6/5/25, 11:30 AM MultiQC Report

Multioc (file:///Users/aseechan/Documents/multiqc\_report.html#)



# (http://multiqc.info/)

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2024-08-08, 16:40 based on data in:

- /gpfs/commons/projects/ak\_intern/aseechan/Project\_MUN\_10873\_B01\_GRM\_WGS/Sample\_AKS/qc
- /gpfs/commons/projects/ak\_intern/aseechan/Project\_MUN\_10873\_B01\_GRM\_WGS/multiqc

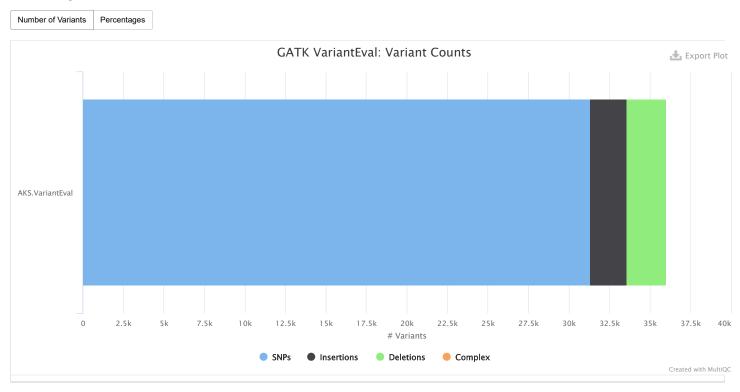
## **General Statistics**

♣ Copy table	<b>Ⅲ</b> Configure Columns	<b>₄Î</b> Plot	Showing $^2/_2$ rows and $^5/_8$ columns.			
Sample Name	% Aligned		Insert Size	% Dups	Median Coverage	Bases ≥ 30X
AKS.final						
AKS.mem						

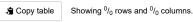
## **GATK**

GATK (https://www.broadinstitute.org/gatk/) is a toolkit offering a wide variety of tools with a primary focus on variant discovery and genotyping.

#### Variant Counts



#### Compare Overlap



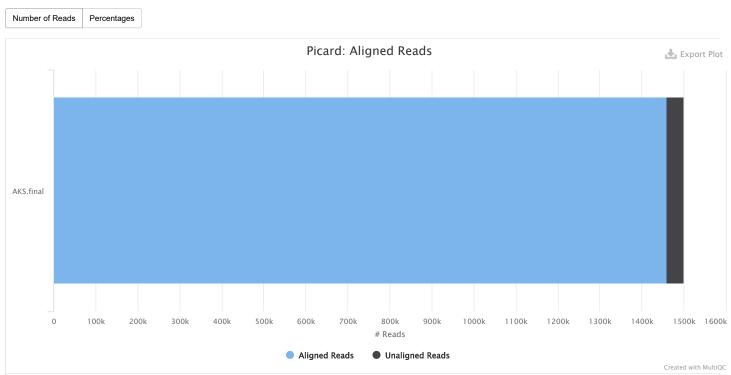
Sample Name

## **Picard**

Picard (http://broadinstitute.github.io/picard/) is a set of Java command line tools for manipulating high-throughput sequencing data.

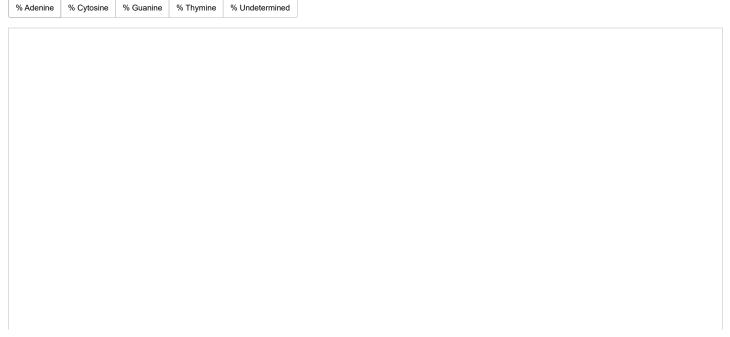
## **Alignment Summary**

Plase note that Picard's read counts are divided by two for paired-end data.



#### **Base Distribution**

Plot shows the distribution of bases by cycle.



