

Enrichment Mapping Report

Project Number: TP53_web

Sample: TP53

Run Type: ONT

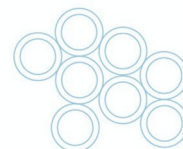
Genome: Homo_sapien_hg38.p13

Region of Interest: [7668402-7687550]

Detection Sequence(s): [7675778-7675939]

Validation Sequence(s): [7673906-7674109]

Date: 2021-11-12



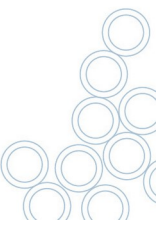
Samplix Aps
Bregnerødvej 96
DK - 3460 Birkerød

cvr: 32 30 93 21
bank: 3409 0011673171

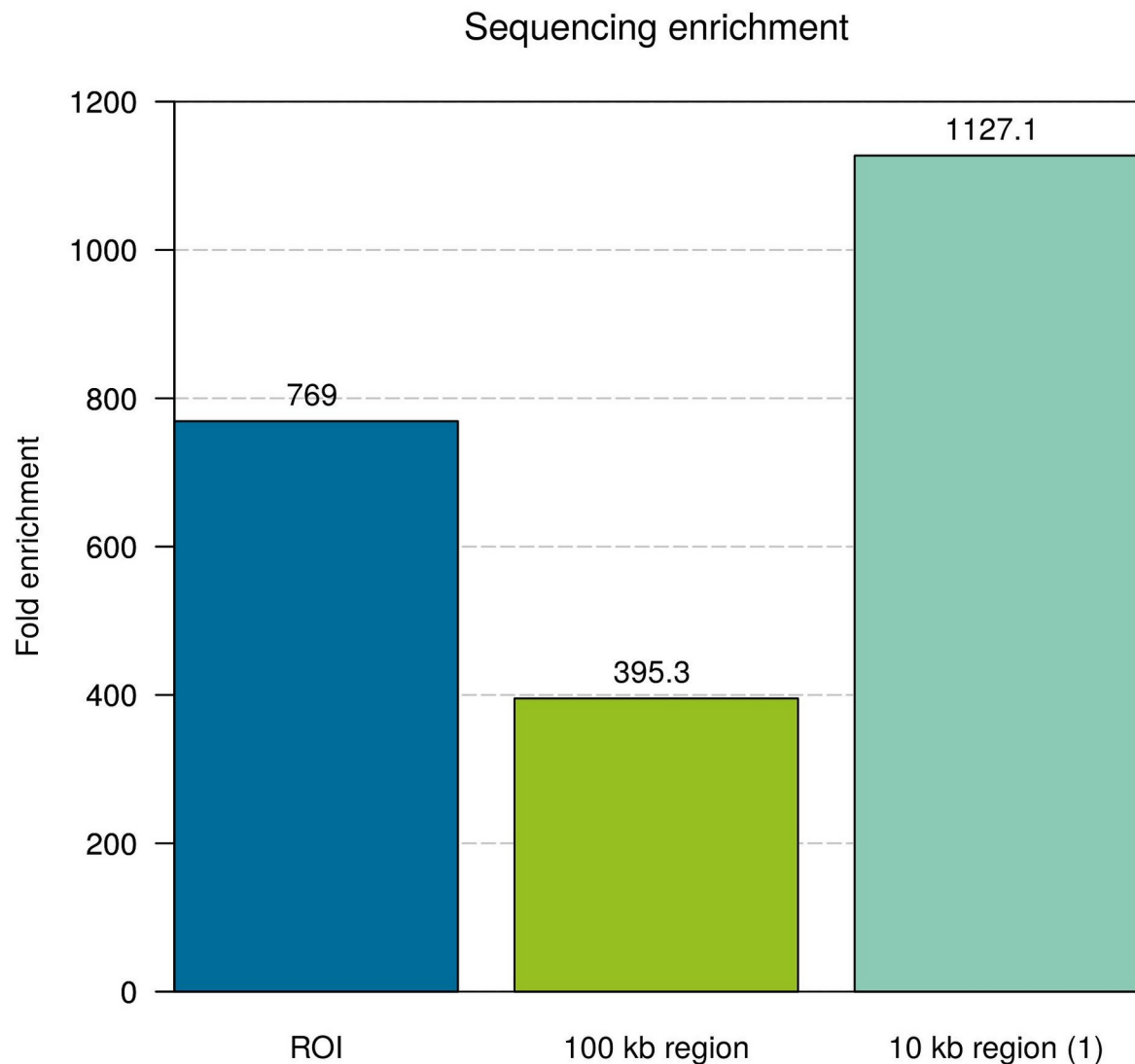


Contents

Sequencing enrichment.....	3
