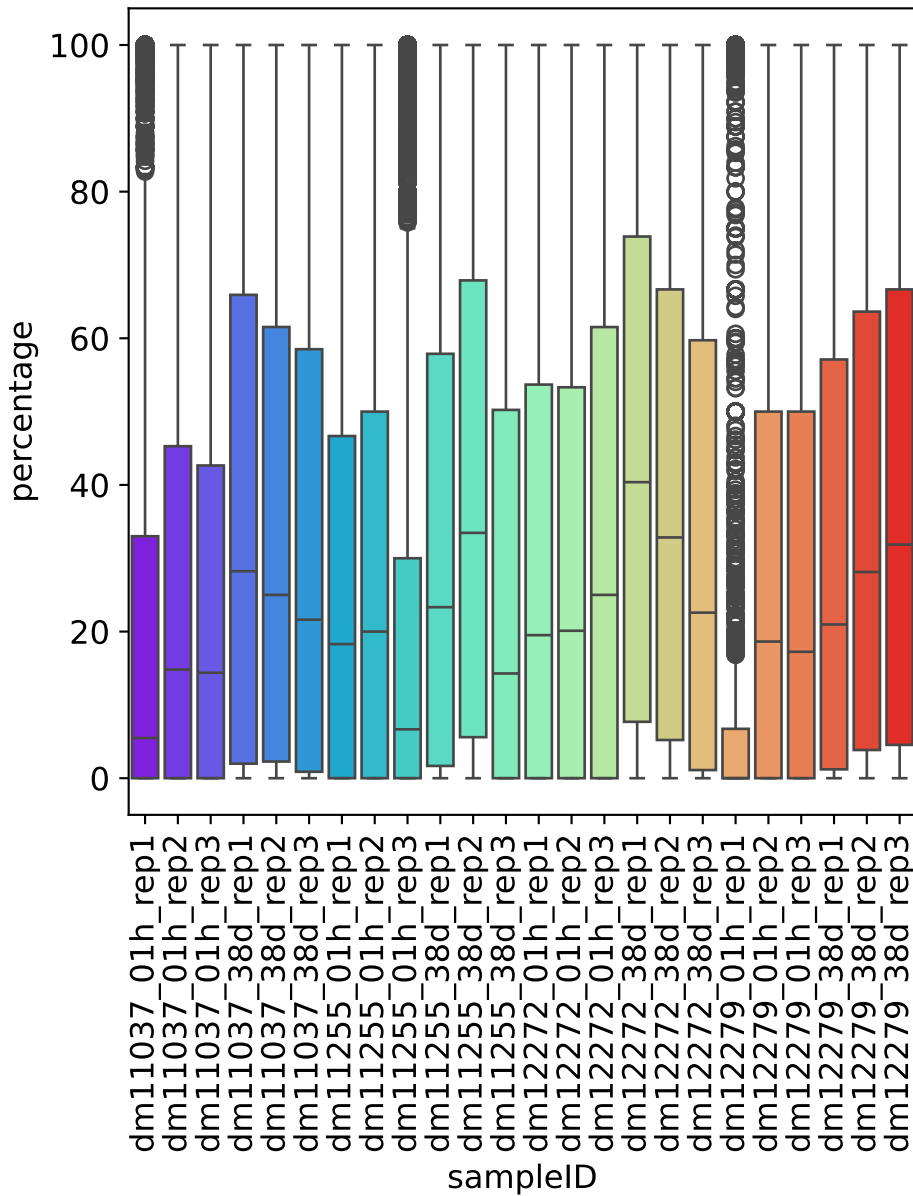


Number of Genes Detected

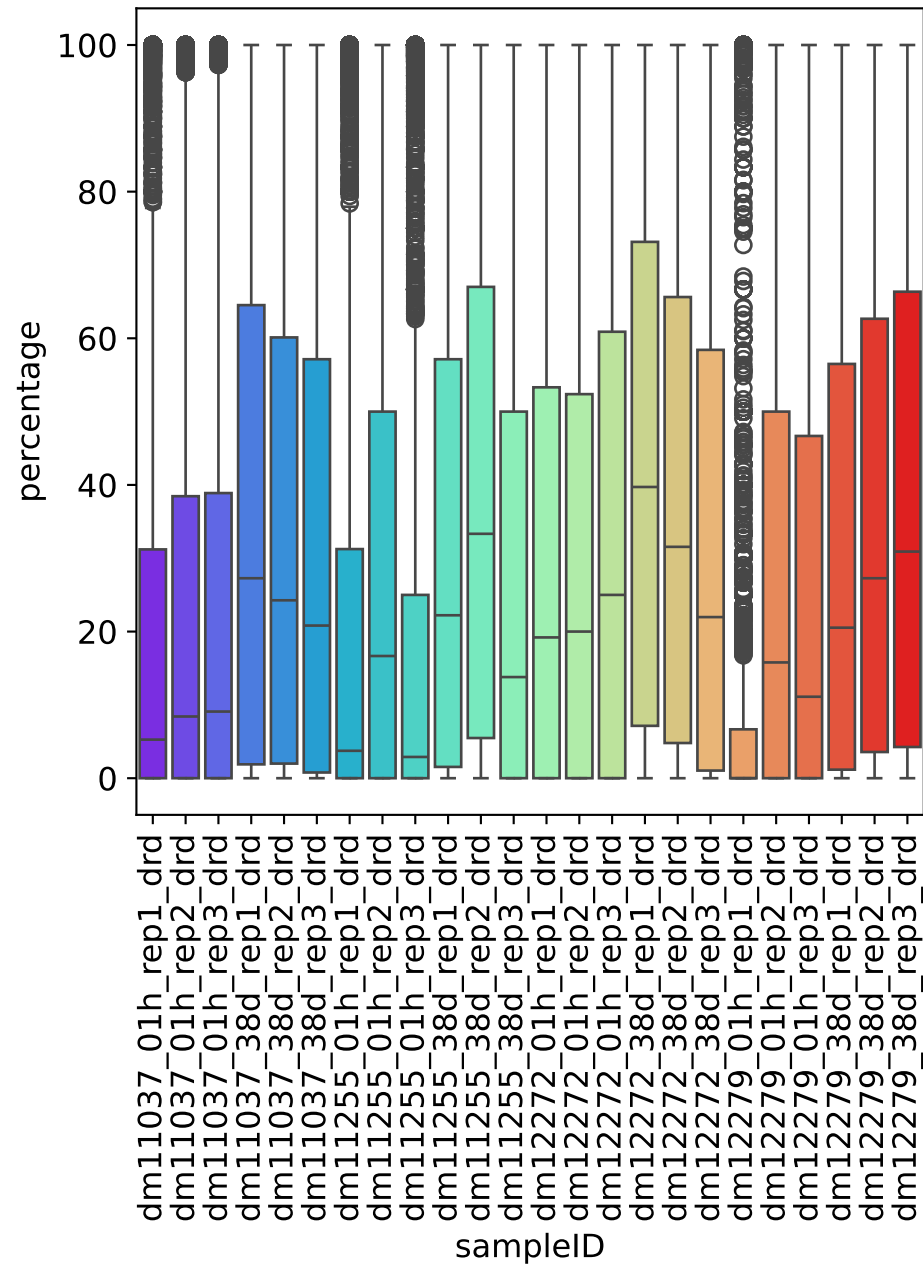


Gene distribution - percent_full-splice_match

basecalls = default

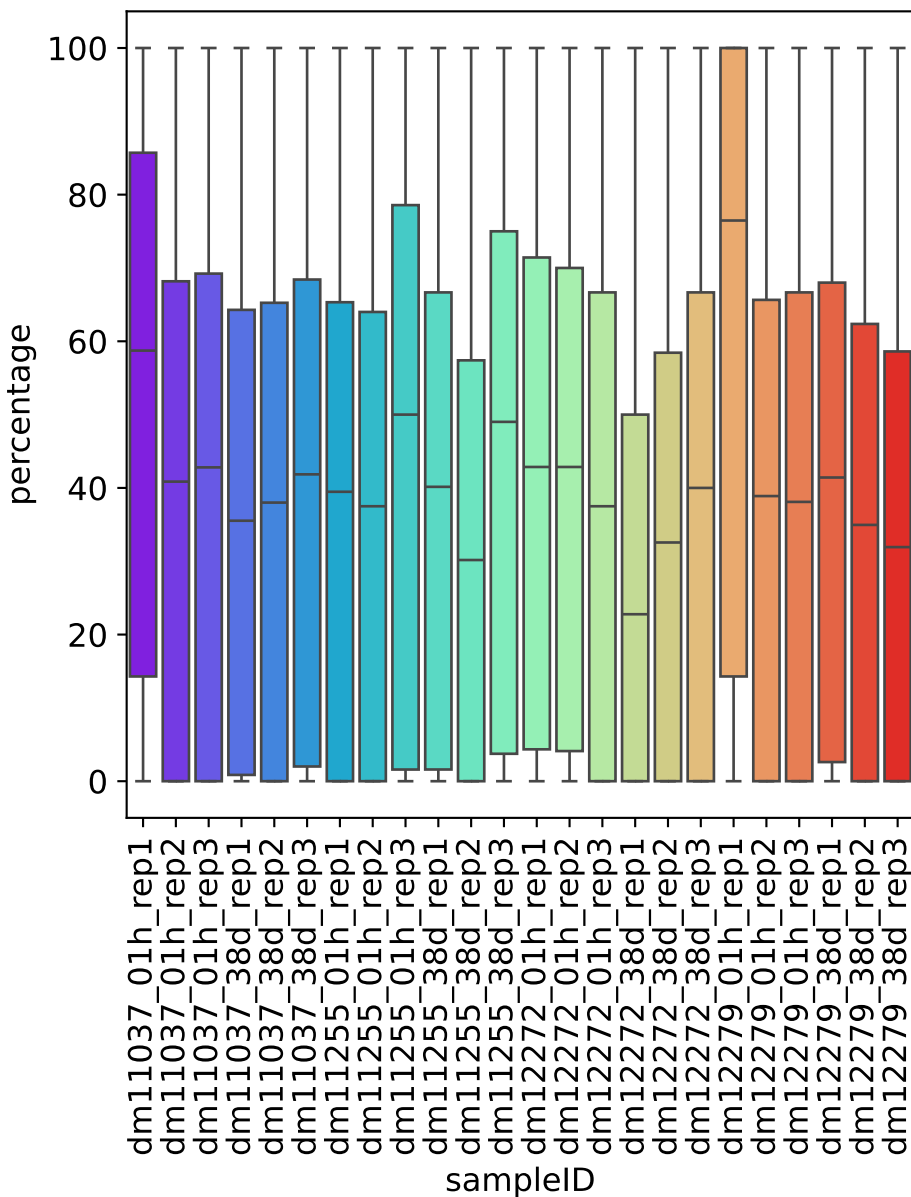


basecalls = dorado

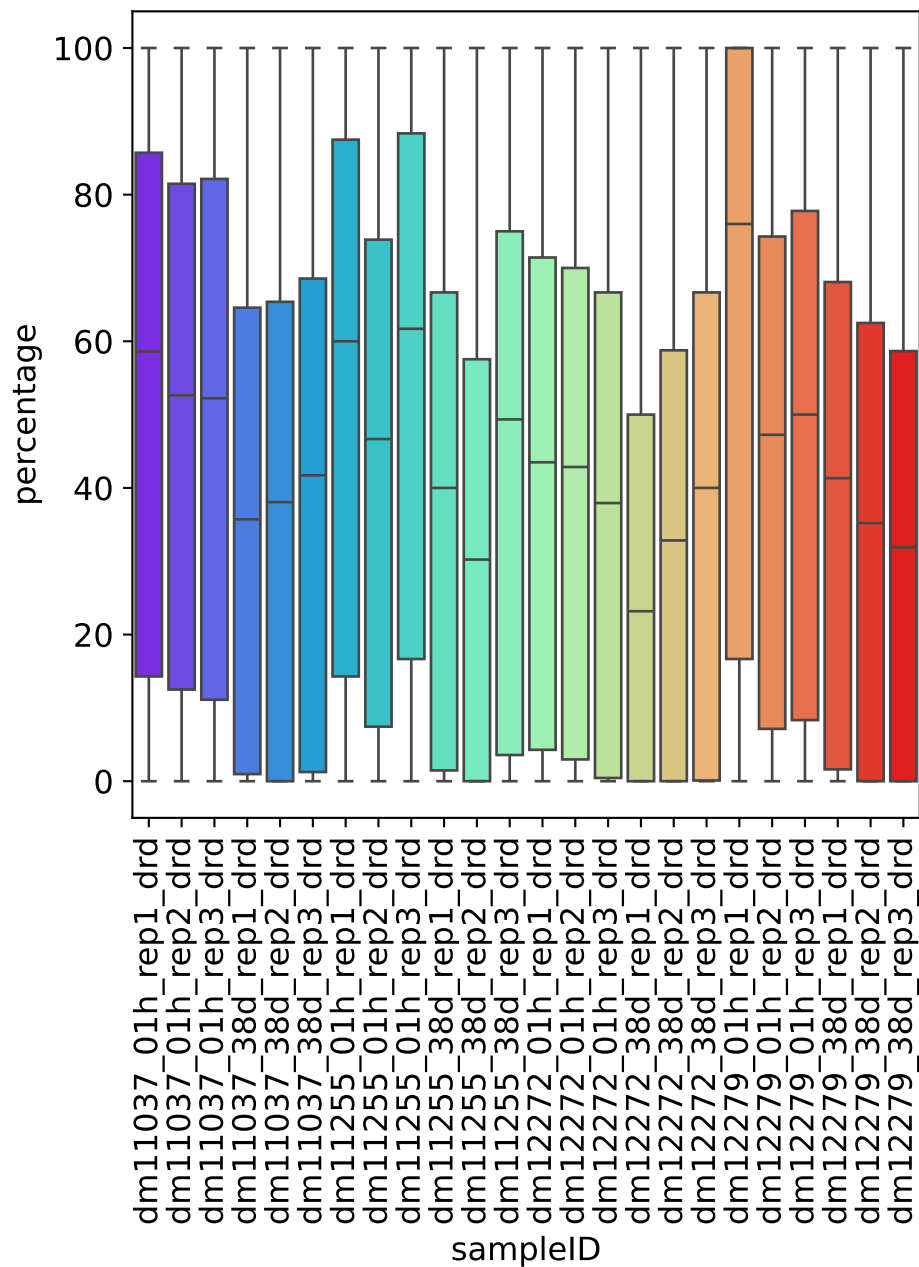


