

# Sample Report

M.Kaller\_14\_05 - P1170\_101

## Sample Information

<b>Report Date</b>	2014-11-13
<b>User Contact</b>	phil.ewels@scilifelab.se
<b>Project Name</b>	M.Kaller_14_05 (Swedish Genomes Pilot v3 )

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<b>Project Name</b>	M.Kaller_14_05 (Swedish Genomes Pilot v3 )
<b>User Sample Name</b>	Test Sample #1290
<b>NGI Sample Name</b>	P1170_101
<b>UPPMAX Project ID</b>	b2014832
<b>Sequencing Platform</b>	Illumina
<b>Library Preparation Method</b>	<b>A:</b> All samples were sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup.The Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale used is Sanger / phred33 / Illumina 1.8+.
<b>Sequencing Centre</b>	NGI Stockholm
<b>Reference Genome</b>	gatk_bundle/2.8/b37/human_g1k_v37.fasta
<b>Flow Cells</b>	140815_SN1025_0222_BC4HAPACXX 140815_SN1025_0223_BC4HAPACXX

## Library Statistics

<b>Total Reads</b>	908,585,160
<b>Aligned Reads</b>	99.47% - 903,806,933
<b>Duplication Rate</b>	1.9%
<b>Median Insert Size</b>	369 bp
<b>Av. Autosomal Coverage</b>	28.92X
<b>≥ 30X Coverage</b>	51.72% of reference
<b>GC Content</b>	39.87%

See below for more information about coverage and insert size. The `qualimapReport.html` report in your delivery folder contains additional library statistics. Note that the duplication rate above is calculated using [Picard Mark Duplicates](#). Qualimap calculates duplicates differently and the figure in the report will be different to the Picard result..

## Distribution of sequencing coverage

Calculating the coverage of a genome tells you how much information you have about the sequence content of any given position. More coverage means more data and so greater confidence in your results. A specific locus with 30X coverage will have 30 unique reads covering that location. Different positions in the genome may have different coverages due to variations in how well reads map to the underlying sequence. Other factors such as GC bias in library preparation may also have an effect.

To calculate the plot below, we create rolling windows across the genome and count the frequencies of the different coverages observed. This was done using the [QualiMap](#) tool and plotted with an [NGI script](#).

## Proportion of library with increasing coverage depths

Another way to assess coverage is to look at the proportion of the reference genome with a certain coverage. The plot below shows what percentage of the reference genome is covered with increasing coverage thresholds. As above, this data was calculated using [QualiMap](#) and plotted with an [NGI script](#).

## Library fragment insert sizes

By inspecting where each read pair maps to in the reference genome, we can reconstruct the reads that were present in the library and calculate the range of insert sizes. This gives an insight into the quality of the sequencing library. We counted how many reads with each insert size were seen and plotted this in the histogram below. This was done using the [QualiMap](#) tool and plotted with an [NGI script](#).

## Distribution of reads by GC content

Library preparation and sequencing alignment can be affected by differences in GC content. Here, we plot the proportions of the library reads at each GC content. The red dotted line shows the profile for the reference genome. This data was calculated using [QualiMap](#) and plotted with an [NGI script](#).

## Variants

<b>Change Rate</b>	1 change per 774 bp
<b>Total SNPs</b>	4,004,647
<b>Homotypic SNPs</b>	1,491,592
<b>Heterotypic SNPs</b>	2,513,055
<b>Ts/Tv Ratio</b>	1.9895
<b>Synonymous SNPs</b>	35,078
<b>Non-Synonymous SNPs</b>	30,232
<b>Stop Gained / Lost</b>	273 / 58
<b>Missense SNPs</b>	46.2% - 30,366
<b>Nonsense SNPs</b>	0.4% - 273
<b>Silent SNPs</b>	53.4% - 35,078

Different effects can be attributed to each SNP depending on where it occurs. Here we have used the [snpEff](#) tool to categorise and count different effects. The results were plotted with an [NGI script](#).

See the `snpEff_summary.html` report in your delivery folder for more details.