Read density for reads mapping to genome.....	4
Read mapping to 100 kb region.....	5
Read mapping with read coverage for the 10 kb region around the DS.....	6
Read mapping with read coverage for the Region of Interest.....	7
Statistics.....	8



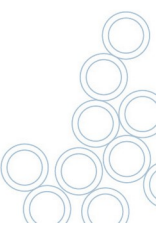
Sequencing enrichment



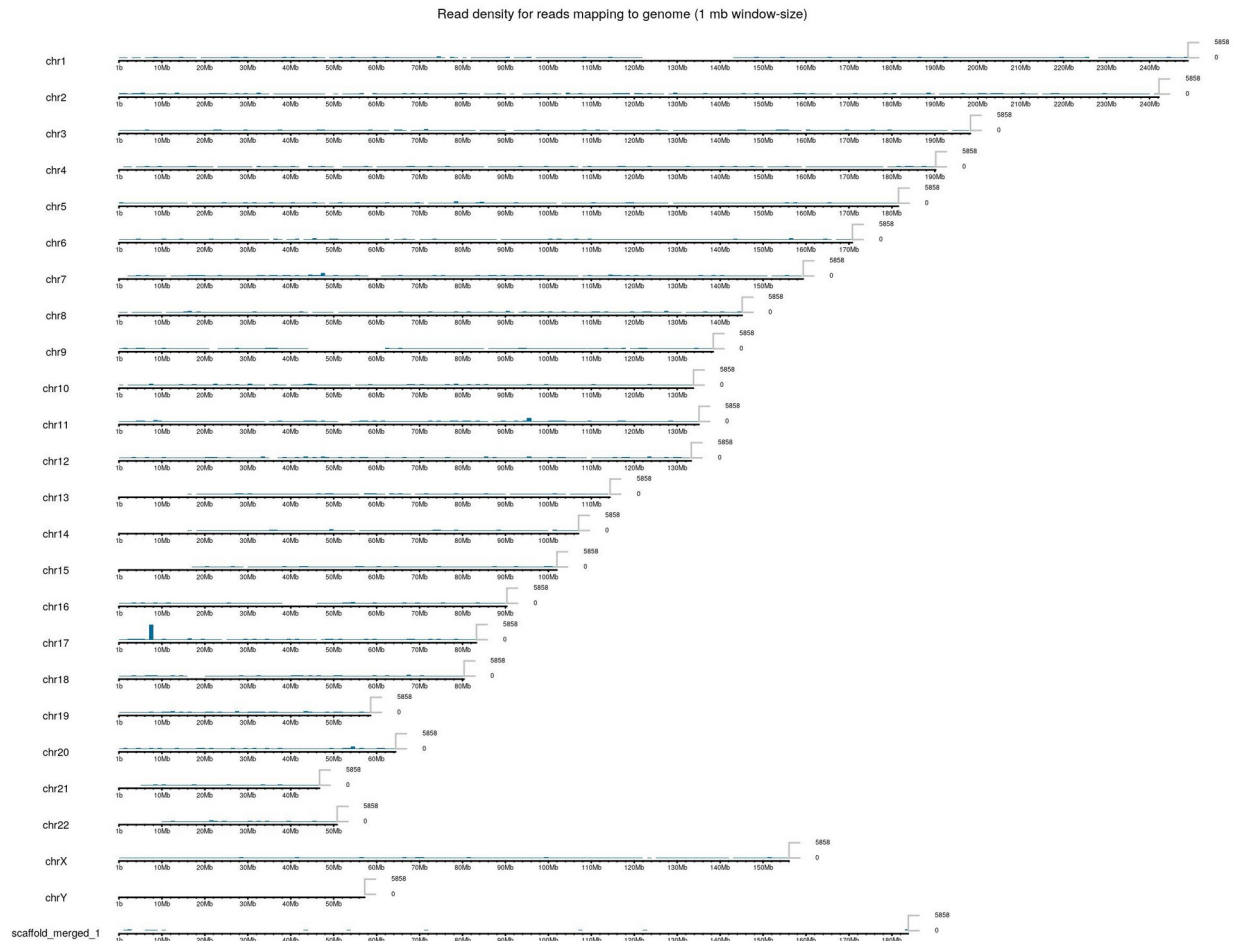
Sequencing enrichment for Region of Interest (ROI) (blue), 100 kb region (green), and 10 kb region around the Detection Sequence(s) (turquoise). Sequencing enrichment is based on the following equation:

