

# Samtools idxstats: Mapped reads per contig

log10 ( Observed over expected counts )

— SPT5\_INPUT\_REP1\_T1
 — SPT5\_T0\_REP1\_T1
 — SPT5\_T0\_REP2\_T1
 — SPT5\_T15\_REP1\_T1
 — SPT5\_T15\_REP2\_T1
 — SPT5\_INPUT\_REP2\_T1

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

Chromosome Name