Gene distribution - percent_incomplete-splice_match

basecalls = default

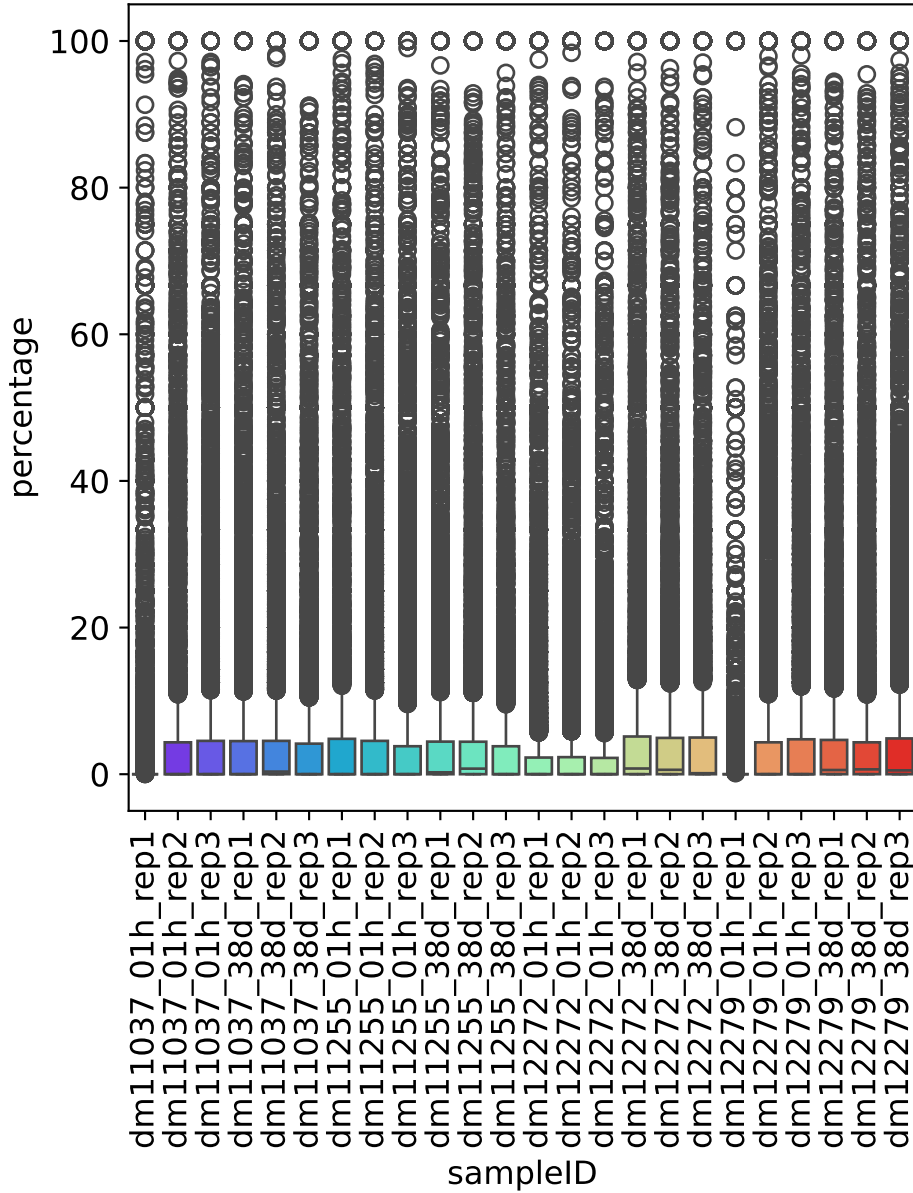


basecalls = dorado

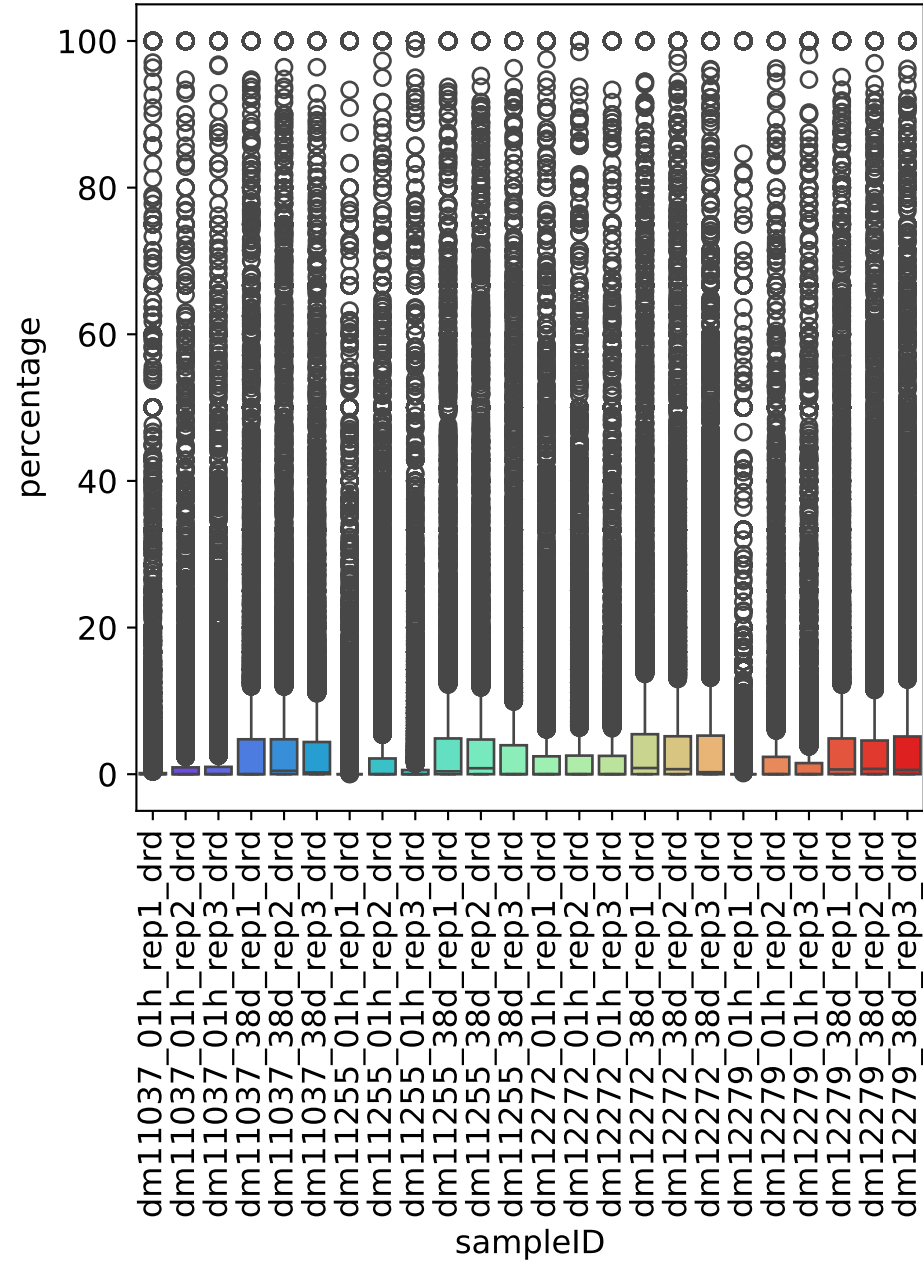


Gene distribution - percent_novel_in_catalog

basecalls = default

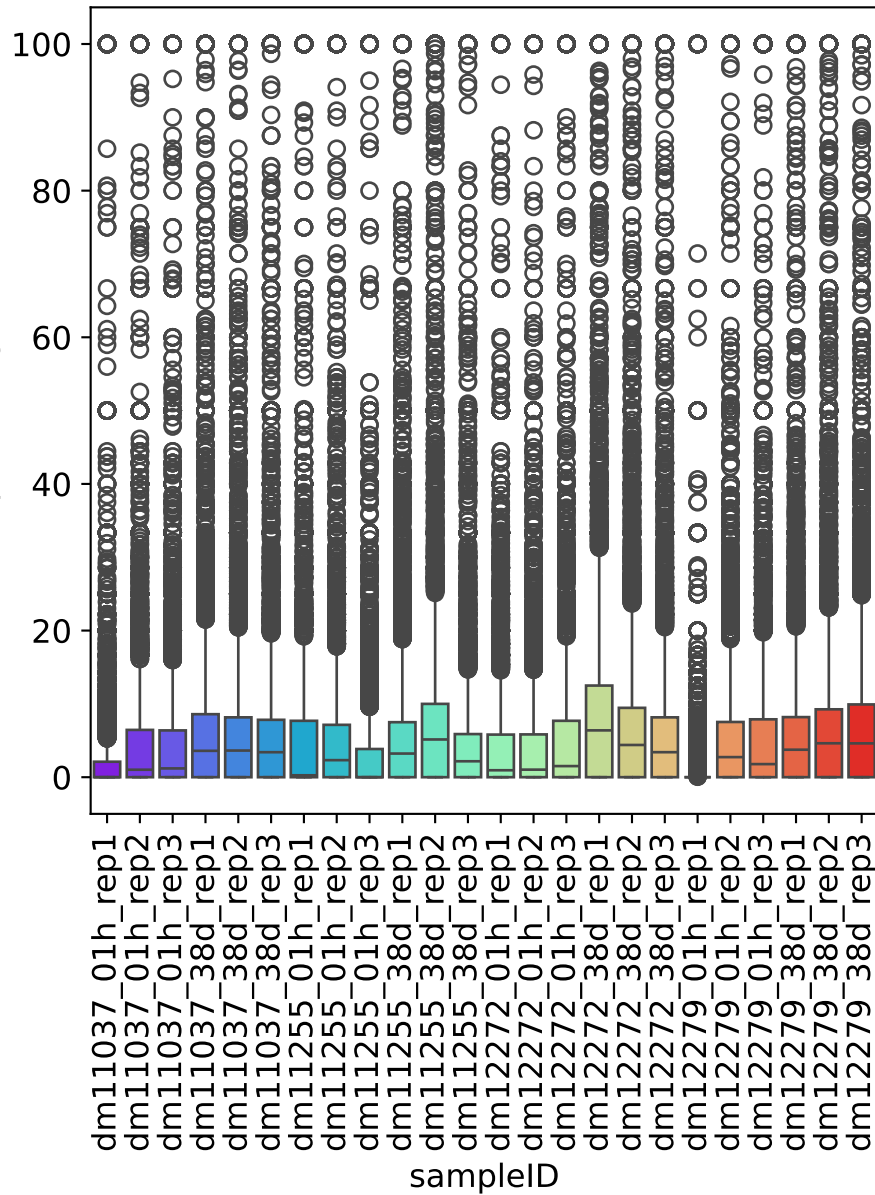