$$\text{Sequencing enrichment} = \frac{\frac{\text{ratio of primary reads mapped to target region}}{\text{target size}}}{\text{reference genome size}}$$

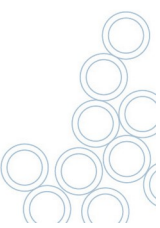
Where the reference genome is the genome provided as reference for the analysis.



Read density for reads mapping to genome

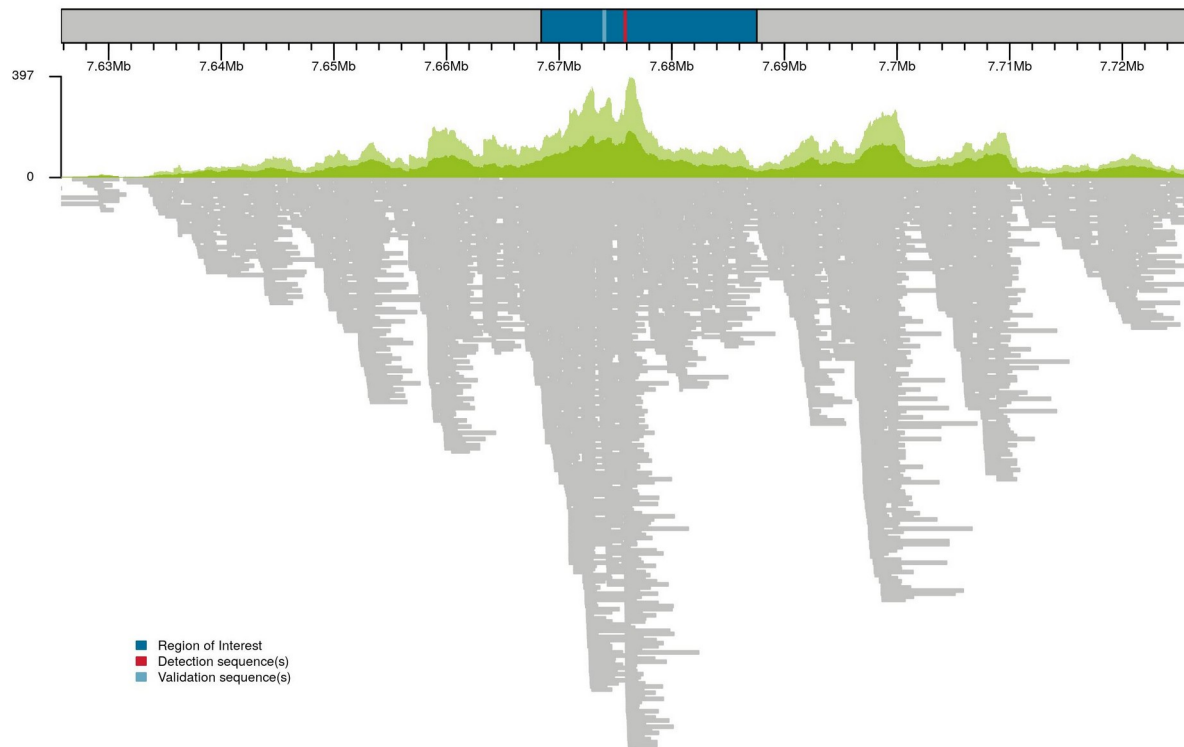


Read density plot of primary and supplementary reads mapped to reference genome. Plot is generated using karyoplotR in R. The read density is plotted as the number of reads detected within 1 MB windows.

