

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:58:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230387.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_SRR6230387 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230387.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:58:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230387.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,698,301
Mapped reads	1,090,574 / 64.22%
Unmapped reads	607,727 / 35.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,344 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	106,841 / 6.29%
Duplication rate	8.44%
Clipped reads	720,893 / 42.45%

2.2. ACGT Content

Number/percentage of A's	16,864,062 / 25.24%
Number/percentage of C's	11,071,572 / 16.57%
Number/percentage of T's	22,930,788 / 34.32%
Number/percentage of G's	15,832,560 / 23.7%
Number/percentage of N's	106,961 / 0.16%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2275
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2.4. Mapping Quality

Mean Mapping Quality	45.61
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2.5. Mismatches and indels

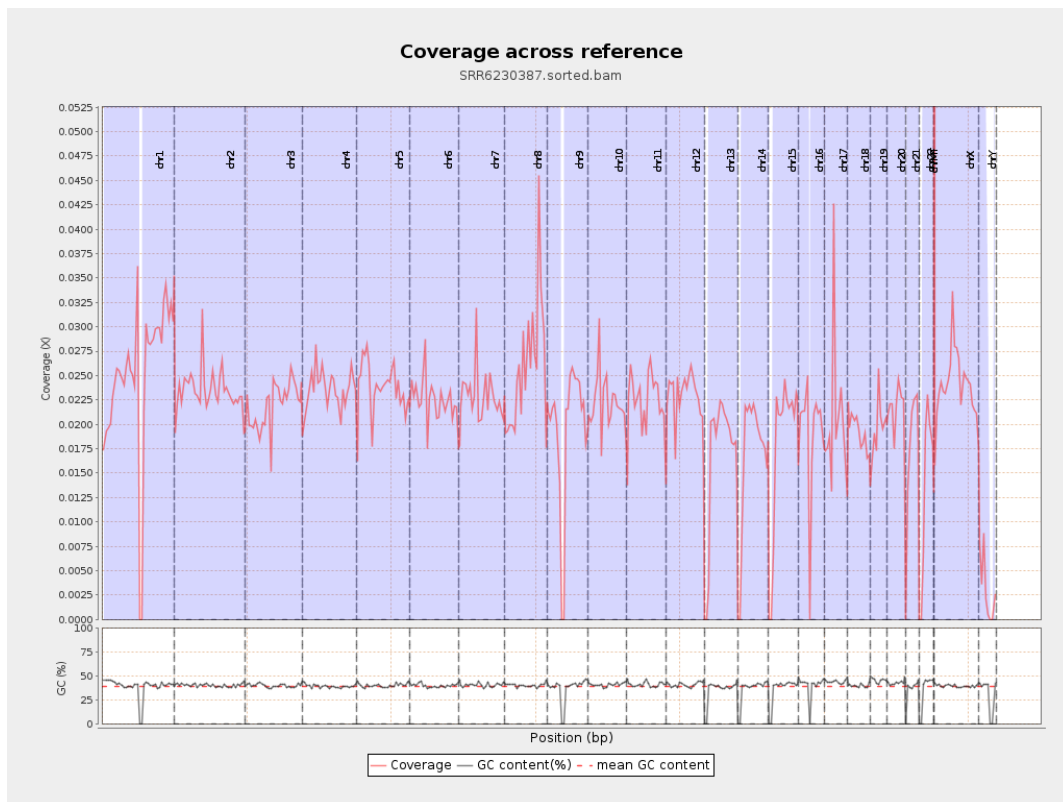
General error rate	1.16%
Mismatches	763,183
Insertions	5,586
Mapped reads with at least one insertion	0.51%
Deletions	23,668
Mapped reads with at least one deletion	2.14%
Homopolymer indels	48.81%