basecalls = dorado

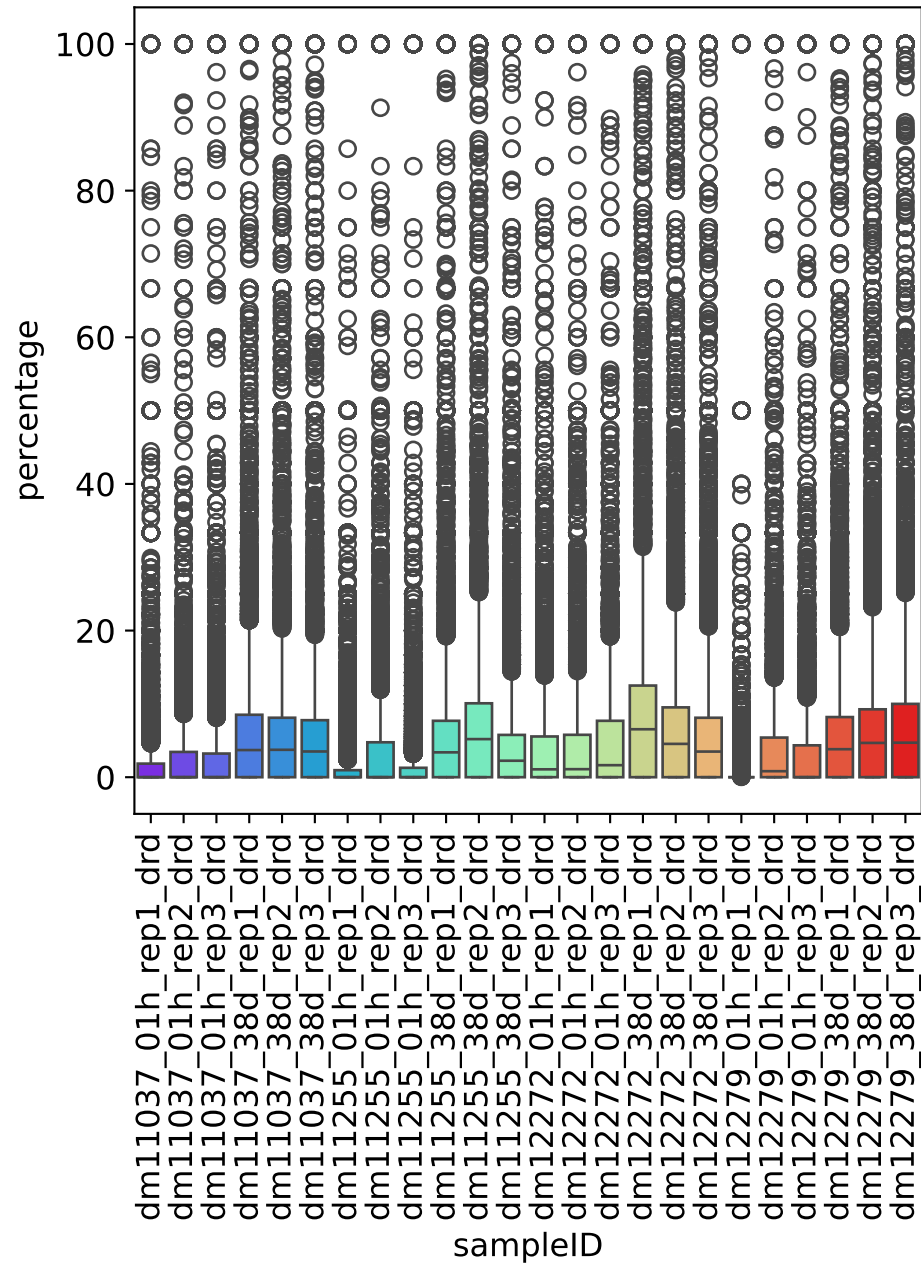


Gene distribution - percent_novel_not_in_catalog

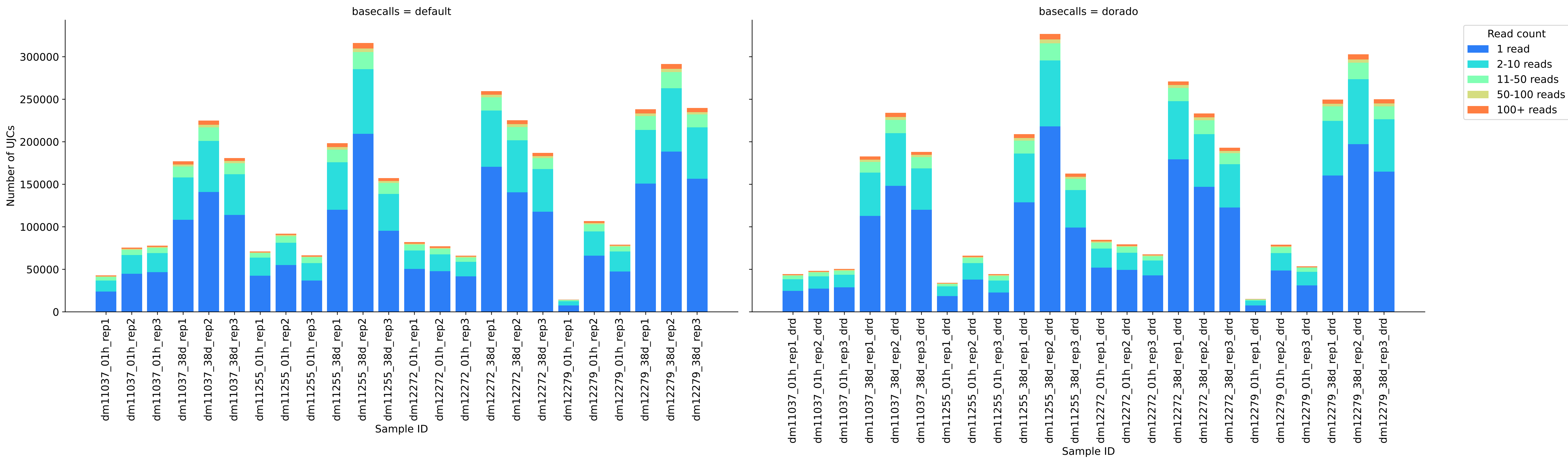
basecalls = default



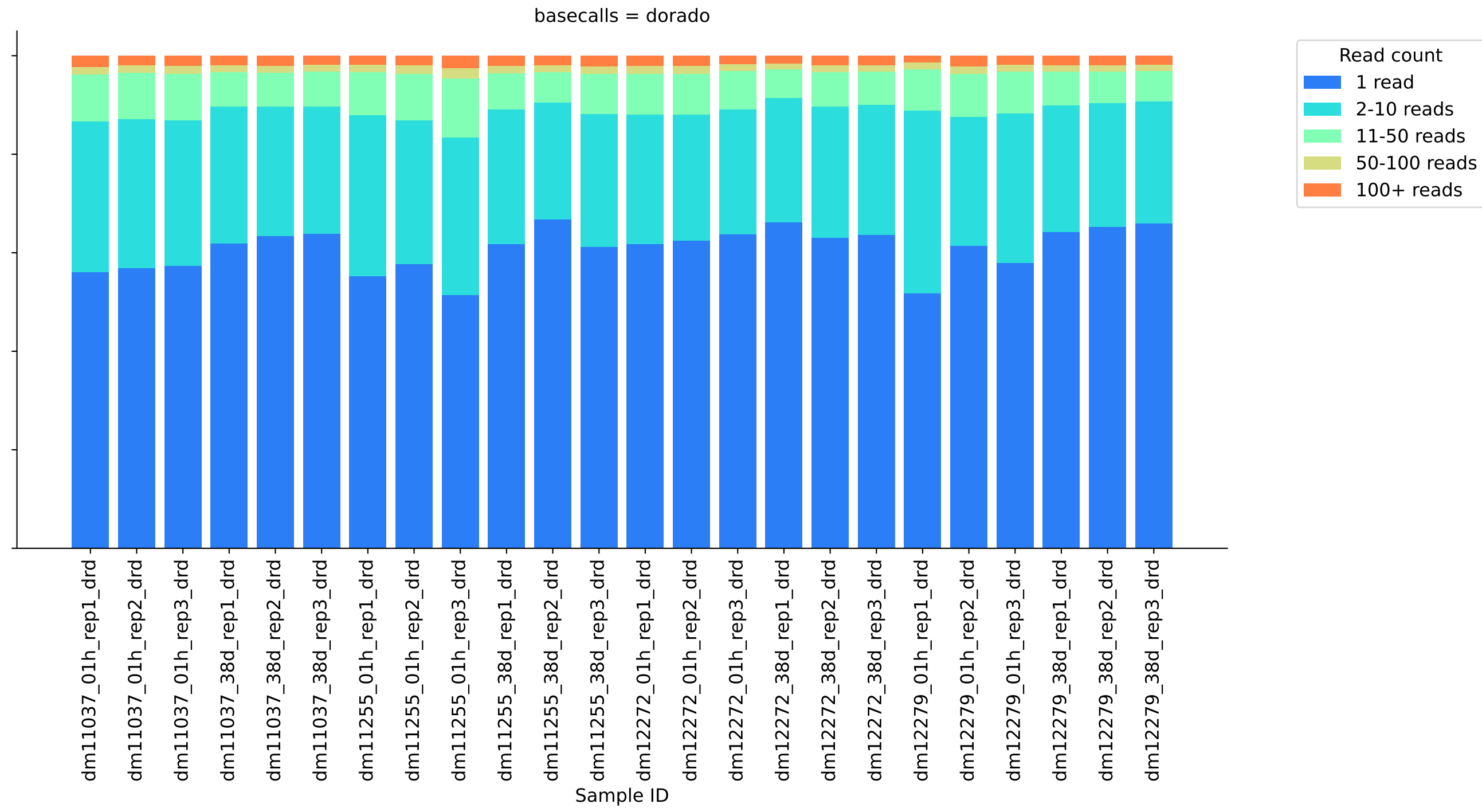
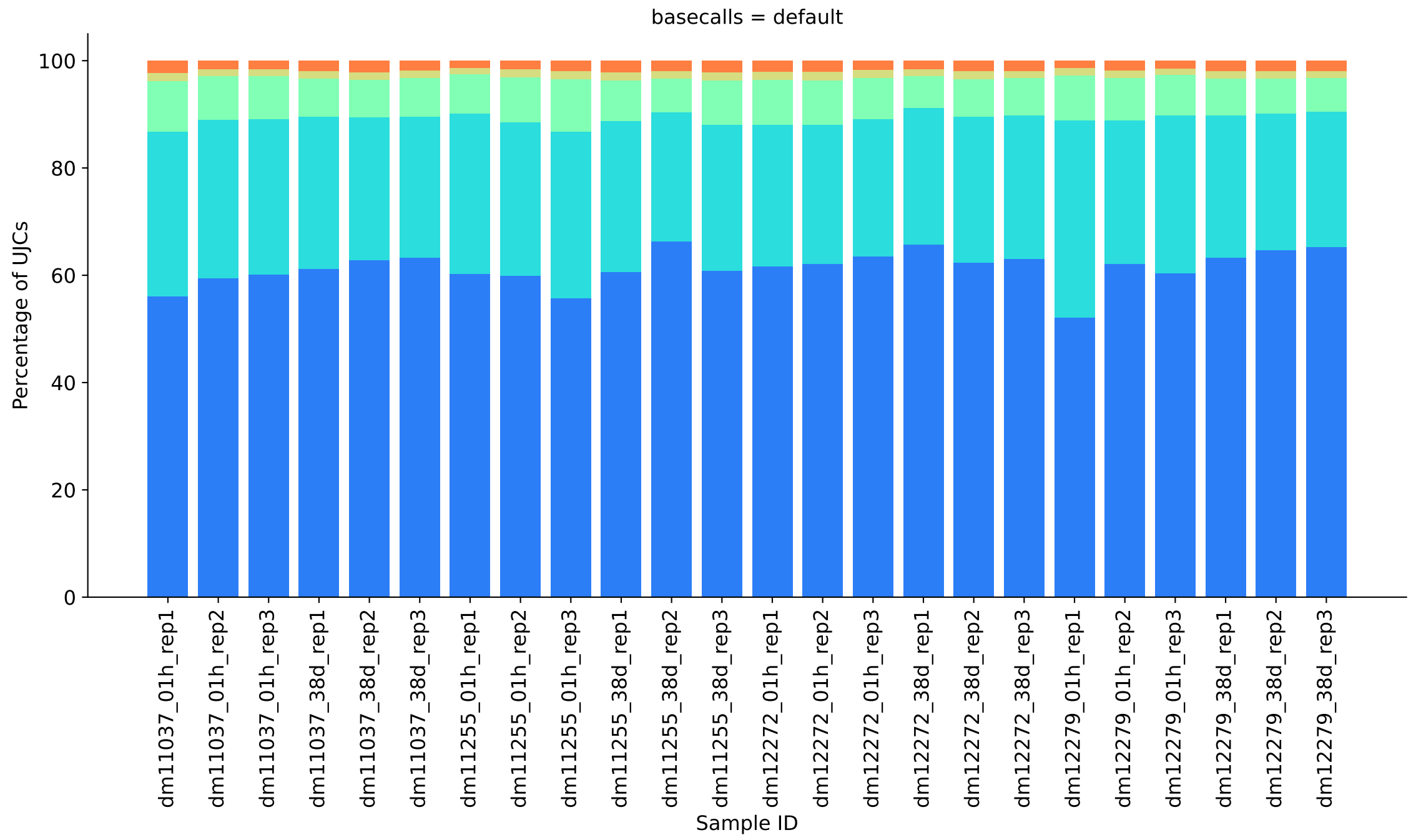
basecalls = dorado