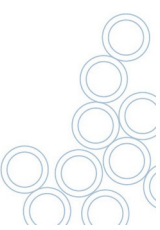


Read mapping to 100 kb region

chr17: 100 kb region

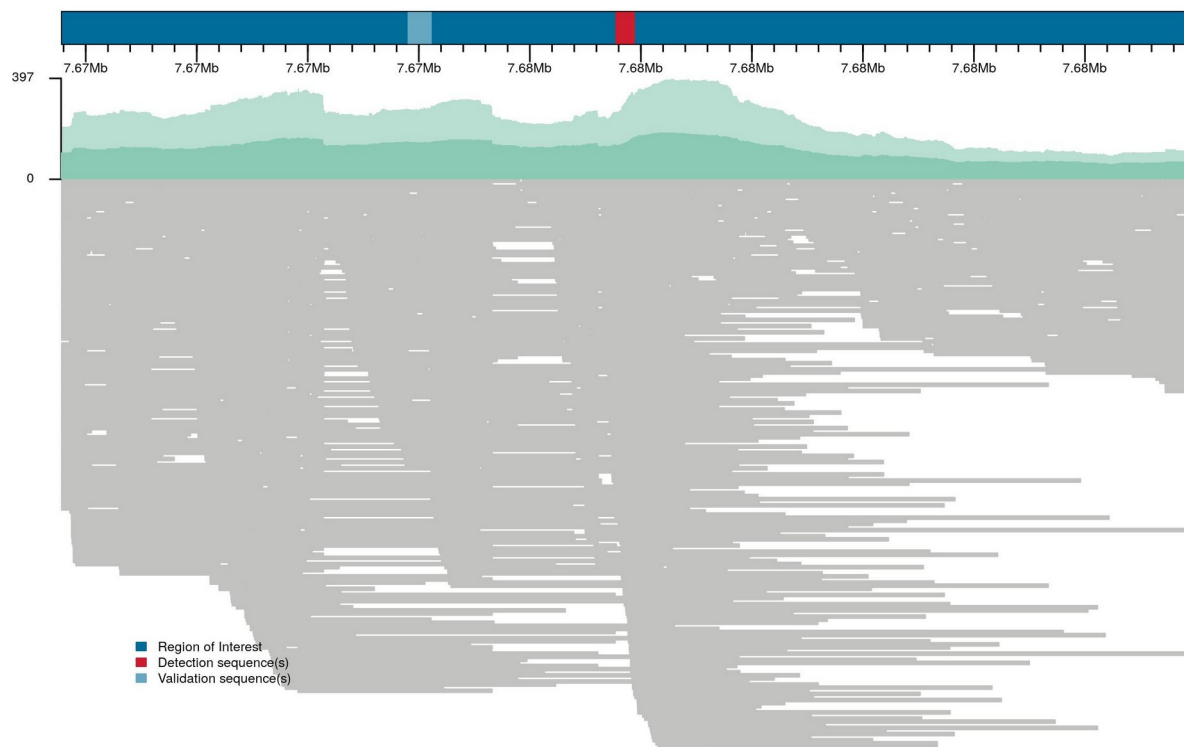


Upper bar shows genomic context of reads mapping to a 100 kb region. Below, read coverage of primary (dark green) and supplementary (light green) reads mapped to a 100 kb region on chr17 with primary read mapping (grey) depicted below. Note that read mapping is based only on start and end position of primary reads (extracted from the CIGAR of the bam files), hence insertion, deletion and mismatches are not shown.

