

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:26:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238646.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6238646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:26:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,922,071
Mapped reads	2,638,164 / 90.28%
Unmapped reads	283,907 / 9.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,038 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	308,526 / 10.56%
Duplication rate	9.43%
Clipped reads	1,728,272 / 59.15%

2.2. ACGT Content

Number/percentage of A's	39,143,292 / 24.26%
Number/percentage of C's	28,127,240 / 17.43%
Number/percentage of T's	54,501,840 / 33.78%
Number/percentage of G's	39,574,903 / 24.53%
Number/percentage of N's	7,711 / 0%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0521

Standard Deviation	0.7596
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.3
----------------------	------

2.5. Mismatches and indels

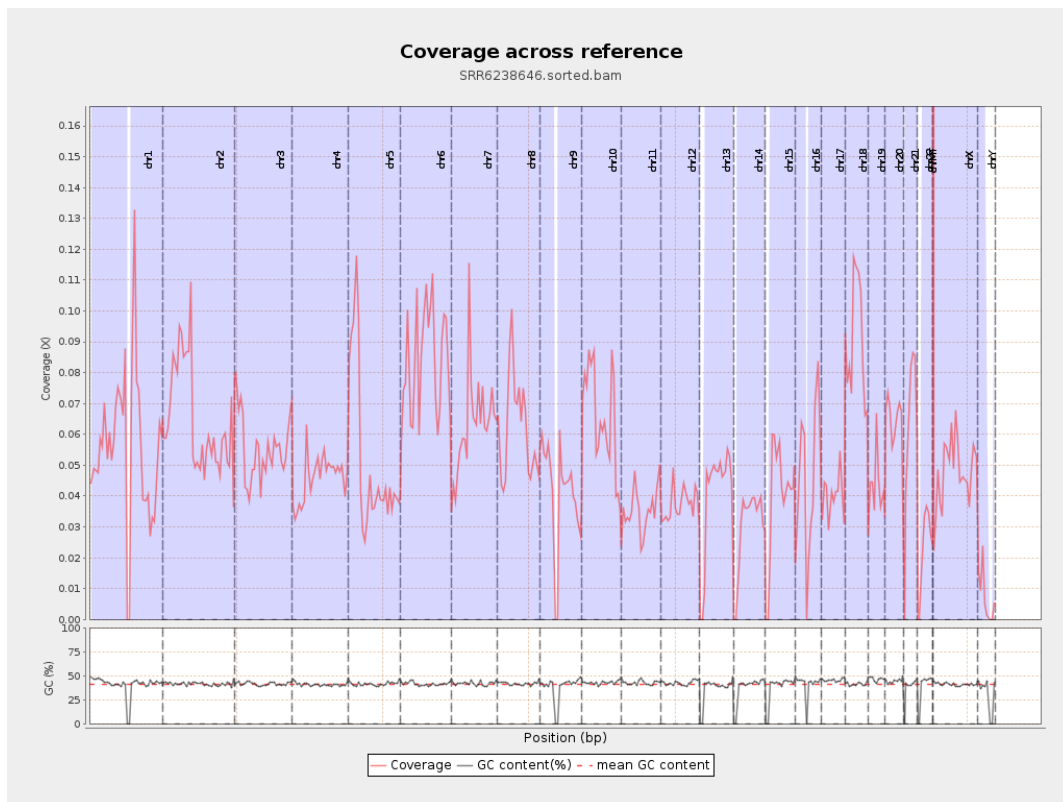
General error rate	0.58%
Mismatches	917,393
Insertions	11,104
Mapped reads with at least one insertion	0.42%
Deletions	38,850
Mapped reads with at least one deletion	1.46%
Homopolymer indels	41.3%

