DEMO | wf-human-variation CNV report

Results generated through the wf-human-variation nextflow workflow provided by Oxford Nanopore Technologies.

Research use only | 2024-05-22 | 2.2.0

Introduction

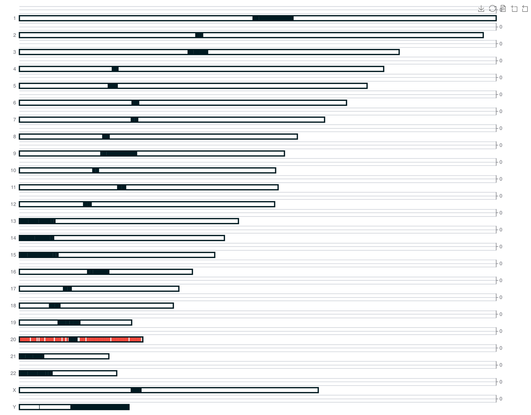
This report contains CNVs detected using QDNAseq, as part of the wf-human-variation workflow.

Chromosomal Sex	Median Read Length	Total Reads
Undetermined	8244bp	414,758

Chromosome Copy Summary

0 copies	1 copies	2 copies	3 copies	4 copies
-	-	1 10 11 12 13 14 15 16 17 18 19 2 21 22 3 4 5 6 7 8 9 X Y	-	20

Ideoplot



Red: Increased copy number detected

Blue: Decreased copy number detected

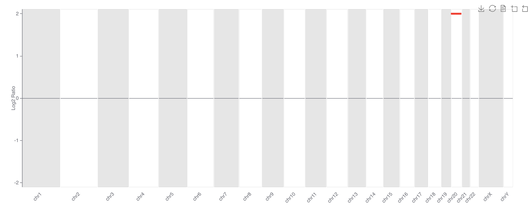
Yellow: QDNASeq no call

Black: 'acen', 'gvar', or 'stalk'; Read counts of < -2 converted to 2

Detailed CNV Results

QDNASeq Smoothed Read Counts

Bin size 500Kbp, No call not displayed



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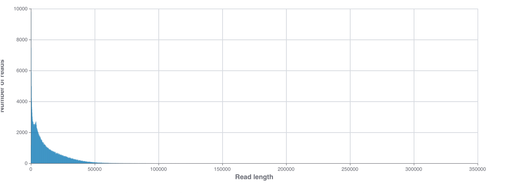
chr	start	end	genes	read count	call
chr20	0	500000	Genes	11.904	2
chr20	500000	1000000	Genes	11.725	2
chr20	1000000	1500000	Genes	11.809	2
chr20	1500000	2000000	Genes	11.686	2
chr20	2000000	2500000	Genes	11.775	2
chr20	2500000	3000000	Genes	11.756	2
chr20	3000000	3500000	Genes	11.737	2
chr20	3500000	4000000	Genes	11.741	2
chr20	4000000	4500000	Genes	11.771	2
chr20	4500000	5000000	Genes	11.782	2

Showing 1 to 10 of 106 entries | 1 2 3 4 5 6 7 ... 11 ›

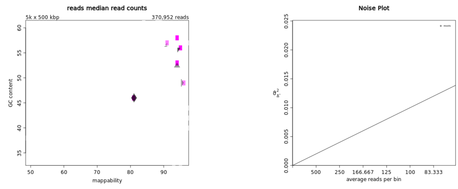
Quality Control Data

Histogram of Read Lengths



N.B. The read length affects the results of QDNASeq analysis. In future versions we will provide preset parameters based on detected read length

QDNASeq Copy Number QC Plots



Median read counts per genomic bin shown as a function of GC content and mappability Read count relationship between sequence depth and noise

Software versions

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Name	Version
pysam	0.21.0
R	4.2.2
QDNAseq	1.34.0
samtools	1.17

Showing 1 to 4 of 4 entries

Workflow parameters

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Key	Value
help	False
version	False
disable_ping	False
threads	40
aws_image_prefix	None
aws_queue	None
out_dir	/project/ctb-noncodo/VnanoOperations/wf-human-variation-test/QDNAseq
snp	True
sv	True
mod	False

Showing 1 to 10 of 68 entries | 1 2 3 4 5 6 7 ›

About this report

This report was produced using the epi2me-labs/wf-human-variation nextflow workflow (2.2.0).