<u>Multi⊕</u>C A modular tool to aggregate results from bioinformatics analyses across many samples into a single report. Report generated on 2024-04-29, 14:15 CEST based on data in: /home/BCG\_2024\_vfassi/project/628 Cumulative genome coverage don't show again × **1** Welcome! Not sure where to start? Watch a tutorial video (6:06) GC content distribution **General Statistics** Sequence Quality Histograms Gopy table 
☐ Configure Columns 
☐ Plot 
☐ Showing 3/3 rows and 8/18 columns. Per Sequence Quality Scores Sample Name % GC ≥ 30X Median cov Mean cov % Dups % GC M Seqs % Aligned Per Base Sequence Content 22.8% 24.1X 99.8% 5.0X 43% case628\_child Per Sequence GC Content 18.0X 31.2% 99.9% case628\_father 27.3X 99.8% 31.0% 18.0X 26.3X case628\_mother 50% Sequence Length Distribution Sequence Duplication Levels Overrepresented sequences QualiMap QualiMap is a platform-independent application to facilitate the quality control of alignment sequencing data and its derivatives like feature counts. DOI: 10.1093/bioinformatics/btv566; 10.1093/bioinformatics/btv503. Coverage histogram Y-Limits: on Distribution of the number of locations in the reference genome with a given depth of coverage. Qualimap BamQC: Coverage histogram Export Plot 1400000 1200000 1000000 600000 400000 200000 Coverage (X) Cumulative genome coverage Y-Limits: on Percentage of the reference genome with at least the given depth of coverage. Qualimap BamQC: Genome fraction covered by at least X reads Export Plot Coverage (X) Created with MultiQC GC content distribution Y-Limits: on Each solid line represents the distribution of GC content of mapped reads for a given sample. Qualimap BamQC: GC content distribution Export Plot 0 2.5 5 7.5 10 12.5 15 17.5 20 22.5 25 27.5 30 32.5 35 37.5 40 42.5 45 47.5 50 52.5 55 57.5 80 82.5 85 87.5 80 82.5 80 **FastQC** FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge. Sequence Counts Sequence counts for each sample. Duplicate read counts are an estimate only. Number of reads Percentages FastQC: Sequence Counts Export Plot case628\_child case628\_father case628\_mother Number of reads Unique ReadsDuplicate Reads Created with MultiQC Sequence Quality Histograms Y-Limits: on The mean quality value across each base position in the read. FastQC: Mean Quality Scores Export Plot Position (bp) Created with MultiQC Per Sequence Quality Scores The number of reads with average quality scores. Shows if a subset of reads has poor quality. FastQC: Per Sequence Quality Scores Export Plot 900000 800000 700000 600000 500000 400000 300000 200000 100000 Mean Sequence Quality (Phred Score) Created with MultiQC Per Base Sequence Content 3 The proportion of each base position for which each of the four normal DNA bases has been called. Click a sample row to see a line plot for that dataset. • Rollover for sample name Export Plot Per Sequence GC Content 2 1 The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content. Percentages Counts FastQC: Per Sequence GC Content Export Plot % GC Per Base N Content 3 The percentage of base calls at each position for which an N was called. FastQC: Per Base N Content Export Plot Position in Read (bp) Sequence Length Distribution 3 Y-Limits: on The distribution of fragment sizes (read lengths) found. See the FastQC help FastQC: Sequence Length Distribution Export Plot 2500000 2000000 126 118 120 128 132 Sequence Length (bp) Created with MultiQC Sequence Duplication Levels Y-Limits: on The relative level of duplication found for every sequence. FastQC: Sequence Duplication Levels Export Plot Sequence Duplication Level Created with MultiQC Overrepresented sequences 33333 The total amount of overrepresented sequences found in each library. 3 samples had less than 1% of reads made up of overrepresented sequences Adapter Content 3 The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position. No samples found with any adapter contamination > 0.1% Status Checks Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red). ↓ Sort by highlight Min: 0 FastQC: Status Checks Export Plot case628\_child case628\_father case628\_mother Per Base Sequence Qu Per Sequence Quality Per Base Sequence Co Per Sequence GC Cont Sequence Length Dist Sequence Duplication Adapter Content Per Base N Content Overrepresented Sequ **Basic Statistics** Section Name Created with MultiQC MultiQC v1.14 - Written by Phil Ewels, available on GitHub.

General Stats

Coverage histogram

Sequence Counts

Per Base N Content

Adapter Content

Status Checks

QualiMap

FastQC