2.6. Chromosome stats

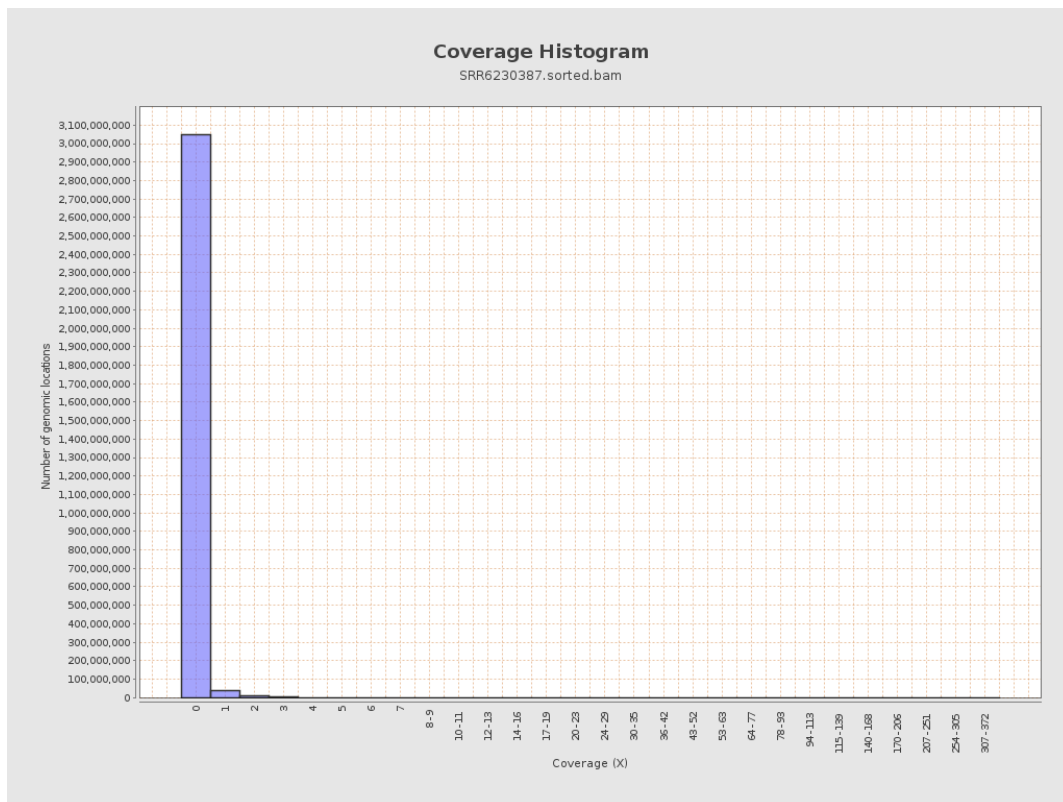
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6274925	0.0252	0.3376
chr2	243199373	5719595	0.0235	0.2467
chr3	198022430	4335929	0.0219	0.191
chr4	191154276	4505172	0.0236	0.2026
chr5	180915260	4357586	0.0241	0.2011
chr6	171115067	3847374	0.0225	0.2219
chr7	159138663	3645375	0.0229	0.259

chr8	146364022	3777059	0.0258	0.2975
chr9	141213431	2743543	0.0194	0.21
chr10	135534747	3004640	0.0222	0.2198
chr11	135006516	3062183	0.0227	0.2121
chr12	133851895	3081006	0.023	0.1971
chr13	115169878	1914531	0.0166	0.1658
chr14	107349540	1785898	0.0166	0.1706
chr15	102531392	1832857	0.0179	0.1743
chr16	90354753	1701715	0.0188	0.1807
chr17	81195210	1665870	0.0205	0.1918
chr18	78077248	1497967	0.0192	0.2913
chr19	59128983	1162496	0.0197	0.2403
chr20	63025520	1356591	0.0215	0.1939
chr21	48129895	847027	0.0176	0.1752
chr22	51304566	699411	0.0136	0.148
chrMT	16571	92862	5.6039	5.2994
chrX	155270560	3753487	0.0242	0.2086
chrY	59373566	177489	0.003	0.0779

