

# Samtools idxstats: Mapped reads per contig

log10 ( Observed over expected counts )

SPT5\_INPUT\_REP1 SPT5\_T0\_REP1 SPT5\_T0\_REP2 SPT5\_T15\_REP1 SPT5\_T15\_REP2 SPT5\_INPUT\_REP2

Chromosome Name

I II III IV IX MT V VI VII VIII X XI XII XIII XIV XV XVI

