

# Samtools idxstats: Mapped reads per contig

log10 ( Observed over expected counts )

1.04

1.02

1.00

0.98

0.96

|

Chromosome Name

RAP1\_IAA\_30M\_REP1

RAP1\_UNINDUCED\_REP1

RAP1\_UNINDUCED\_REP2

WT\_REP1

WT\_REP2