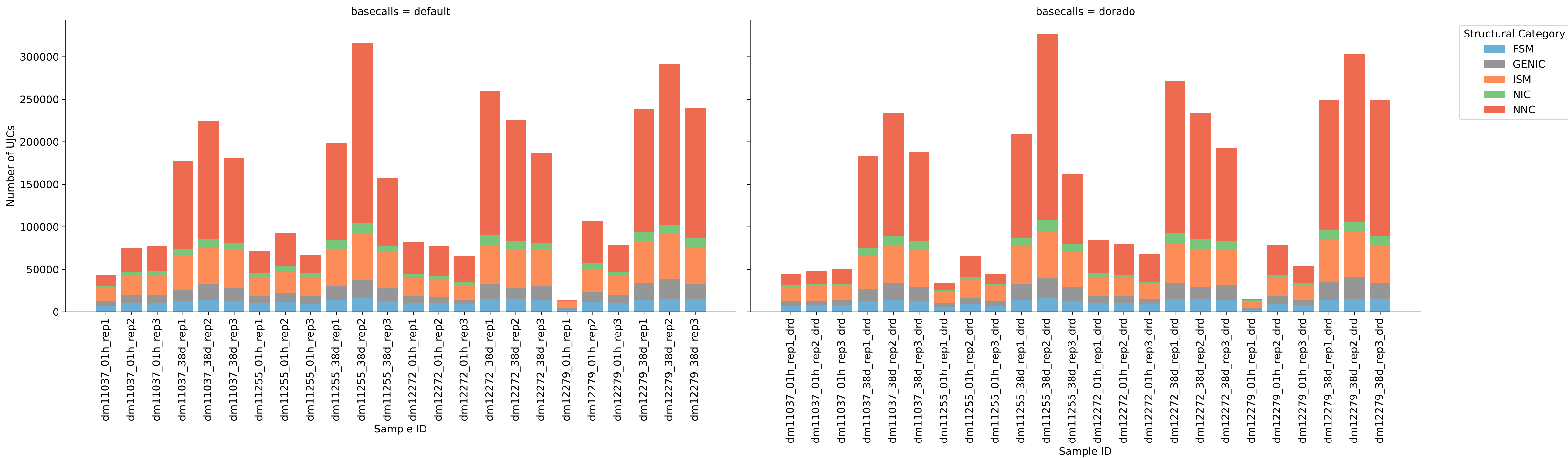
Number of UJCs Detected



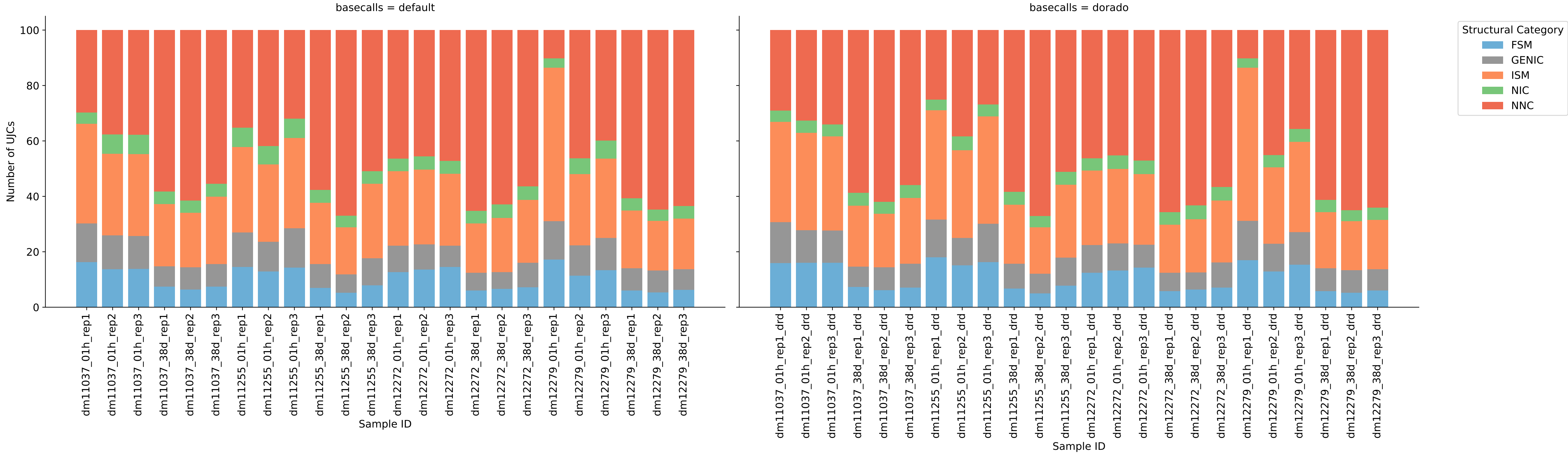
UJCs Detected

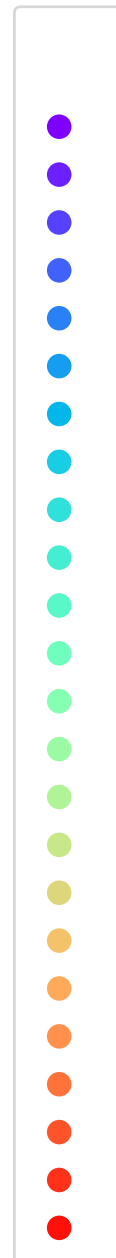
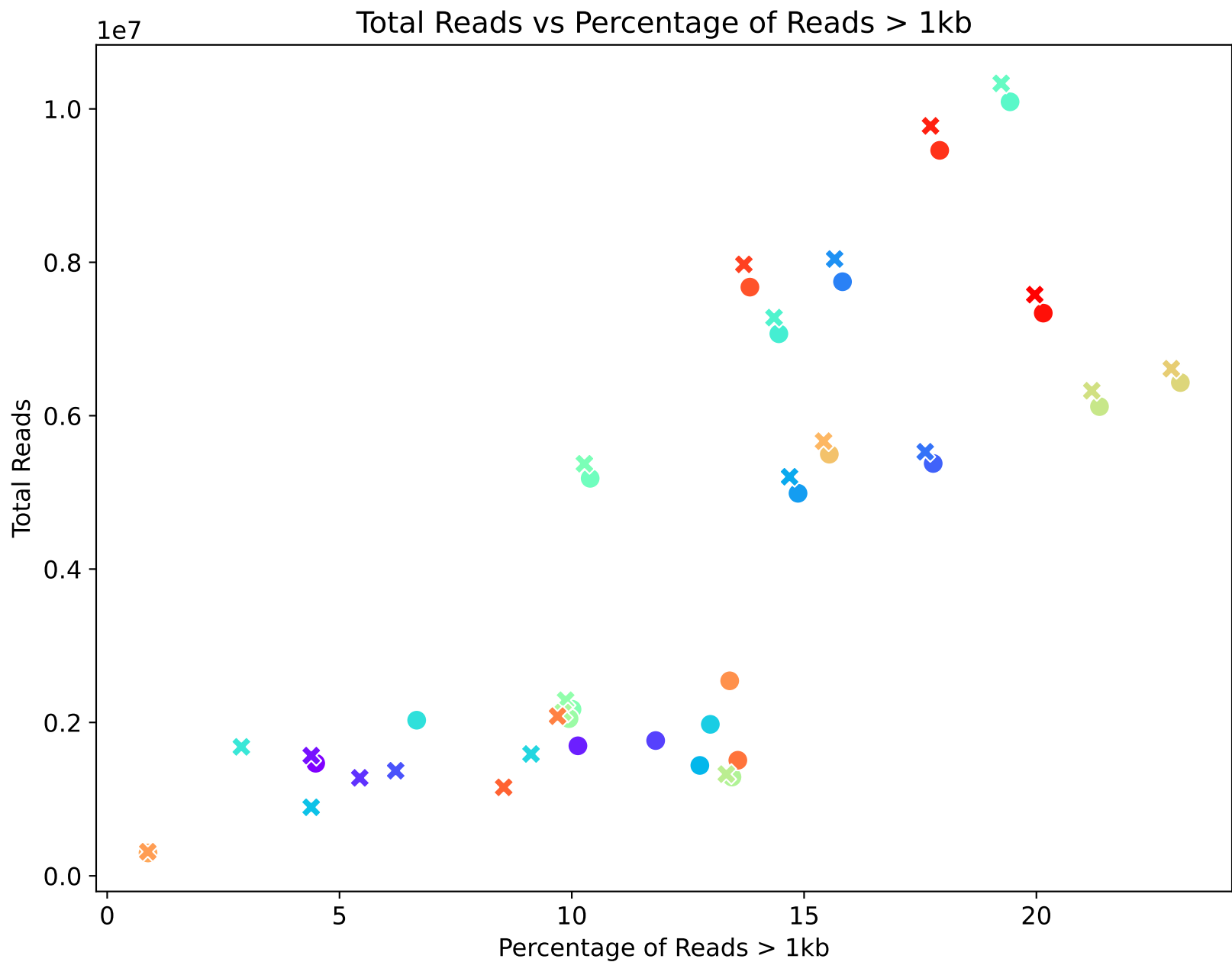