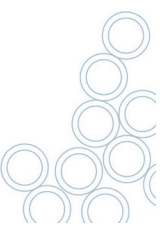


Read mapping with read coverage for the 10 kb region around the DS

chr17: 10 kb region assay 1

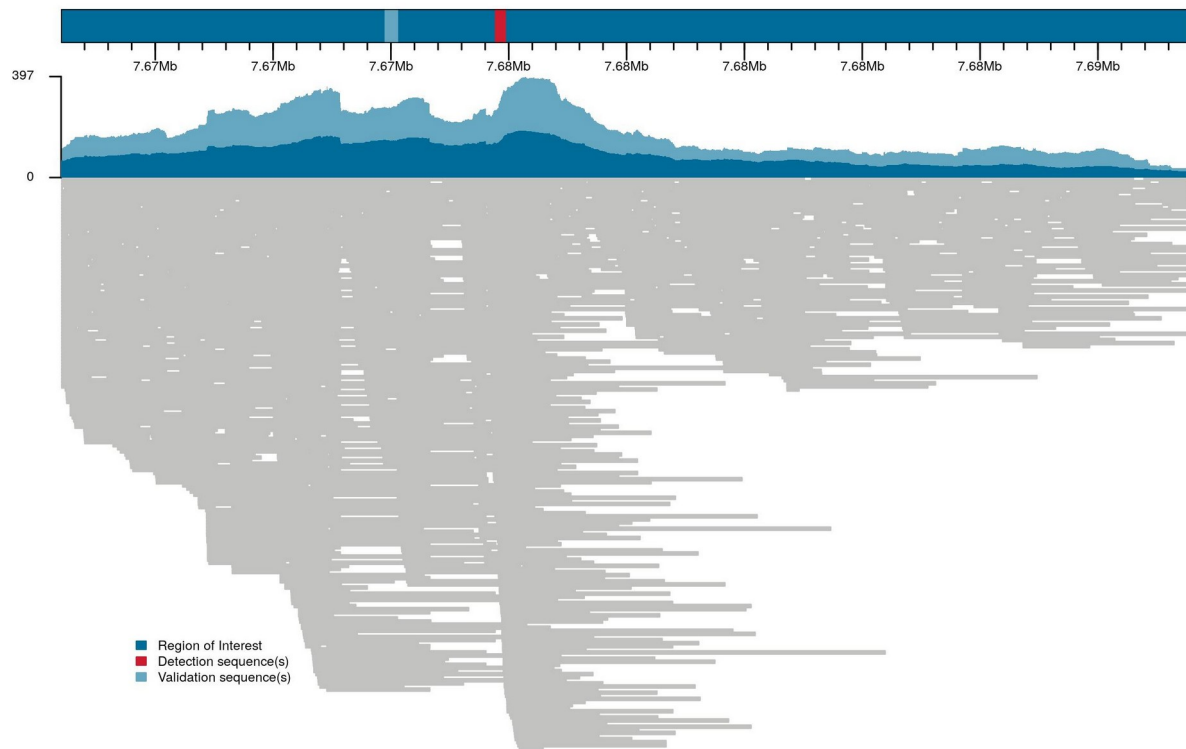


Upper bar shows genomic context of reads mapping to a 10 kb region around the Detection Sequence, with the detection and validation sequences in red and light blue, respectively. Below, read coverage of primary (dark turquoise) and supplementary (light turquoise) reads mapped to the 10 kb region around the Detection Sequence (on chr17), with primary read mapping (grey) depicted below. Note that read mapping is based only on start and end position of primary reads (extracted from the CIGAR of the bam files), hence insertion, deletion and mismatches are not shown.

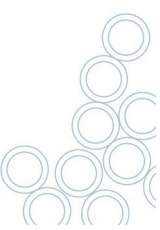


Read mapping with read coverage for the Region of Interest

chr17: Region of Interest



Upper bar shows genomic context of reads mapping to the Region of Interest (highlighted in blue). Below, read coverage of primary (dark blue) and supplementary (light turquoise) reads mapped to the Region of Interest (on chr17), with primary read mapping (grey) depicted below. Note that read mapping is based only on start and end position of primary reads (extracted from the CIGAR of the bam files), hence insertion, deletion and mismatches are not shown.



Statistics

Total bases sequenced (bp)	799442636
Total reads (reads)	155209
Total mapped reads (reads)	153413
Total reads mapped to 100 kb region (reads)	1857
Total reads mapped to 10 kb region assay 1 (reads)	539
Total reads mapped to ROI (reads)	693
Percentage mapped reads to reference (%)	98.84
Percentage mapped reads to 100 kb region (%)	1.21
Percentage mapped reads to 10 kb region assay 1 (%)	0.35
Percentage mapped reads to ROI (%)	0.45
Percentage of bases mapped primary (%)	54.3
Percentage of bases mapped primary incl. suppl. (%)	99
Enrichment 100 kb region (fold)	395.3
Enrichment 10 kb region assay 1 (fold)	1127.1
Enrichment ROI (fold)	769
N50 mapped readlength (bp)	6775
N50 100 kb region readlength (bp)	6834
N50 10 kb region assay 1 readlength (bp)	6890
N50 ROI readlength (bp)	6855
Median mapped readlength (bp)	3810