2.6. Chromosome stats

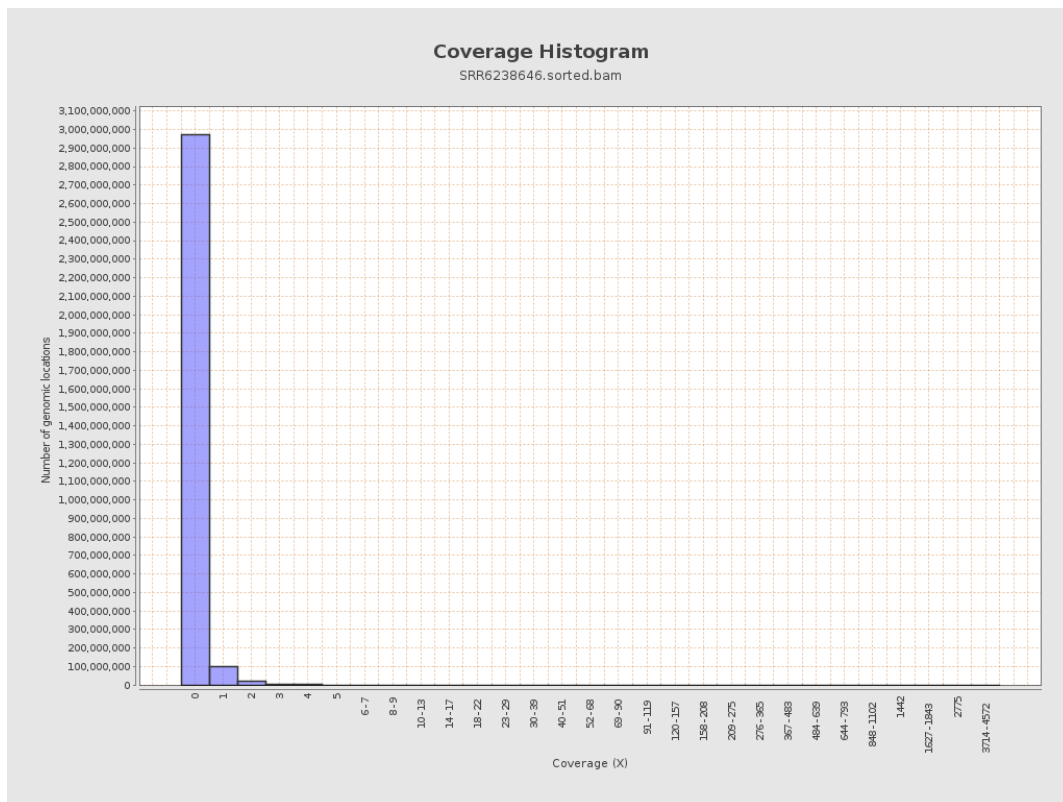
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13705128	0.055	0.7465
chr2	243199373	15752964	0.0648	2.0142
chr3	198022430	10987559	0.0555	0.3187
chr4	191154276	8785214	0.046	0.3022
chr5	180915260	9157465	0.0506	0.3031
chr6	171115067	14368345	0.084	0.752
chr7	159138663	10089440	0.0634	0.9125

chr8	146364022	9038865	0.0618	0.5736
chr9	141213431	5828923	0.0413	0.4956
chr10	135534747	8899660	0.0657	0.4446
chr11	135006516	4780036	0.0354	0.3144
chr12	133851895	4968484	0.0371	0.2811
chr13	115169878	4636181	0.0403	0.4464
chr14	107349540	3262295	0.0304	0.2855
chr15	102531392	4029710	0.0393	0.4585
chr16	90354753	3983153	0.0441	0.3606
chr17	81195210	3279646	0.0404	0.2718
chr18	78077248	7087840	0.0908	1.2317
chr19	59128983	2586296	0.0437	0.5275
chr20	63025520	4093725	0.065	0.346
chr21	48129895	3003640	0.0624	0.3632
chr22	51304566	1188086	0.0232	0.1886
chrMT	16571	64162	3.8719	3.618
chrX	155270560	7417355	0.0478	0.317
chrY	59373566	426633	0.0072	0.2934