Number of UJCs detected

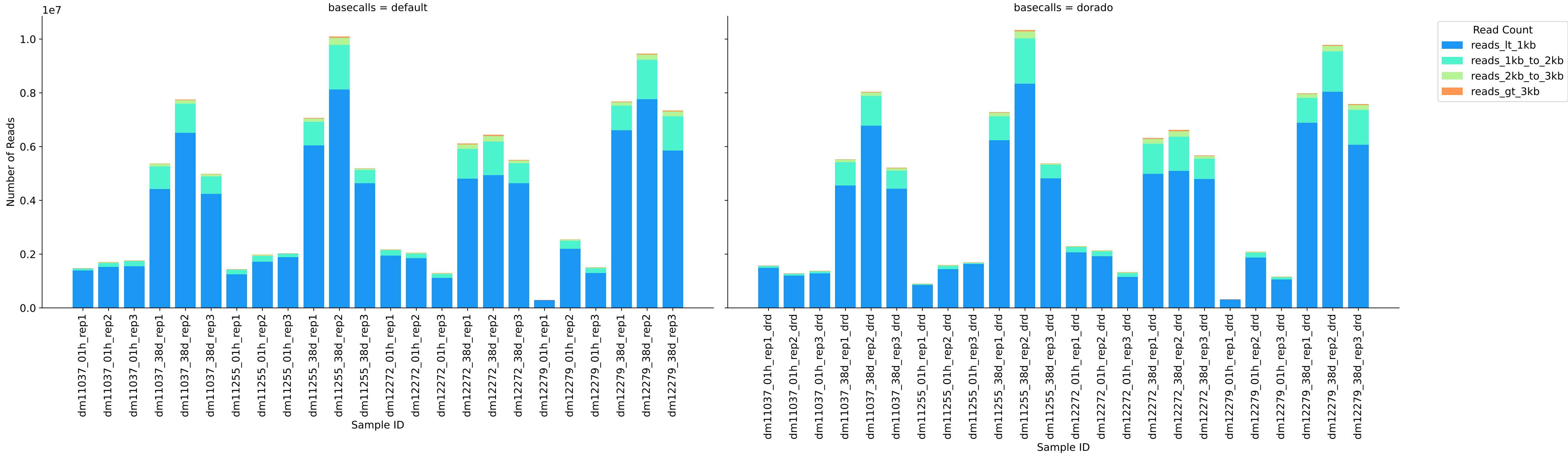


Number of UJCs detected

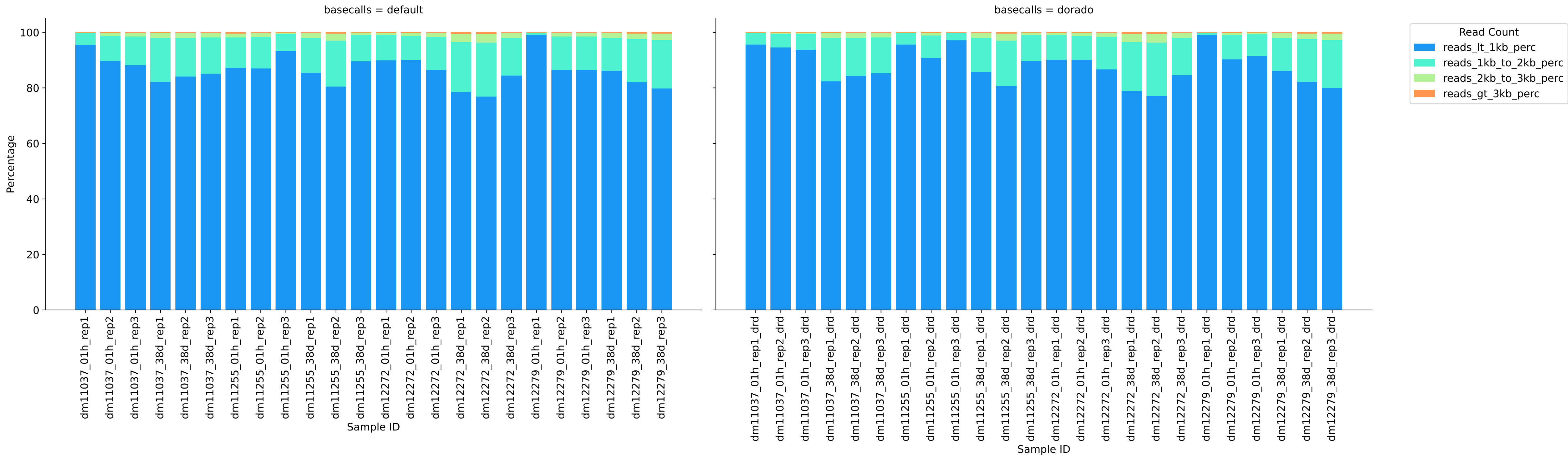




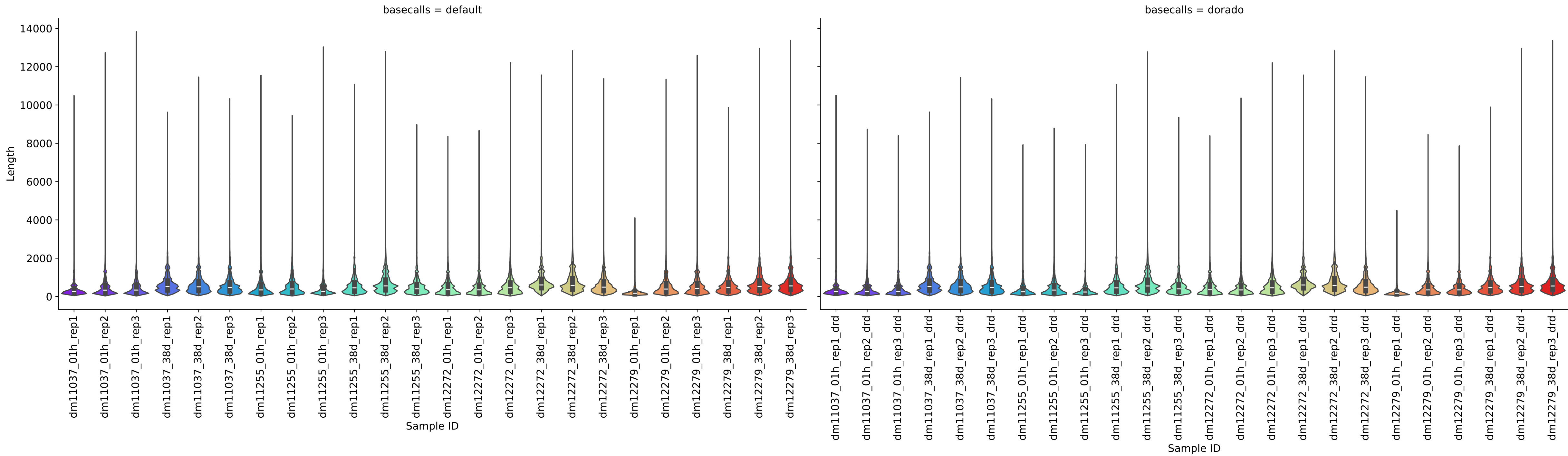
Lengths of All Mapped Reads



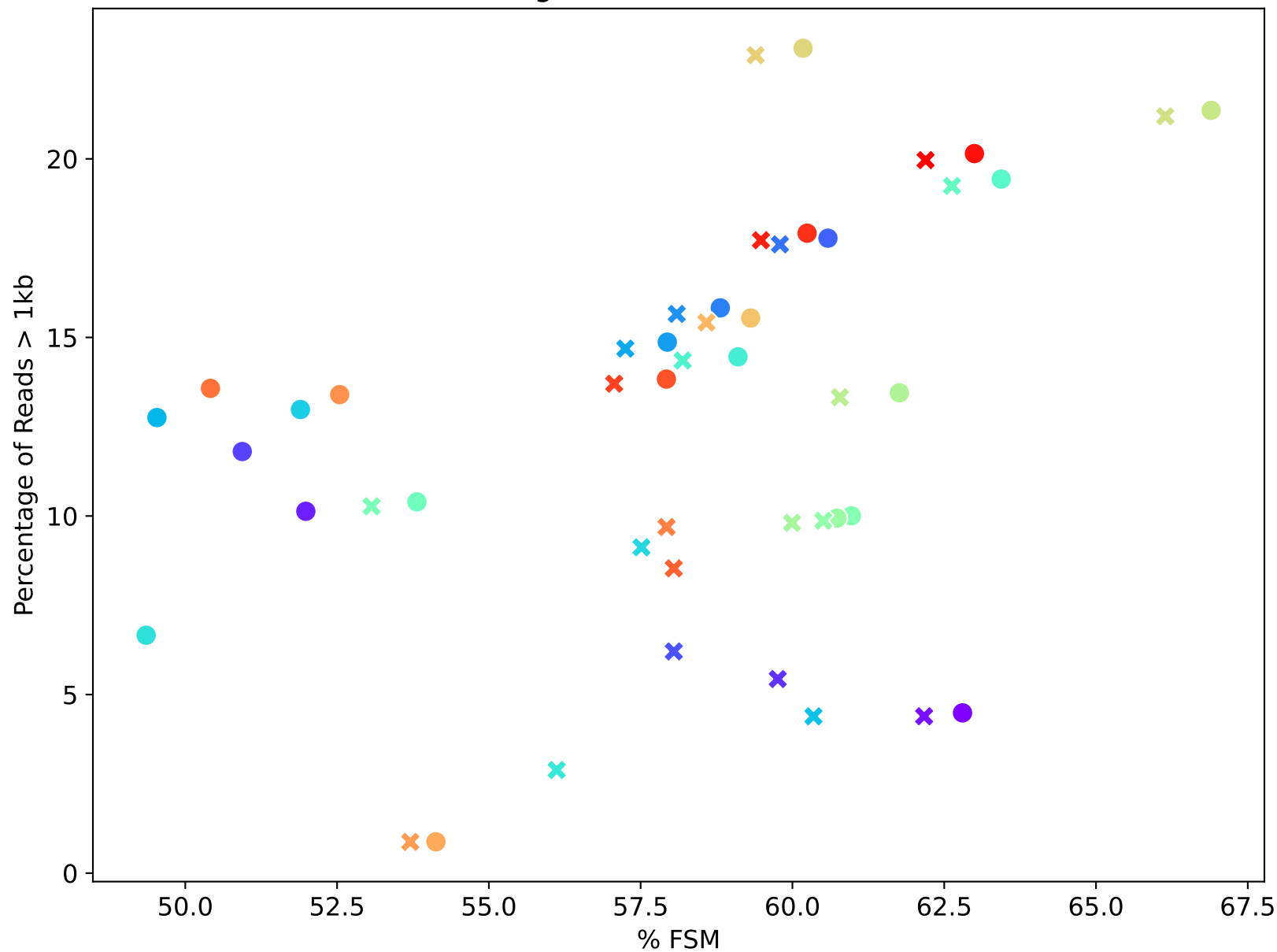
Lengths of All Mapped Reads



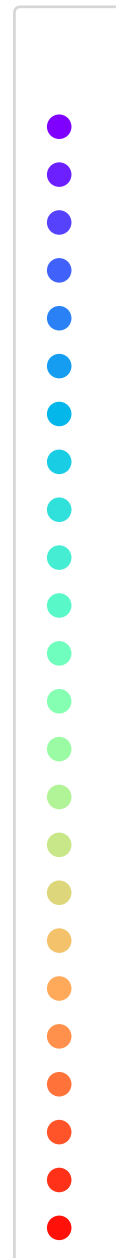
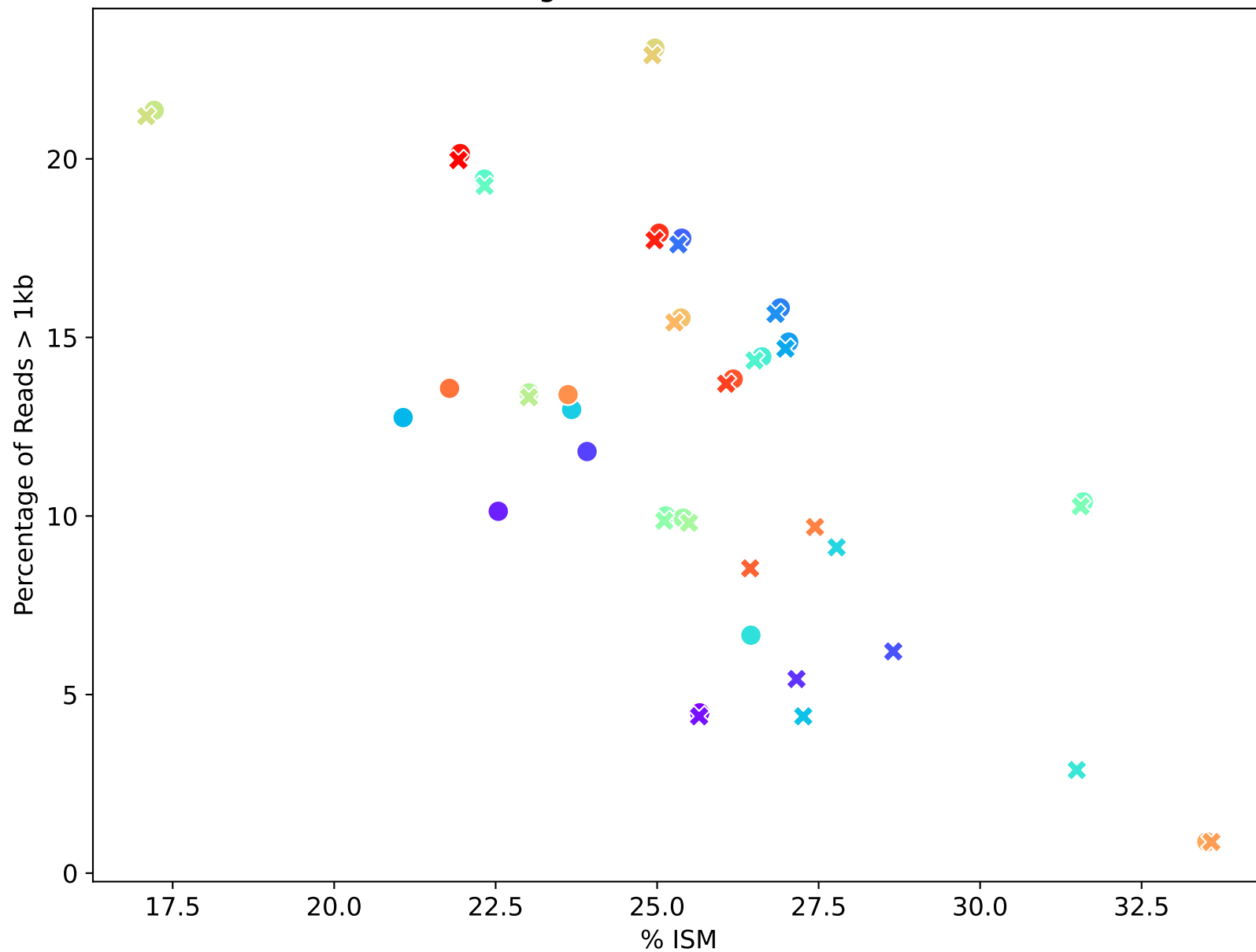
Read Length Distribution