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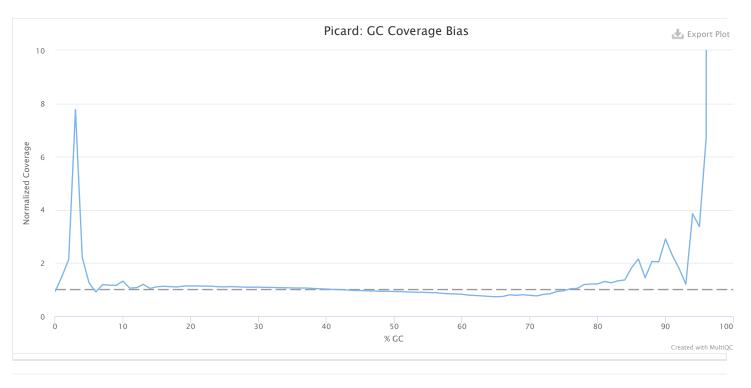
Picard: Base Distribution

100

♣ Export Plot

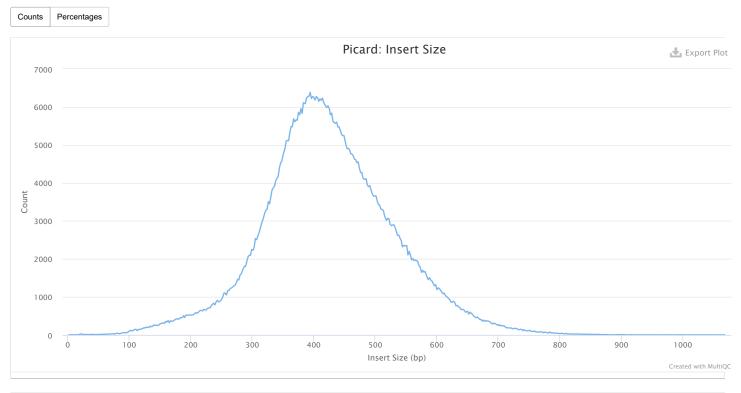
## GC Coverage Bias

This plot shows bias in coverage across regions of the genome with varying GC content. A perfect library would be a flat line at y = 1.



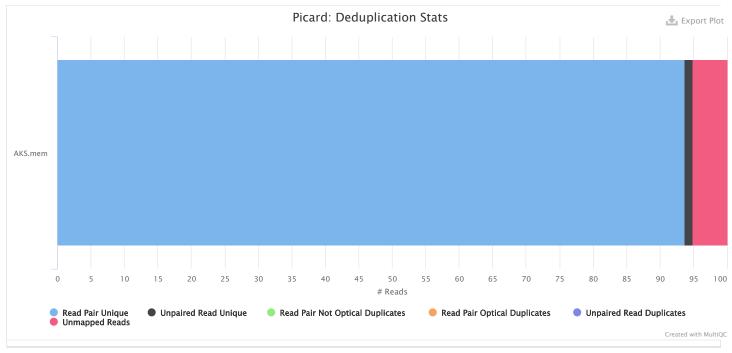
#### Insert Size

Plot shows the number of reads at a given insert size. Reads with different orientations are summed.



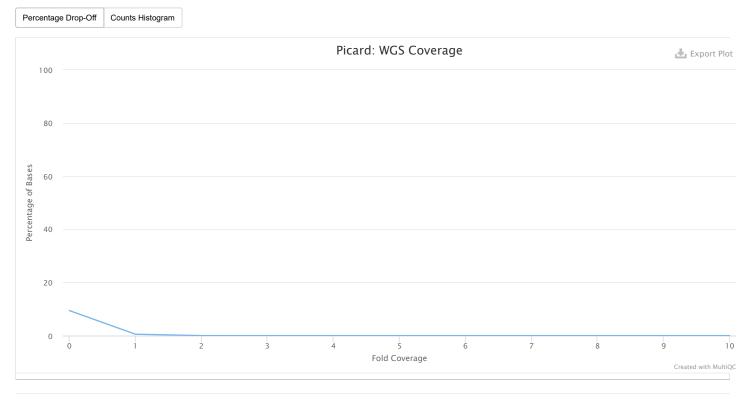
## Mark Duplicates

Number of Reads Percentages



## **WGS** Coverage

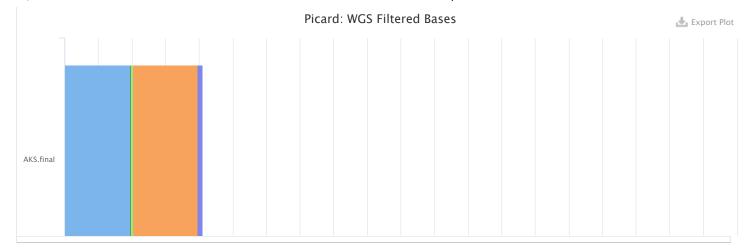
The number of bases in the genome territory for each fold coverage. Note that final 1% of data is hidden to prevent very long tails.



## WGS Filtered Bases

For more information about the filtered categories, see the Picard documentation (http://broadinstitute.github.io/picard/picard-metric-definitions.html#CollectWgsMetrics.WgsMetrics).

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MultiQC v1.8 (http://multiqc.info/) - Written by Phil Ewels (http://phil.ewels.co.uk/), available on GitHub (https://github.com/ewels/MultiQC). This report uses HighCharts (http://www.highcharts.com/), jQuery (https://jquery.com/), jQuery UI (https://jqueryui.com/), Bootstrap (http://getbootstrap.com/), FileSaver.js (https://github.com/eligrey/FileSaver.js) and clipboard.js (https://clipboardjs.com/).

