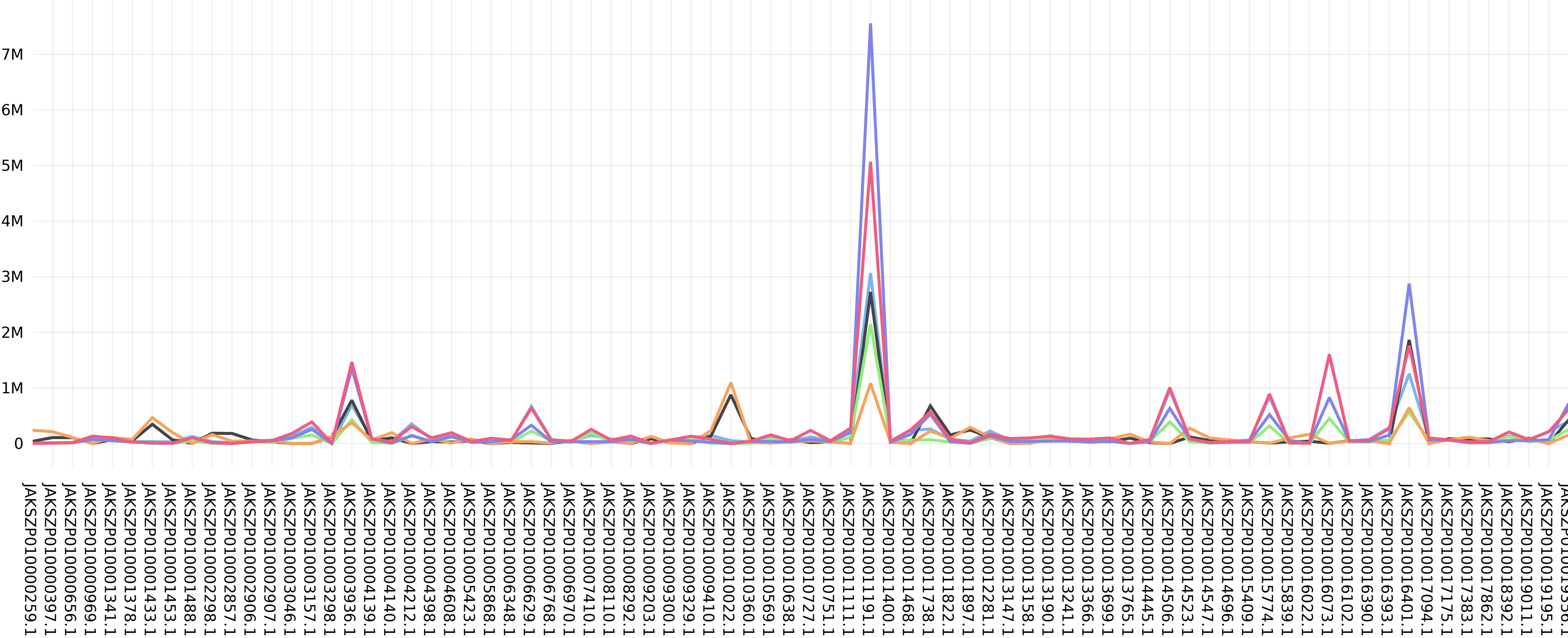


# Samtools: idxstats: Mapped reads per contig

Raw Counts, 6 samples

# mapped reads



Chromosome name