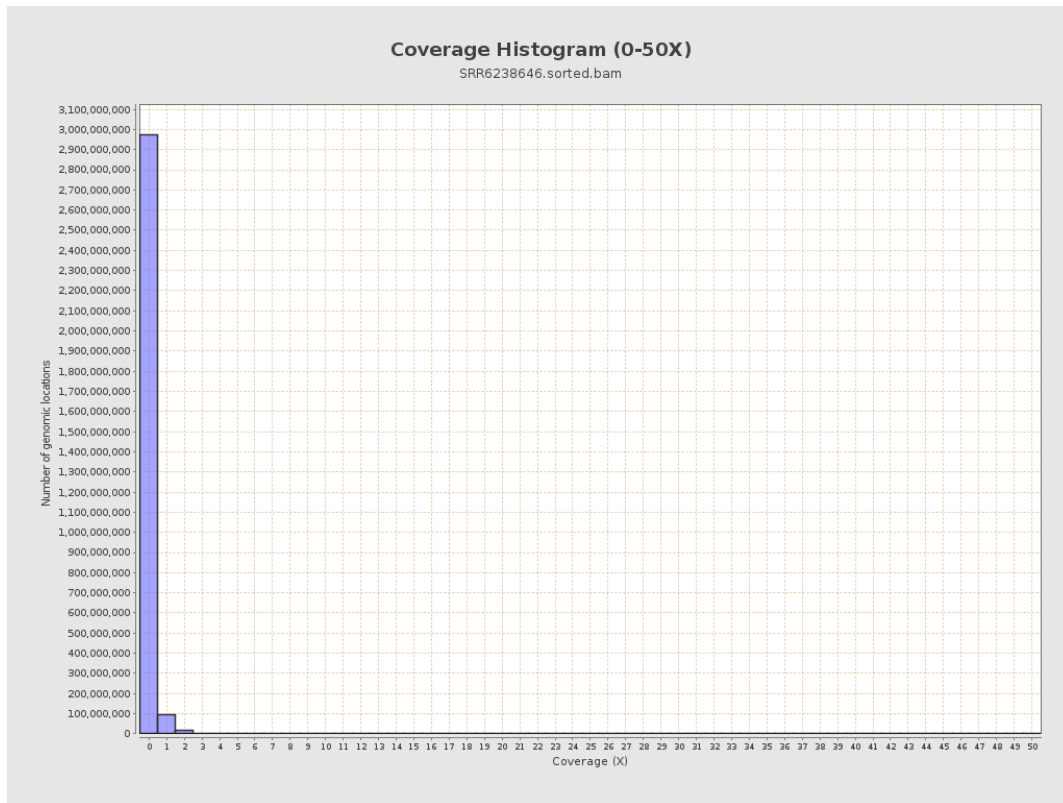
3. Results : Coverage across reference



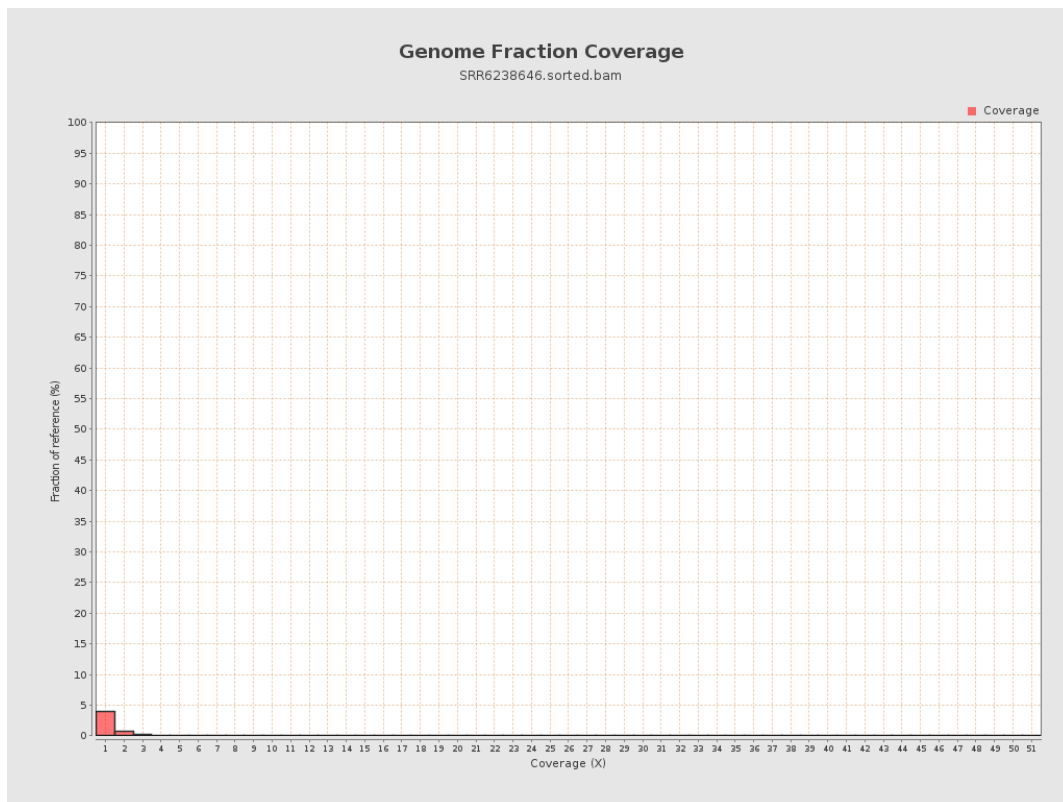
