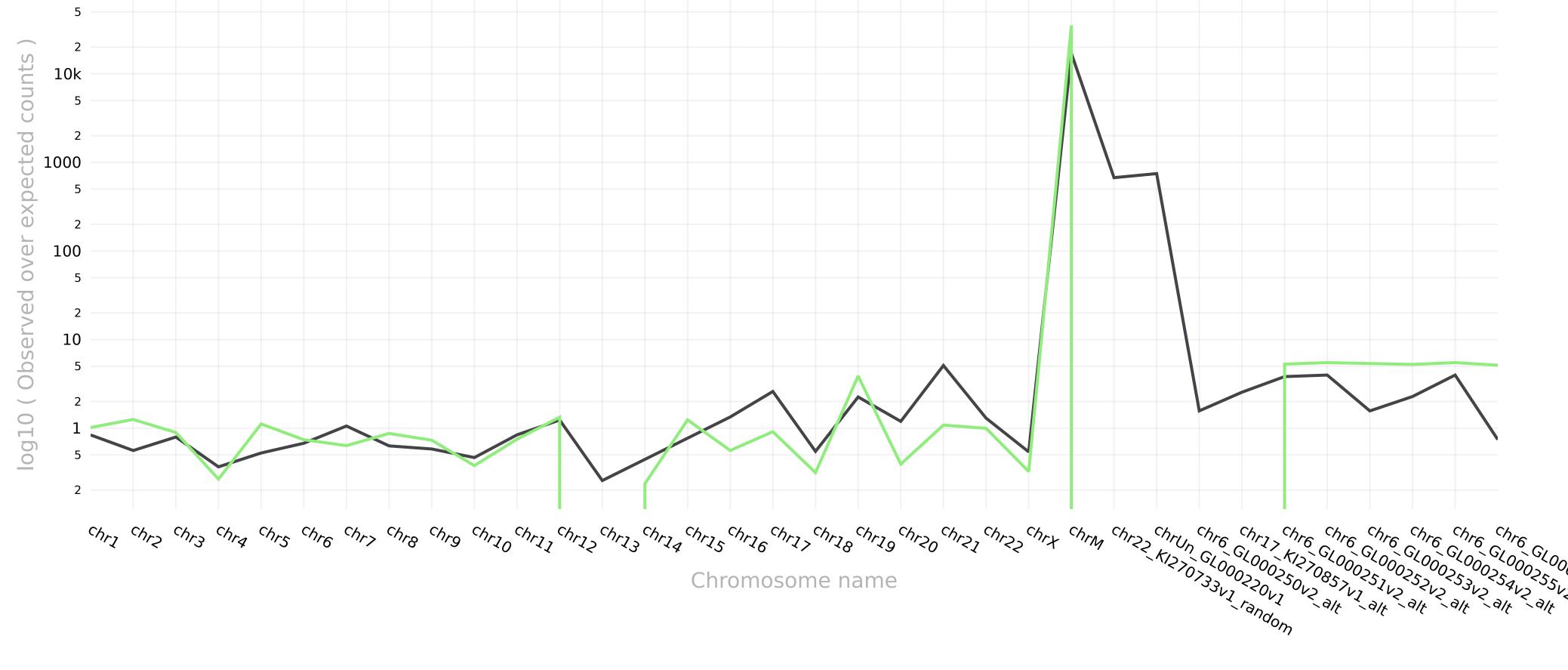
Samtools: idxstats: Mapped reads per contig

Observed over Expected Counts, 3 lines



Chromosome name