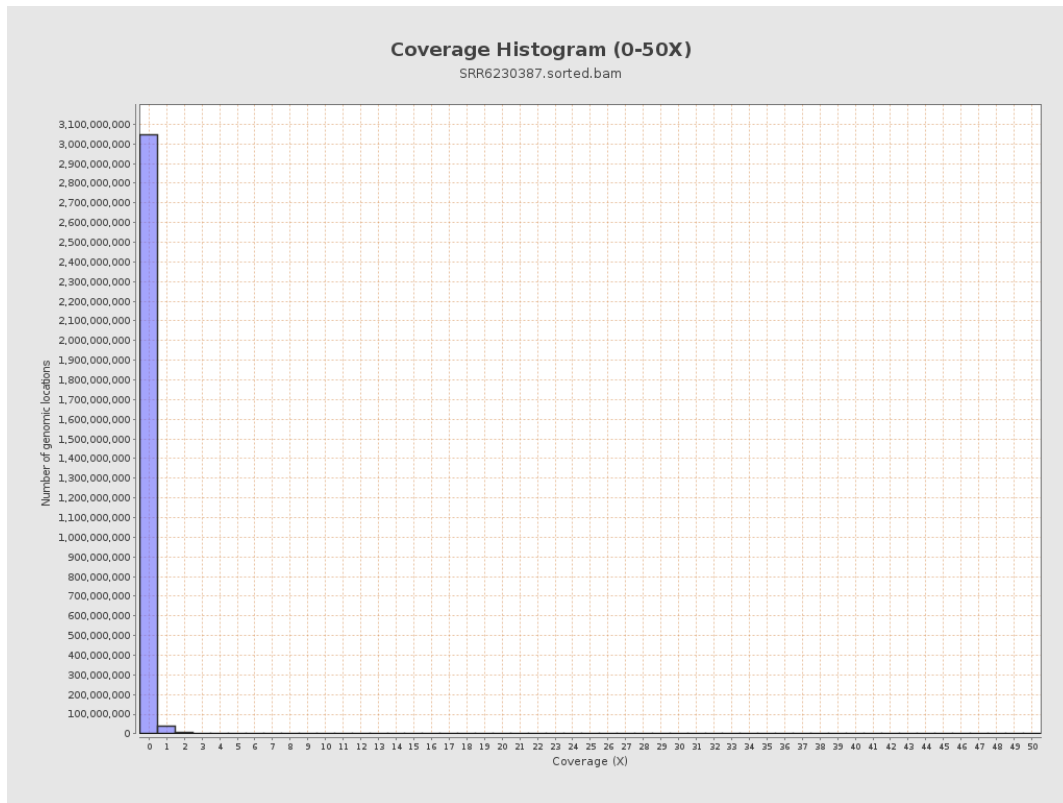
3. Results : Coverage across reference



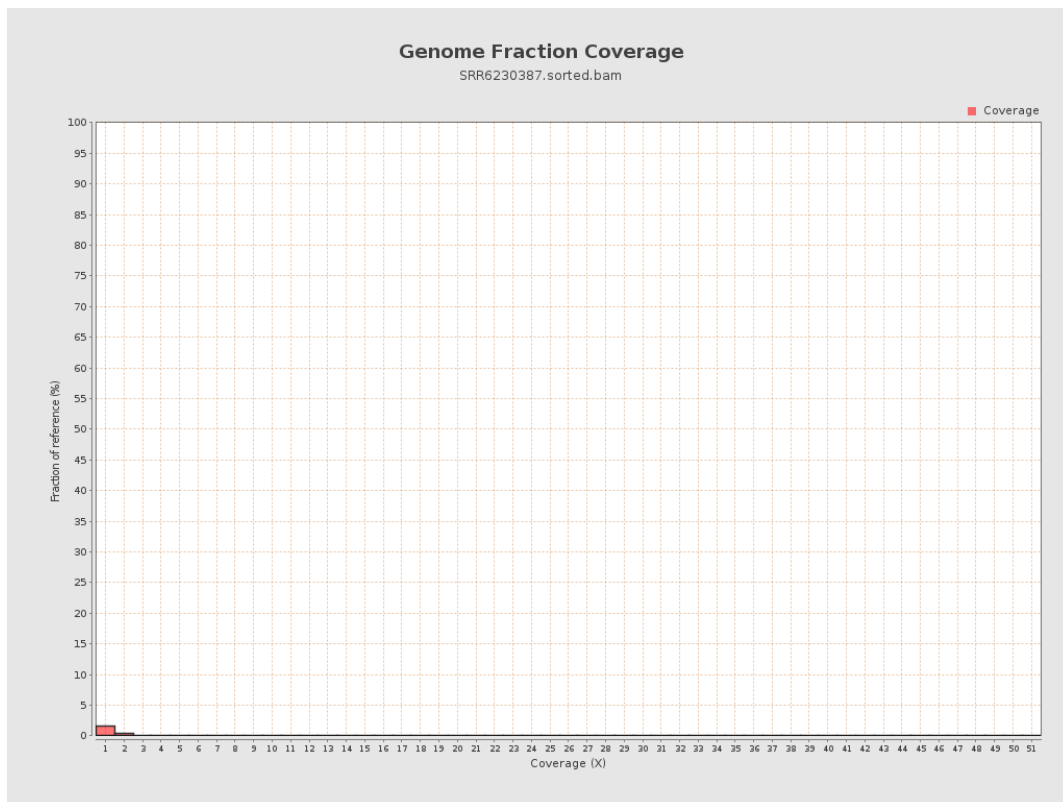
4. Results : Coverage Histogram



