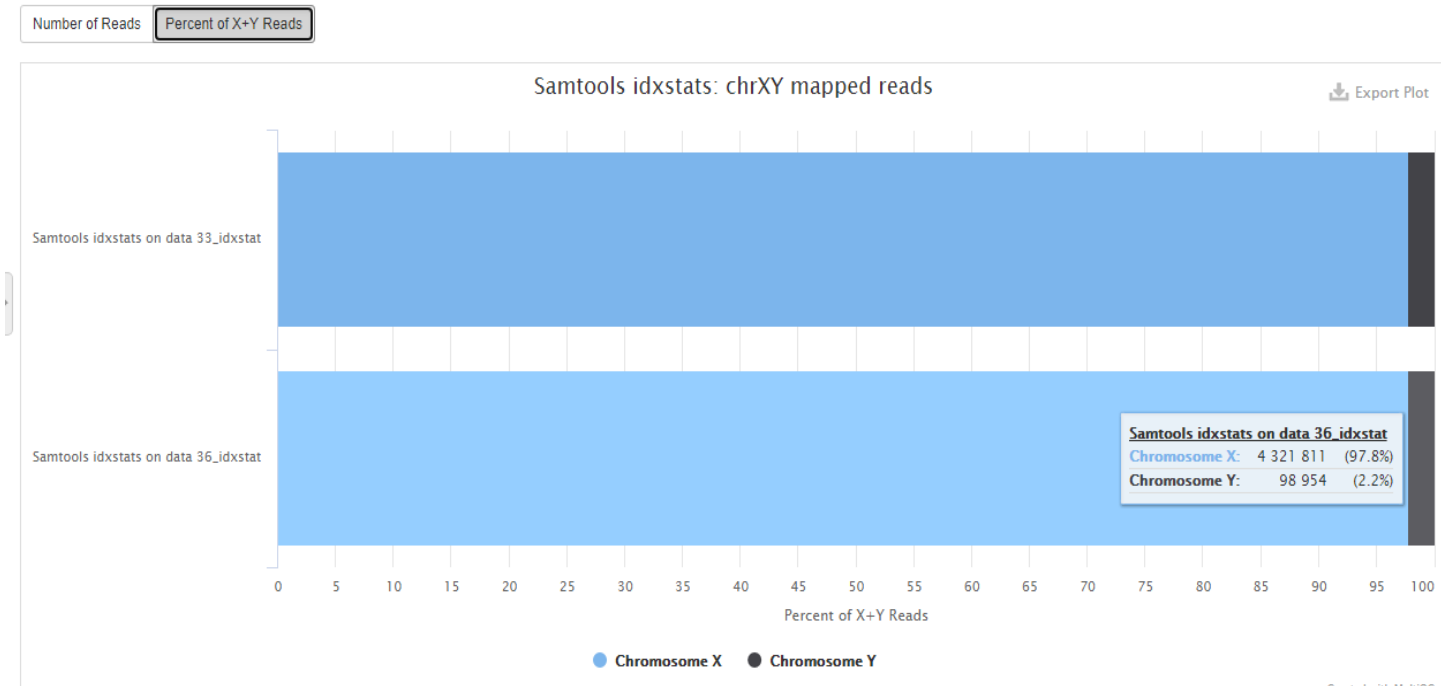


CHECKING NUMBER OF READS MAPPED TO EACH CHROMOSOME USING **Samtools Idxstats** AND AGGREGATING THE LOGS USING **MultiQC**

Samtools
Samtools is a suite of programs for interacting with high-throughput sequencing data.

XY counts



Mapped reads per contig
The `samtools idxstats` tool counts the number of mapped reads per chromosome / contig. Chromosomes with < 0.1% of the total aligned reads are omitted from this plot.

