



S
E
C



S
C

PiG

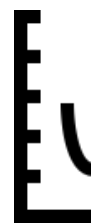
INPUTS

Sample Sheet for
experimental
designs.

Settings file to
configure tools.

ix-RNAseq

READ C



BED



IMPROVE
READ QUALITY



TRIM-GALORE

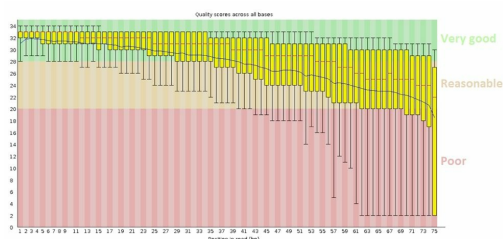
ALIGN
TO THE



S



CHECK
SEQUENCING
QUALITY



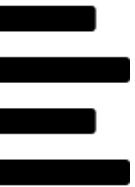
COVERAGE



TOOLS



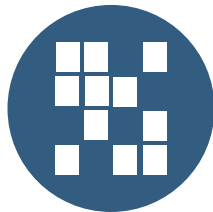
N READS
E GENOME



TAR



QUANTIFY
EXPRESSION



STAR / SALMON



ANALYSE
DIFFERENTIAL
EXPRESSION



DESeq2



PAN-SAMPLE
QUALITY CHECK



MultiQC



OUTPUTS



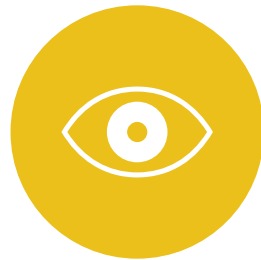
preprocessed data
FASTQ, BAM, BigWig
BEDGRAPH, TSV



Log files for tasks



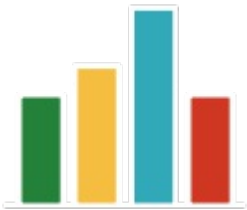
HTML reports for
quality diagnostics



HTML report for
exploration and
differential expression

PiGx-RNAseq

FIND ENRICHED GO TERMS



g:ProfileR

multiQC