4. Results : Coverage Histogram



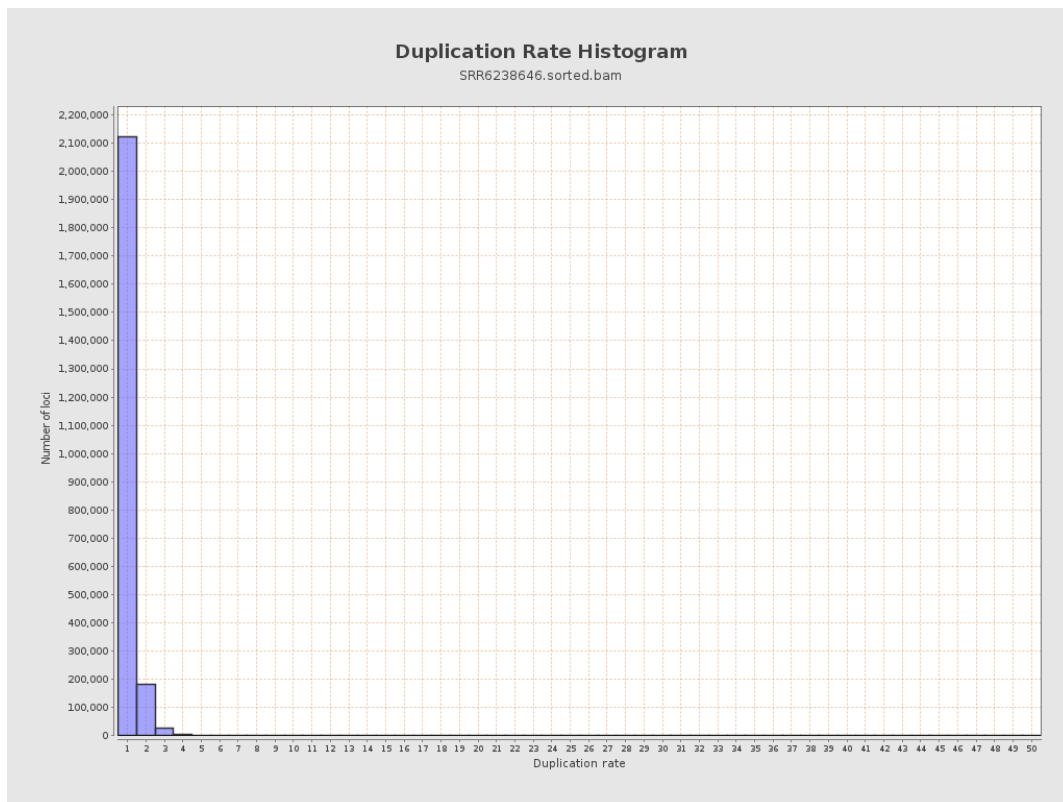
5. Results : Coverage Histogram (0-50X)



