

fastqc
sample: SRR12904817

fastqc
sample: SRR12904818

fastqc
sample: SRR12904821

multiqc

all

```
graph TD; S1["fastqc<br/>sample: SRR12904817"] --> M["multiqc"]; S1 --> A["all"]; S2["fastqc<br/>sample: SRR12904818"] --> M; S2 --> A; S3["fastqc<br/>sample: SRR12904821"] --> M; S3 --> A; M --> A;
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The diagram illustrates a workflow for processing FastQC data. At the top, three boxes represent individual FastQC samples: 'fastqc sample: SRR12904817', 'fastqc sample: SRR12904818', and 'fastqc sample: SRR12904821'. These samples are processed by 'multiqc' (a central box) and then aggregated into an 'all' directory (the bottom box). Arrows indicate the flow of data from each sample to both 'multiqc' and 'all', and from 'multiqc' to 'all'.