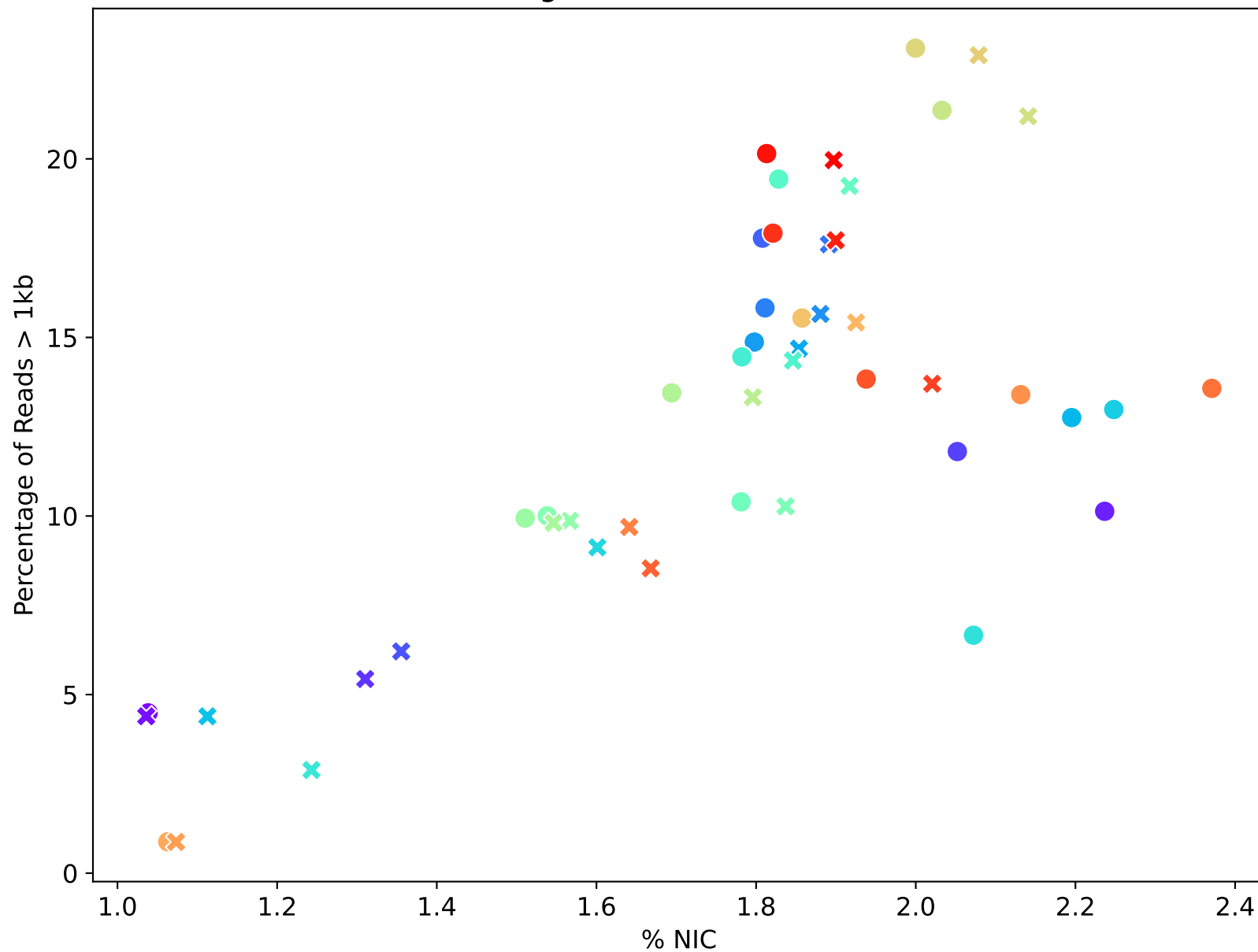
Percentage of Reads > 1kb vs %FSM



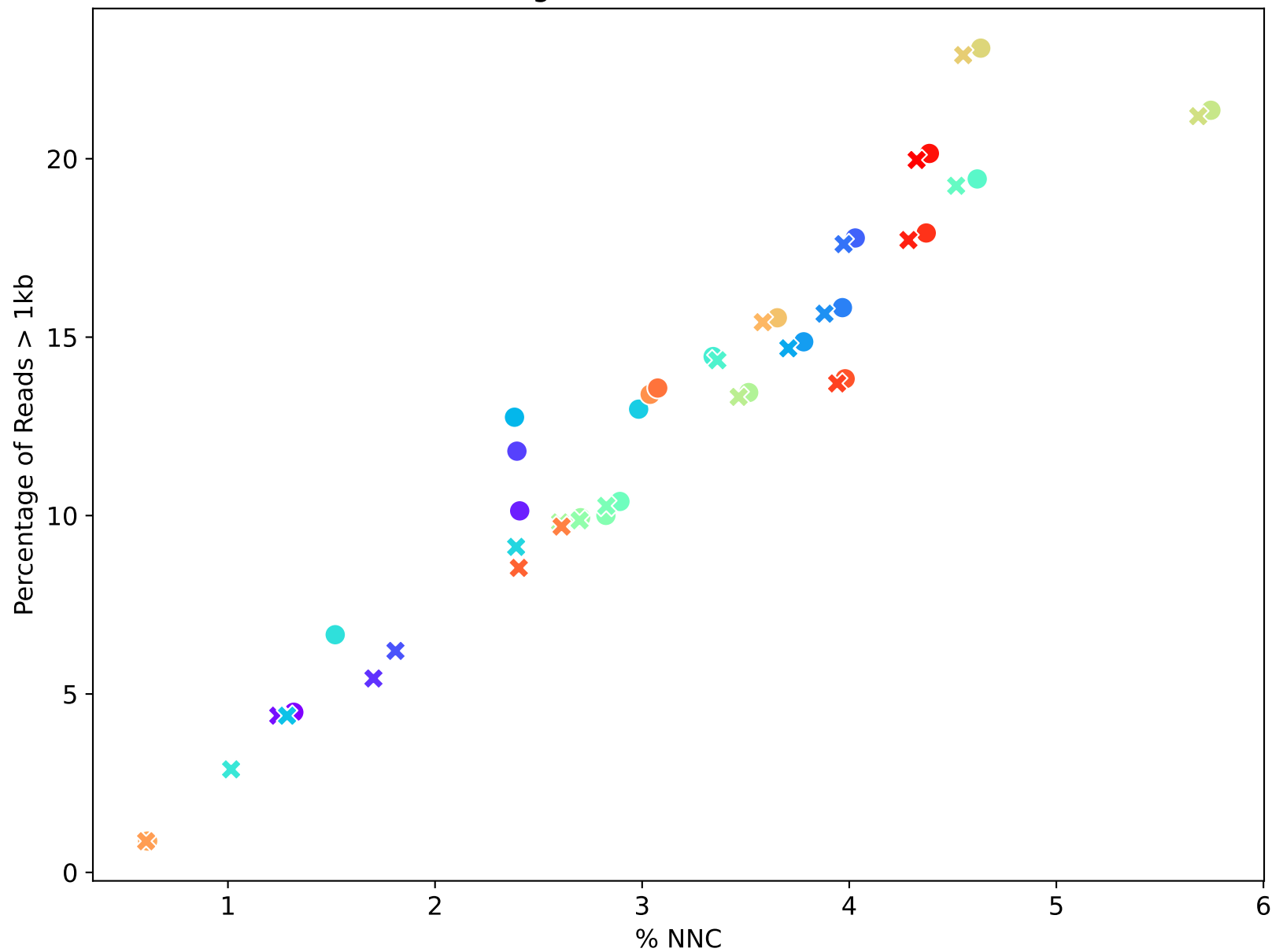
Percentage of Reads > 1kb vs %ISM



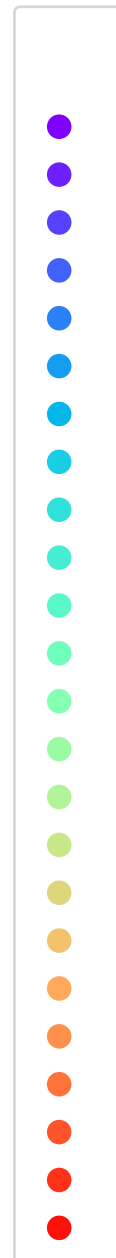
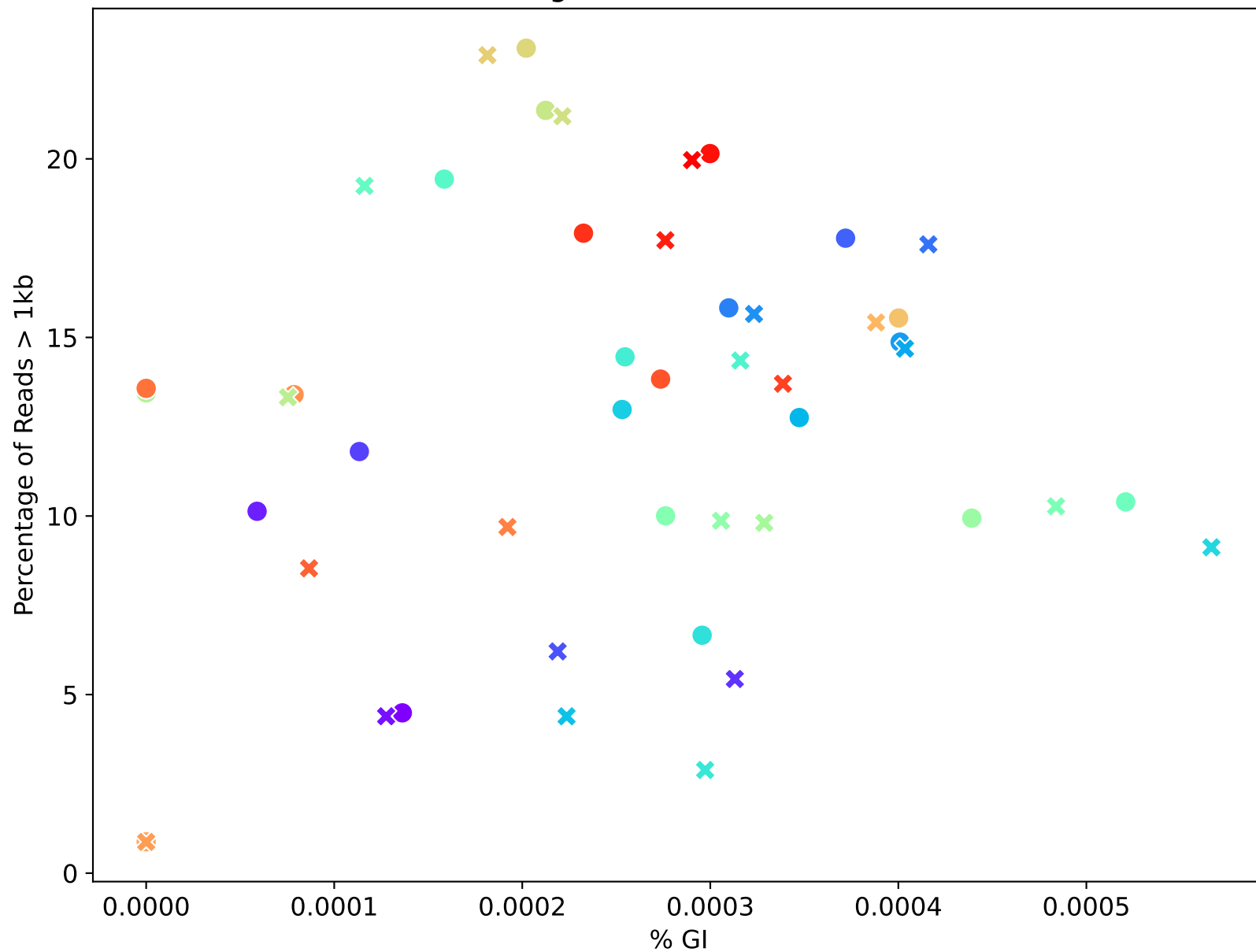
Percentage of Reads > 1kb vs %NIC