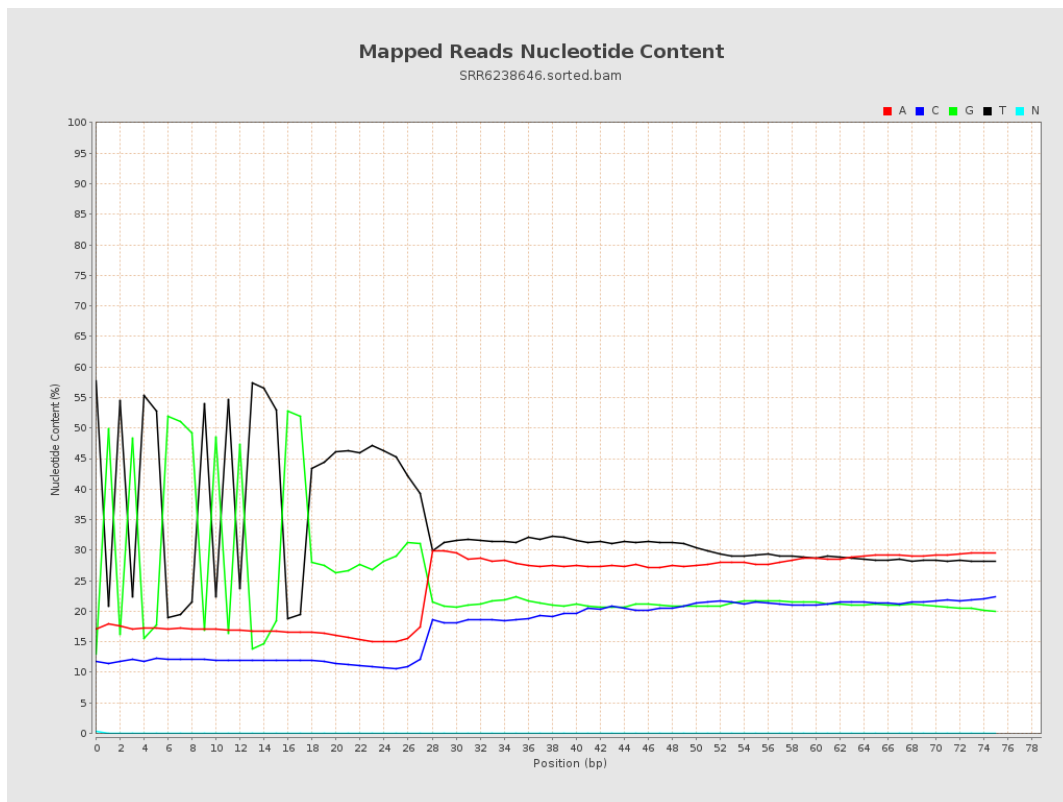
6. Results : Genome Fraction Coverage



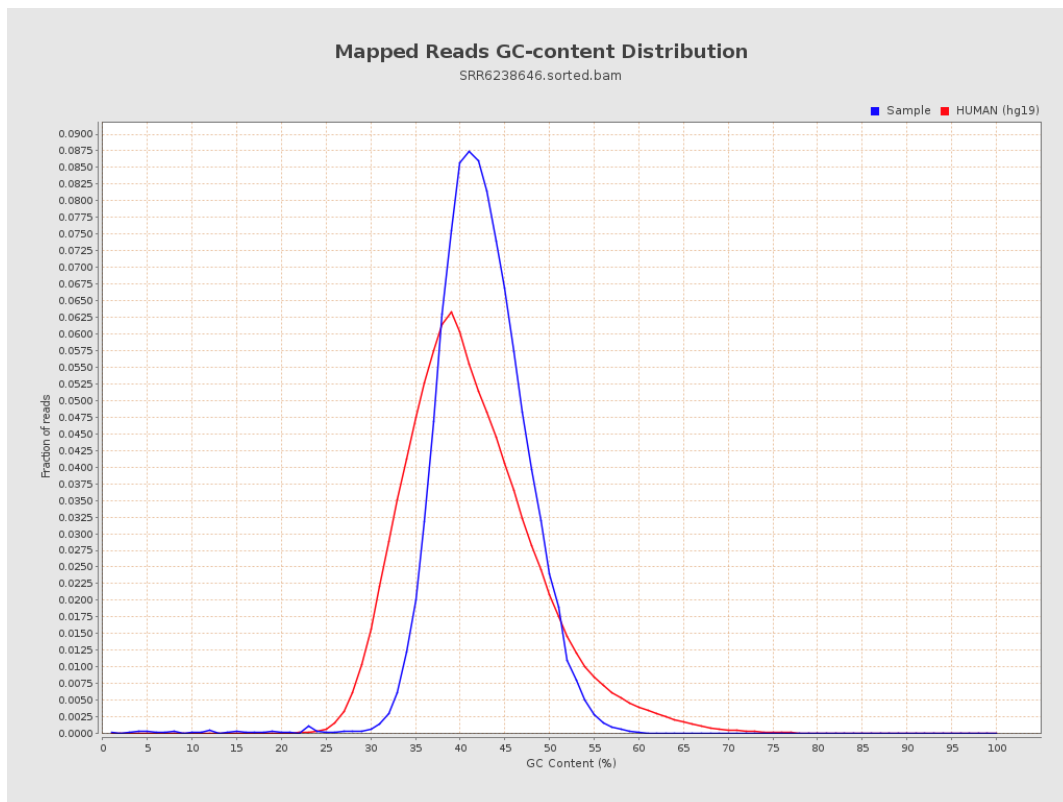
