MultiQC <u>Multi⊕</u>C A modular tool to aggregate results from bioinformatics analyses across many samples into a single report. Report generated on 2019-10-23, 13:24 based on data in: /data/storage/SAYRES/NASONIA/Heini/Processing/Clark/RNA/raw_FastQC Sequence Quality Histograms Per Sequence Quality Scores **1 Welcome!** Not sure where to start? Watch a tutorial video (6:06) don't show again 🗙 Per Base Sequence Content Per Sequence GC Content **General Statistics** Sequence Length Distribution 🗳 Copy table **....** Configure Columns ■ Plot Showing ¹²/₁₂ rows and ³/₅ columns. Sequence Duplication Levels % GC Sample Name M Seqs % Dups Overrepresented sequences 65.3 70.0% 41% SRR1566022 32.7 44% 52.4% SRR1566023 49.4% 38.1 SRR1566024 68.1% 56.3 42% SRR1566028 56.3% 43.9 45% SRR1566029 51.5% 48.0 SRR1566030 60.4% 42% 50.3 SRR2773794 53.0 56.6% 45% SRR2773795 74.8 49.4% 47% SRR2773796 65.2 64.0% 42% SRR2773797 93.7% SRR2773798 52% 57.3 46% 63.9 48.4% SRR2773799 **FastQC** FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge. Sequence Quality Histograms The mean quality value across each base position in the read. See the FastQC help. Y-Limits: on Mean Quality Scores **Export Plot** 40 35 30 Phred Score 15 10 18 20 22 32 50 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. See the FastQC help. Y-Limits: on Per Sequence Quality Scores Export Plot 35000000 30000000 25000000 20000000 15000000 10000000 5000000 22 24 26 Mean Sequence Quality (Phred Score) Created with MultiQC Per Base Sequence Content 6 6 The proportion of each base position for which each of the four normal DNA bases has been called. See the FastQC help. Click a sample row to see a line plot for that dataset. Rollover for sample name %C: -%A: -%G: -Position: -**Export Plot** Per Sequence GC Content The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content. See the FastQC help. Y-Limits: on Percentages Counts Per Sequence GC Content Export Plot 50 95 % GC Created with MultiQC Per Base N Content The percentage of base calls at each position for which an N was called. See the FastQC help. Y-Limits: 0 Per Base N Content Export Plot 24 Position in Read (bp) Created with MultiQC Sequence Length Distribution 5 7 The distribution of fragment sizes (read lengths) found. See the FastQC help. Y-Limits: on Sequence Length Distribution Export Plot 70000000 60000000 50000000 40000000 30000000 20000000 10000000 50 Sequence Length (bp) Created with MultiQC Sequence Duplication Levels 3 9 9 The relative level of duplication found for every sequence. See the FastQC help. Y-Limits: on Sequence Duplication Levels Export Plot >10 >50 >5kSequence Duplication Level Created with MultiQC Overrepresented sequences 5 7 The total amount of overrepresented sequences found in each library. See the FastQC help for further information. Overrepresented sequences Export Plot SRR1566023 SRR1566024 SRR1566028 SRR1566029 SRR1566030 SRR2773794 SRR2773795 SRR2773796 SRR2773797 SRR2773798 SRR2773799 5% 2% 3% 7% 13% 14% 15% 16% 17% 18% 19% 20% Percentage of Total Sequences Sum of remaining over-represented sequences Top over-represented sequence Created with MultiQC Adapter Content The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position. See the FastQC help. Only samples with ≥ 0.1% adapter contamination are shown. Y-Limits: on **Adapter Content** Export Plot % of Sequences 14 16 18 20 22 24 28 34 26 32 38 Position (bp) Created with MultiQC

General Stats

Per Base N Content

Adapter Content

FastQC

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