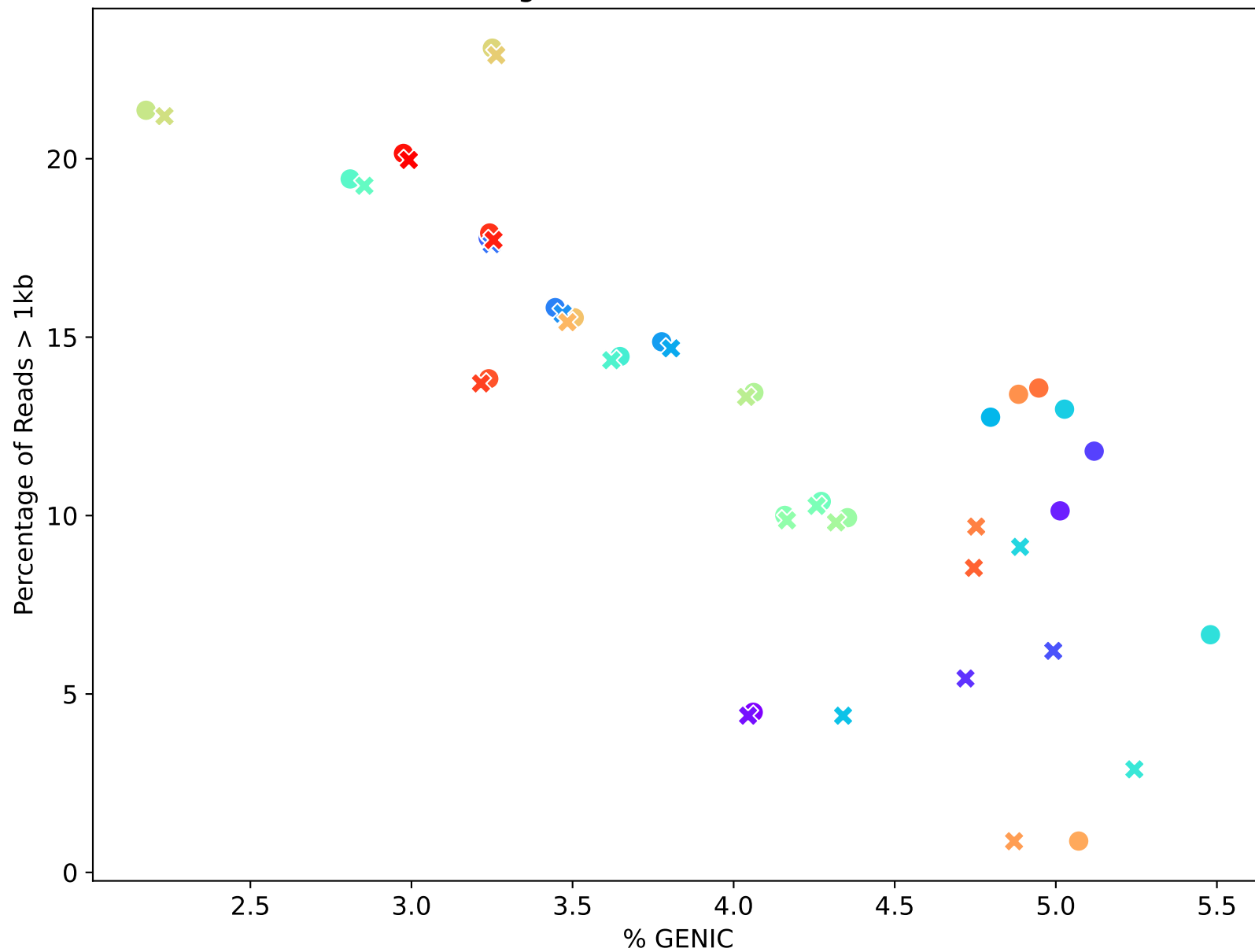
Percentage of Reads > 1kb vs %NNC



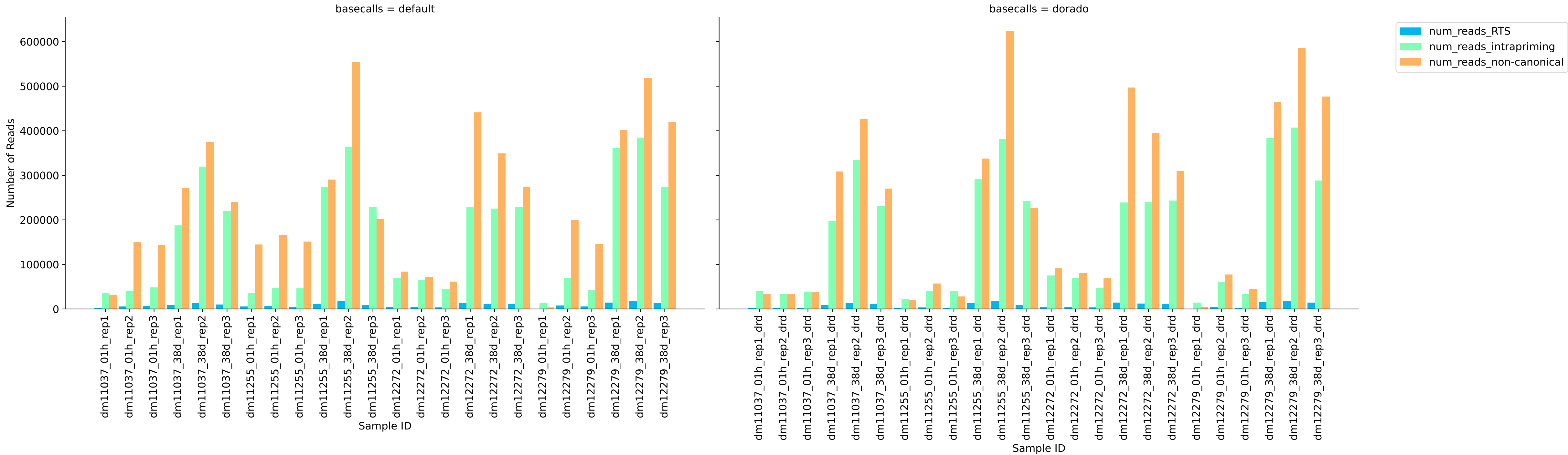
Percentage of Reads > 1kb vs %GI



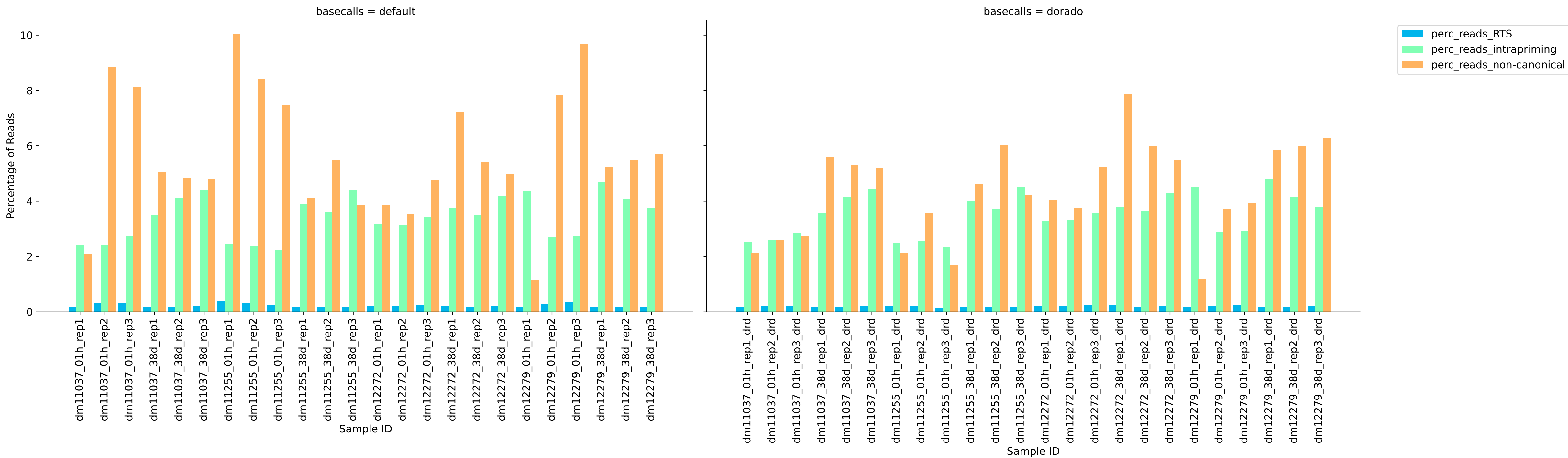
Percentage of Reads > 1kb vs %GENIC



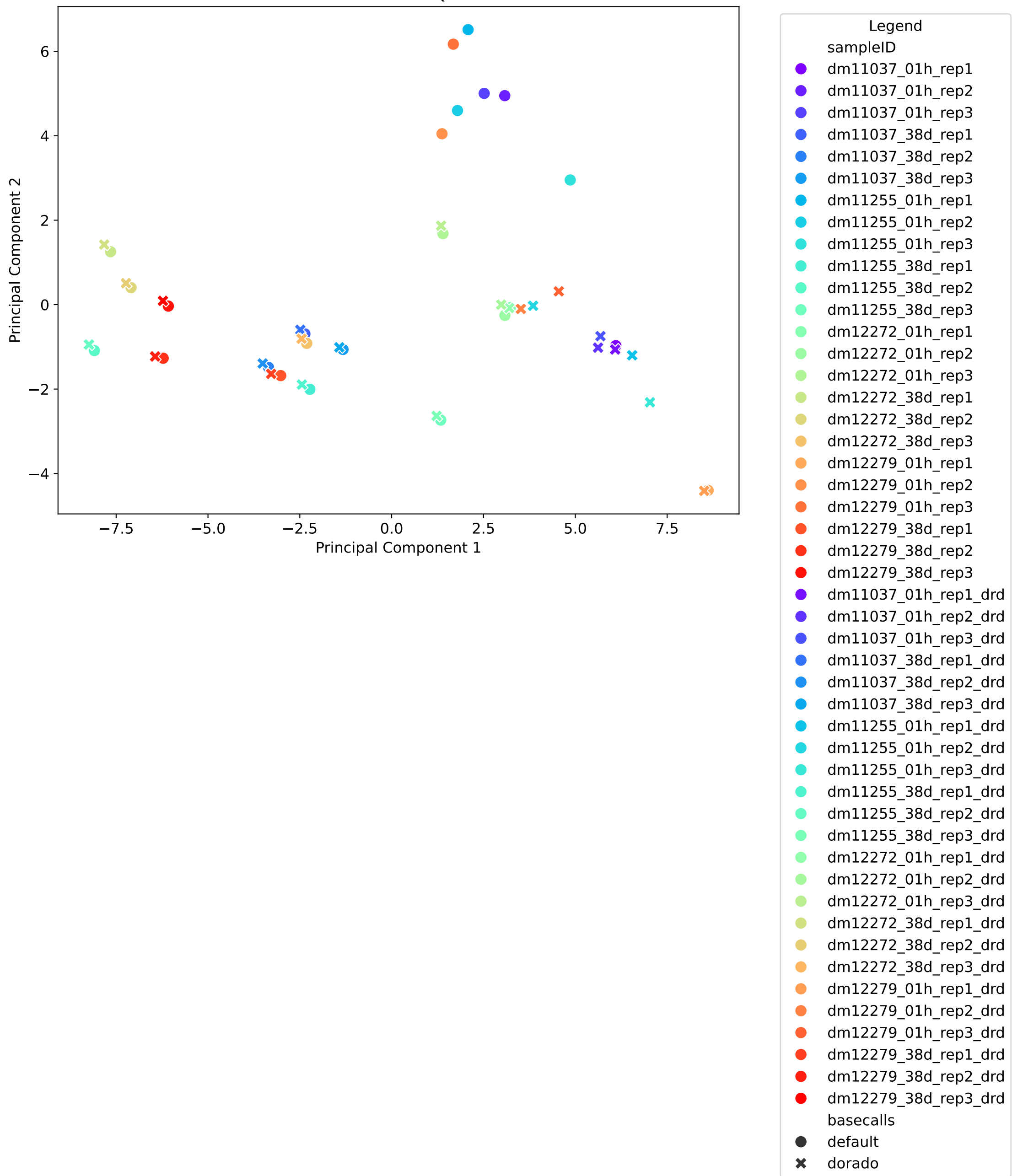
Number of Artefact Reads



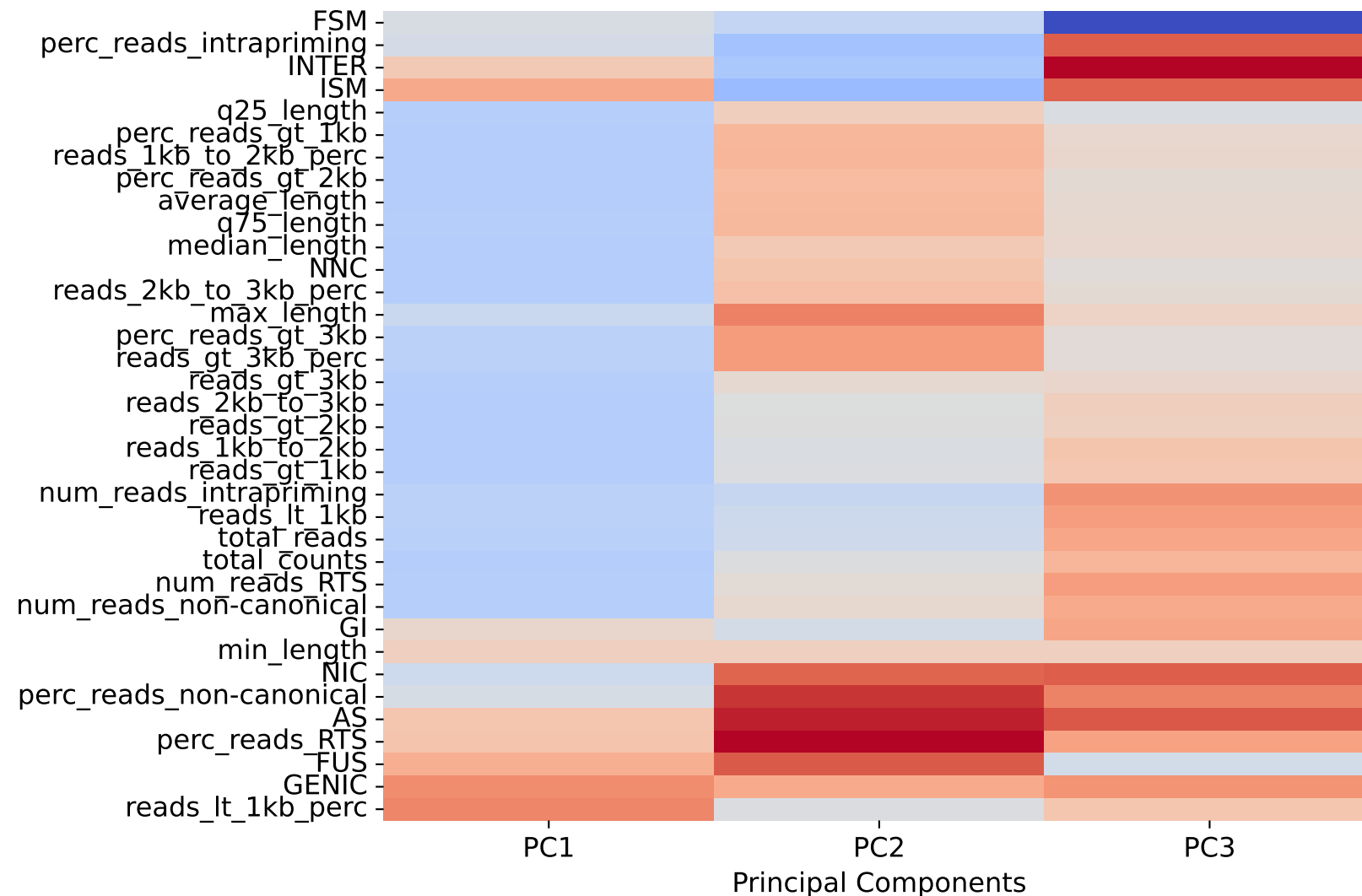
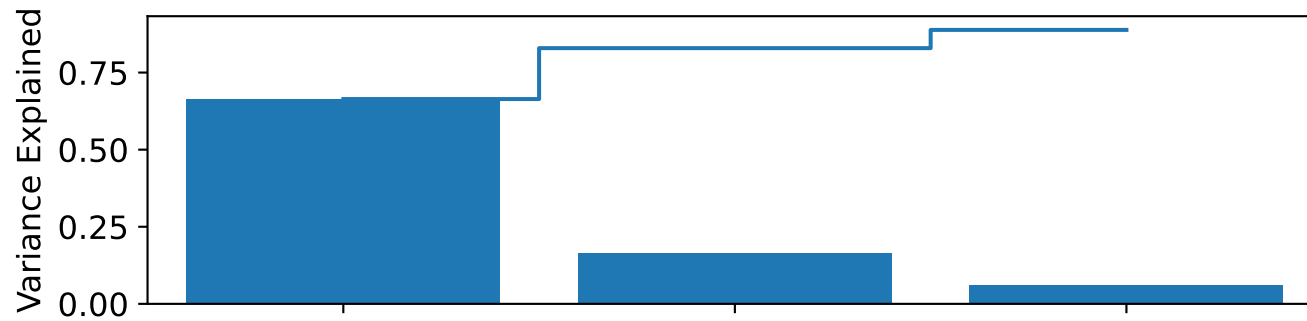
Percentage of Artefact Reads