7. Results : Duplication Rate Histogram



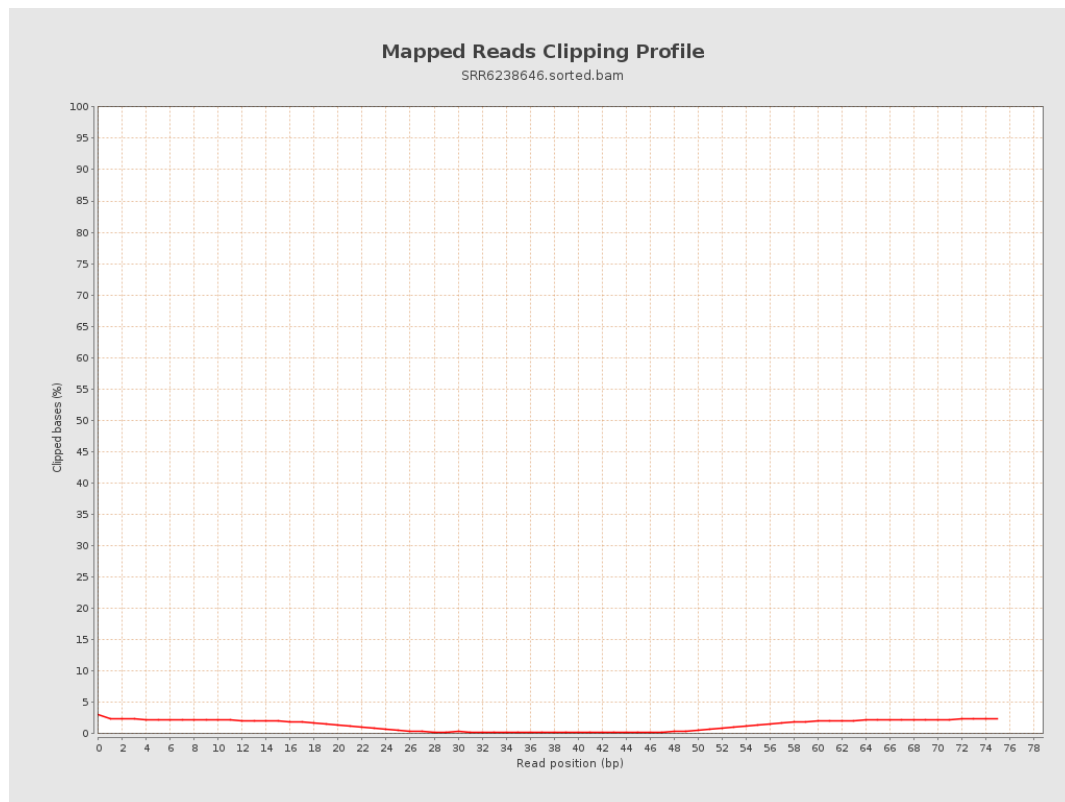
8. Results : Mapped Reads Nucleotide Content



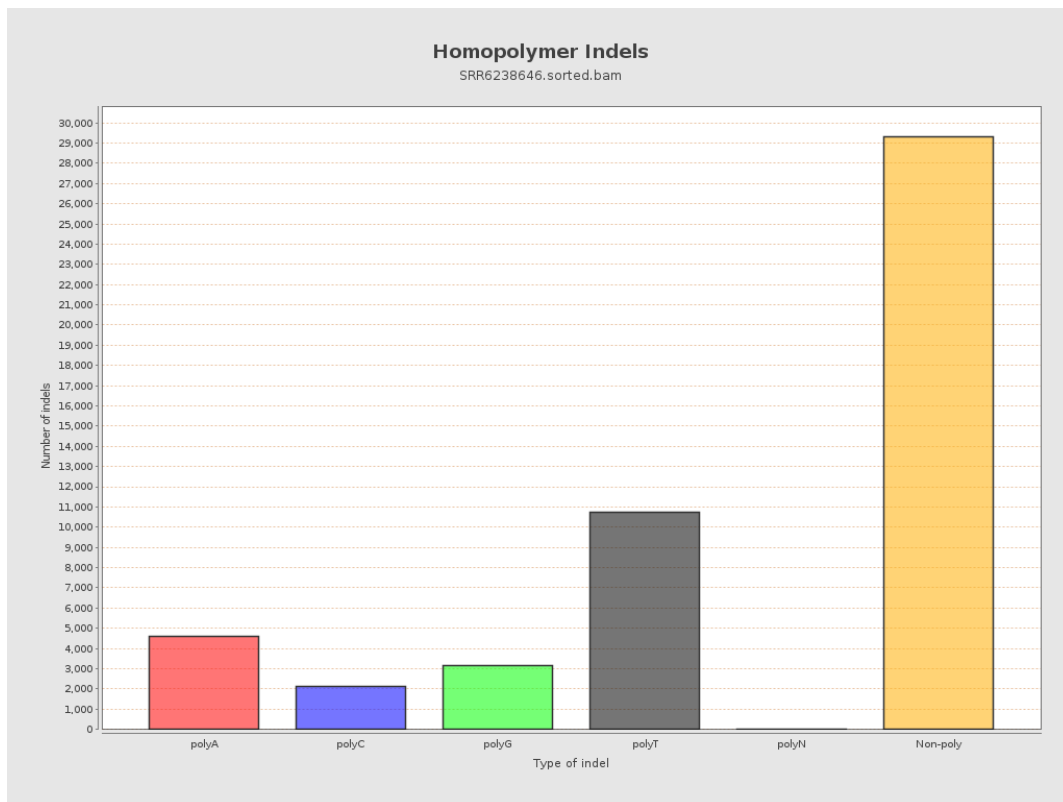
9. Results : Mapped Reads GC-content Distribution



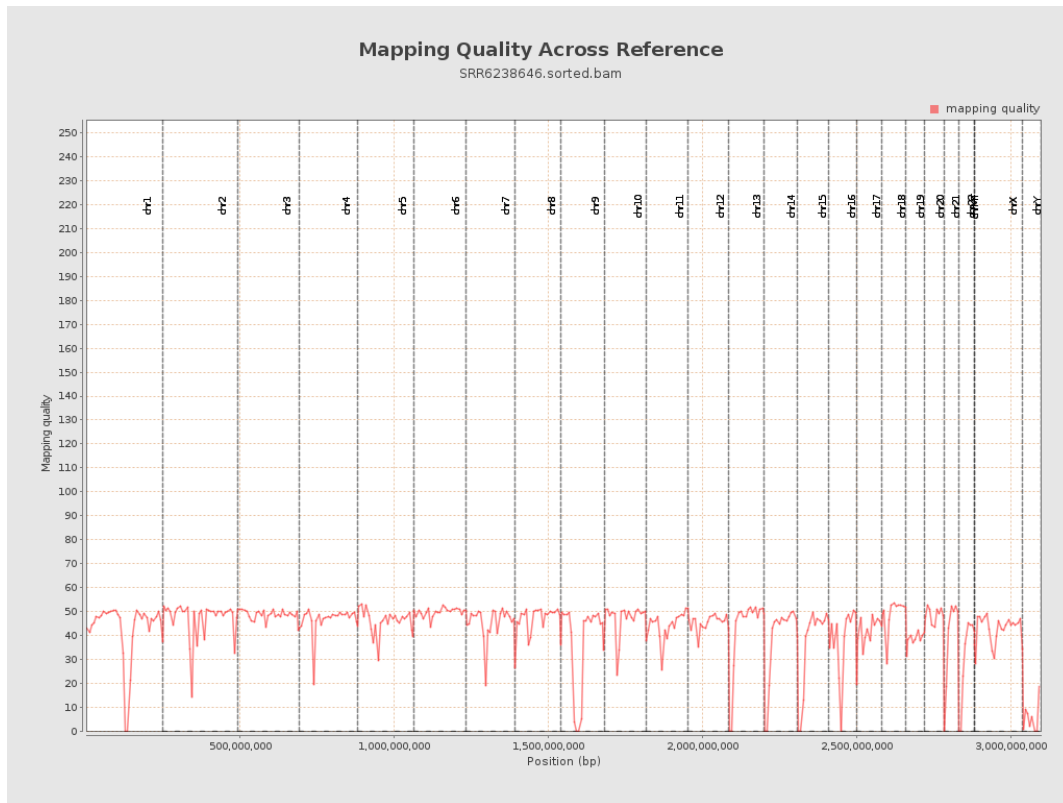
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