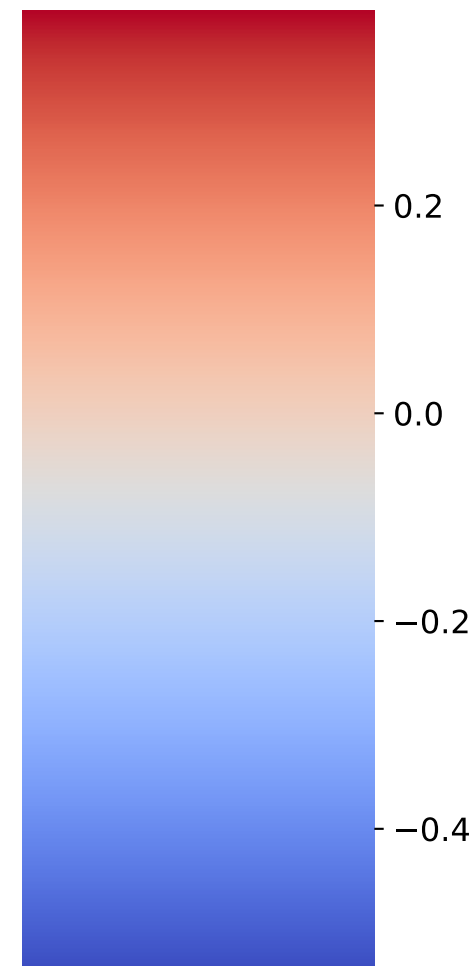
PCA Plot Based on QC metrics



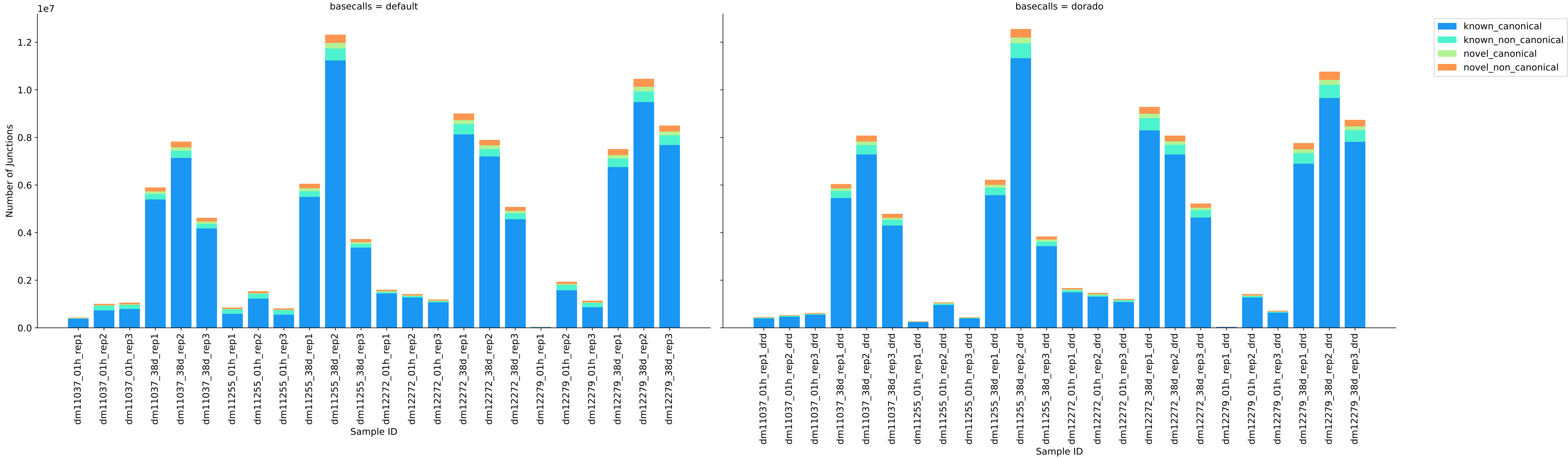
Screeplot and Heatmap of PC loadings



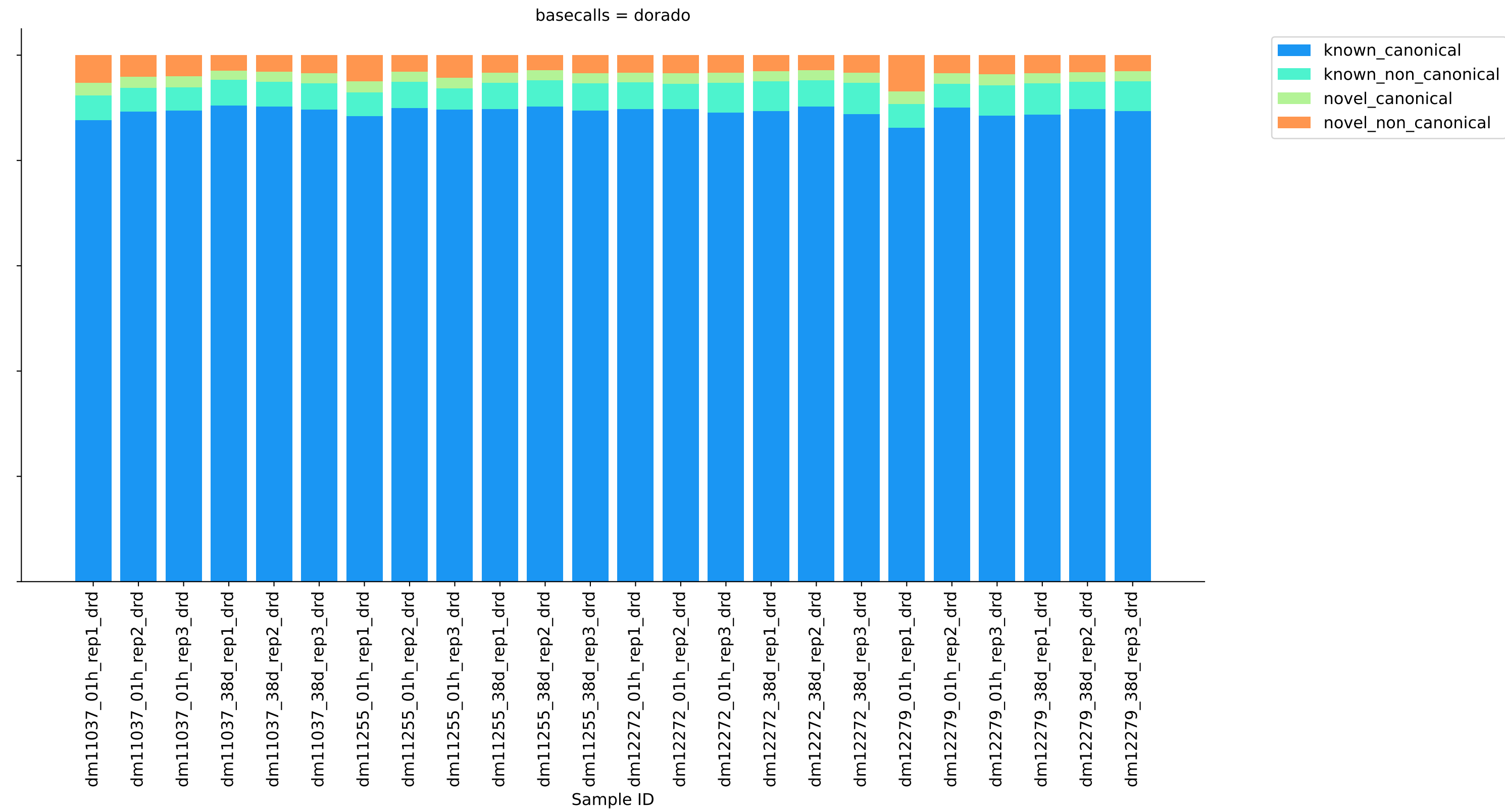
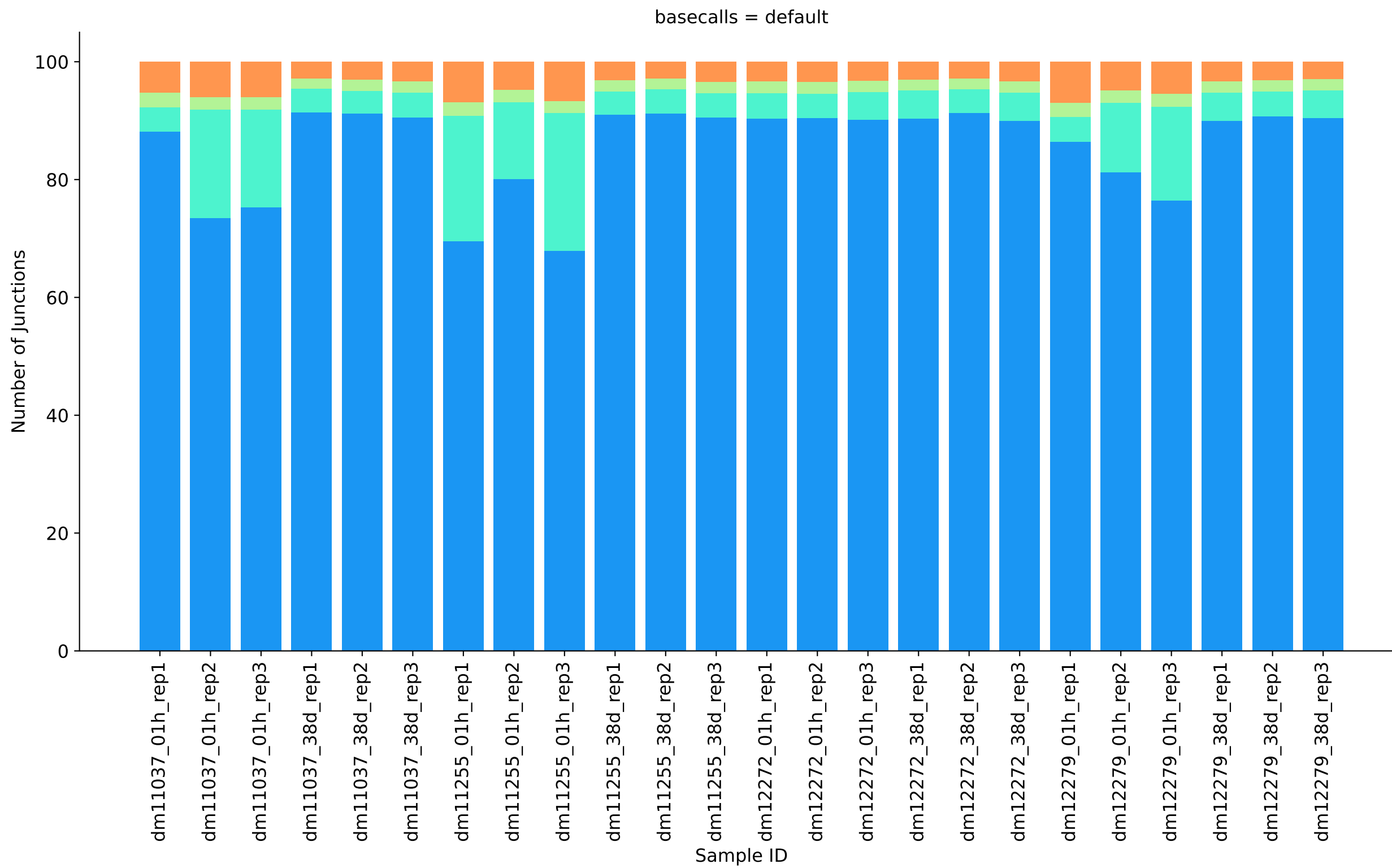
— Cumulative explained variance
■ Individual explained variance



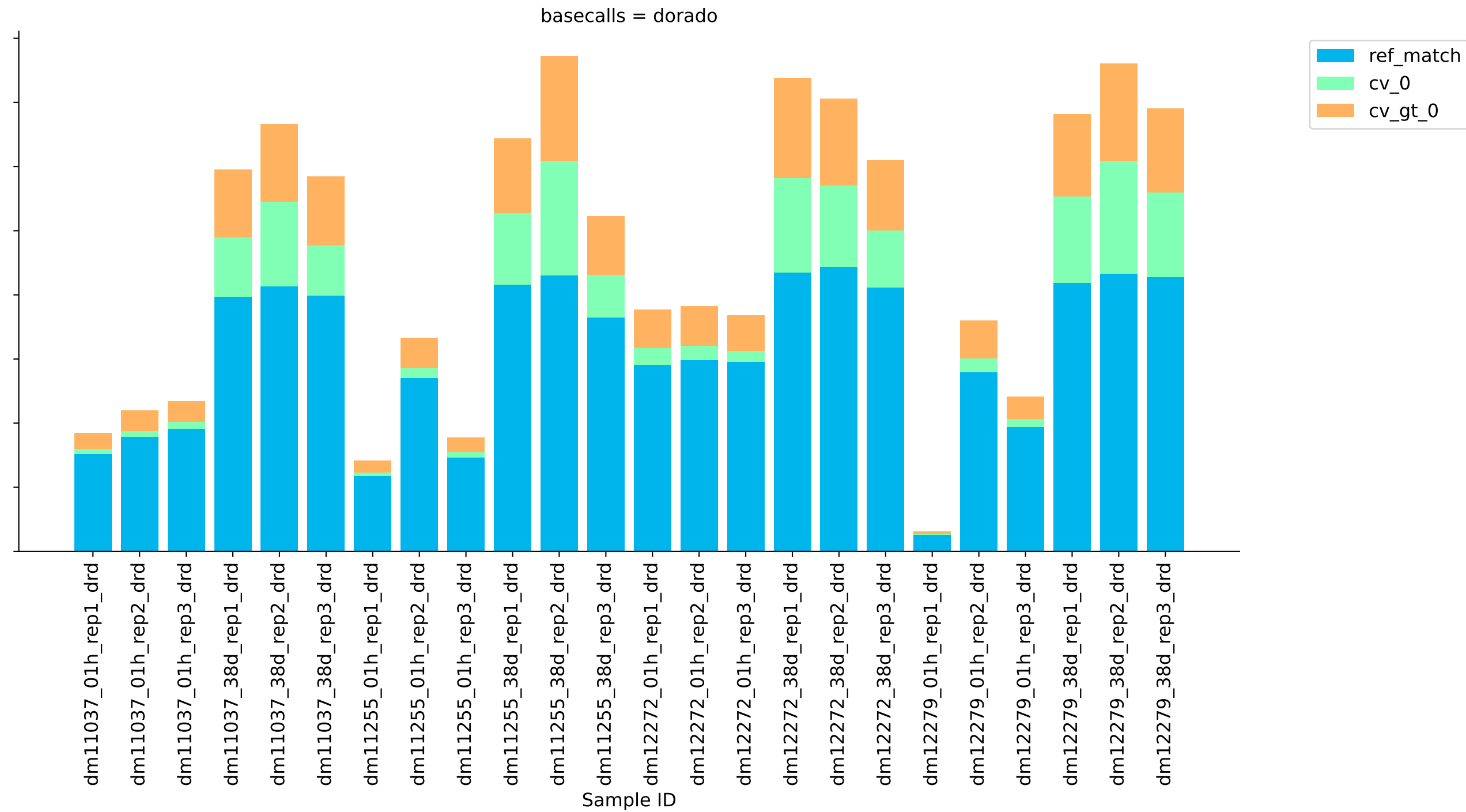
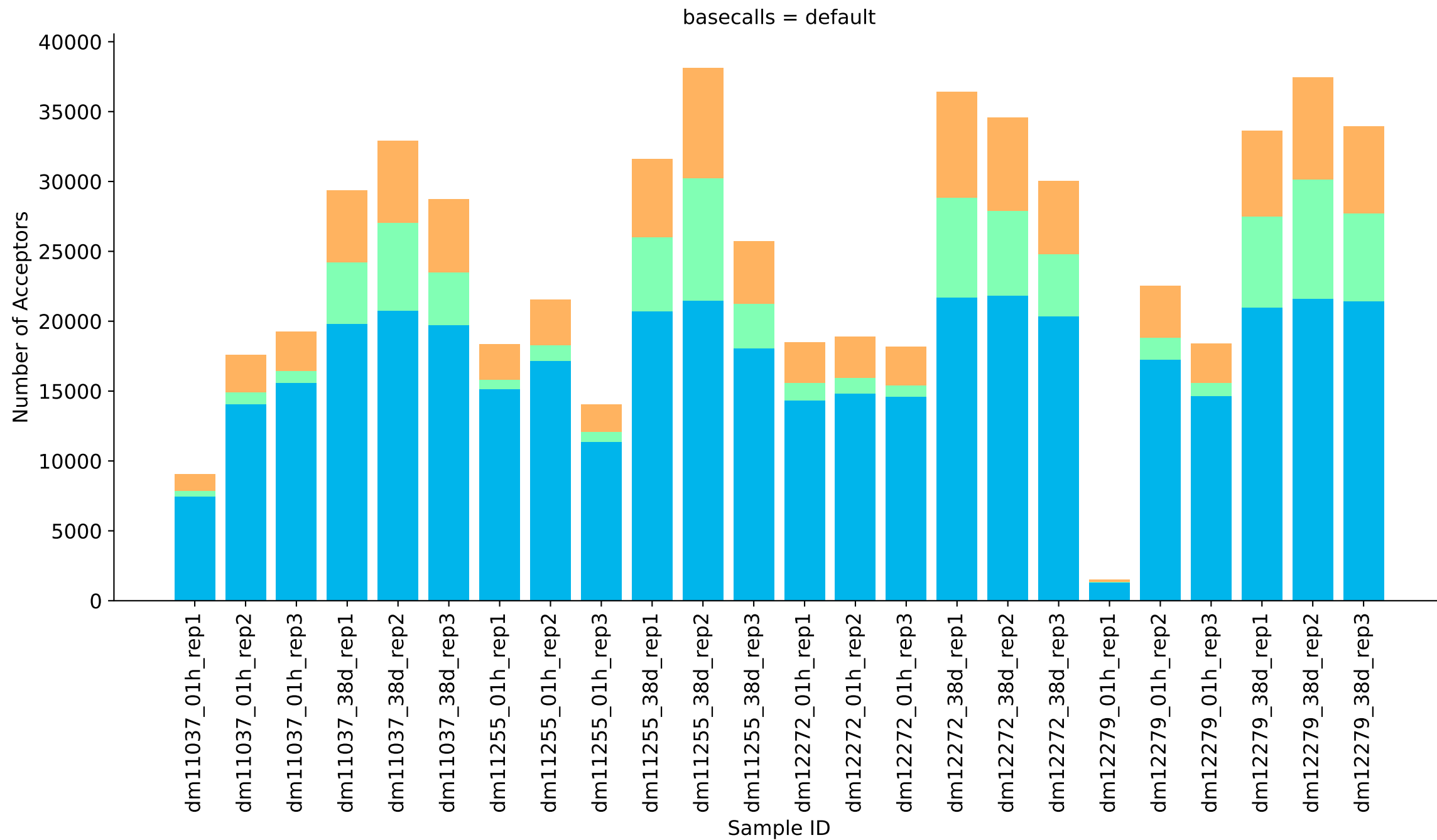
Junctions by Category



Junctions by Category



Acceptors with > 3 reads



Donors with > 3 reads