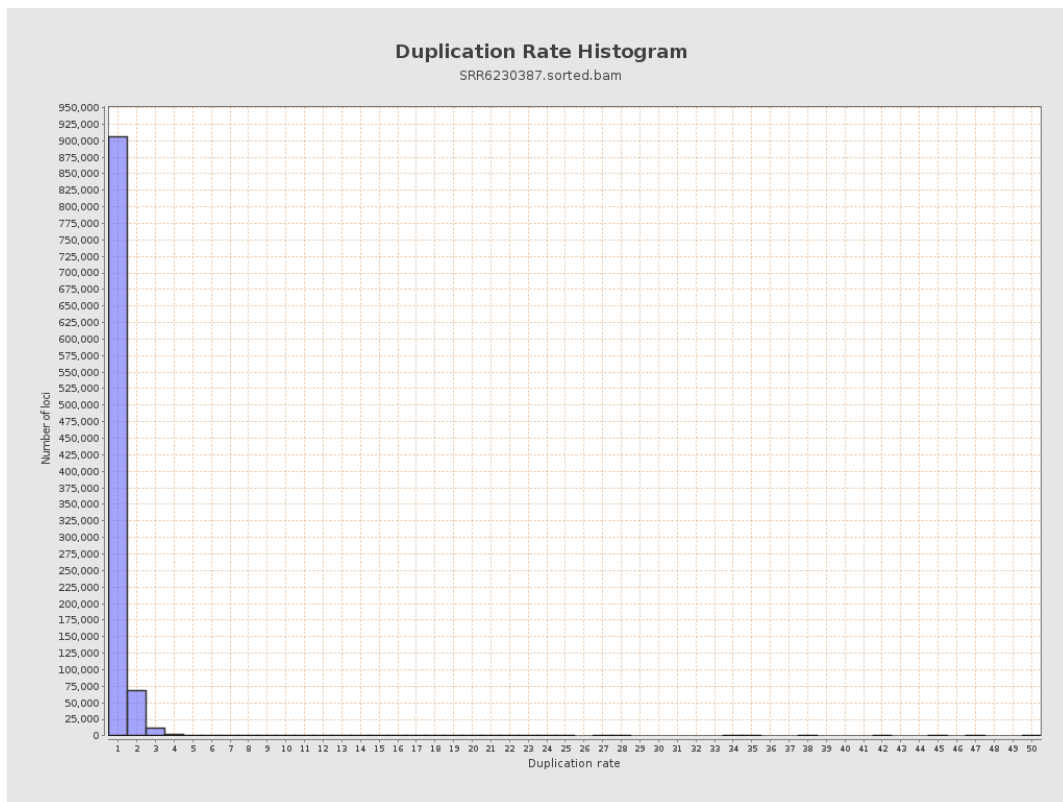
5. Results : Coverage Histogram (0-50X)



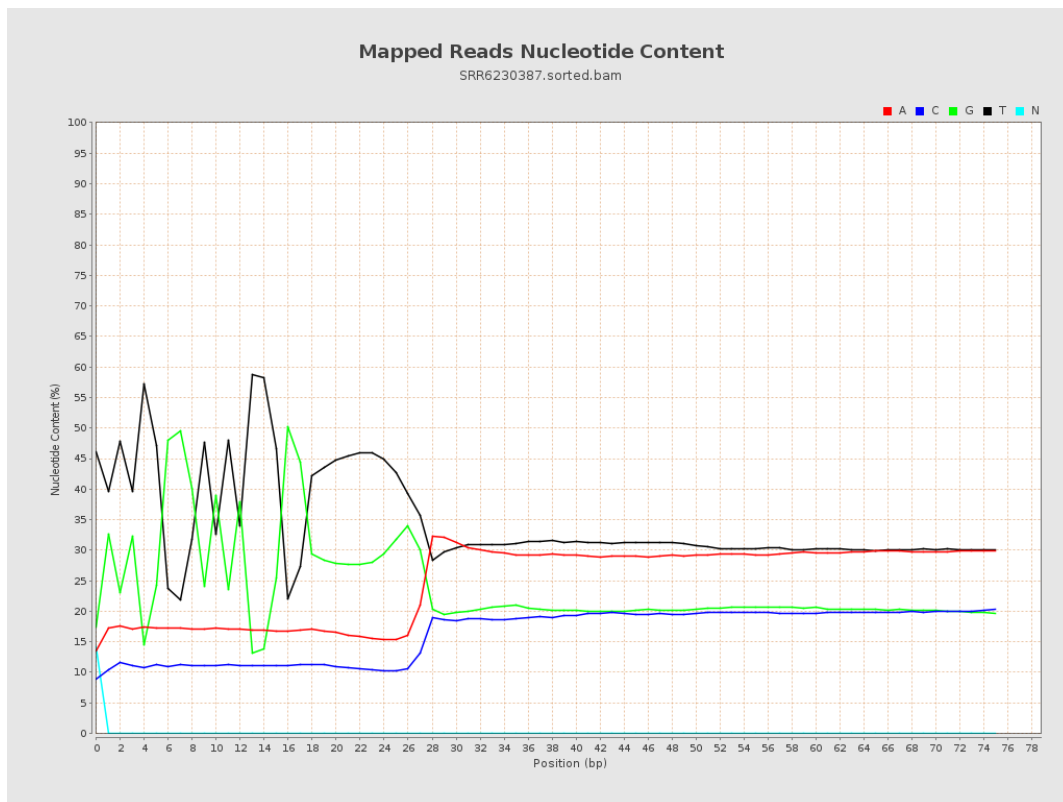
6. Results : Genome Fraction Coverage



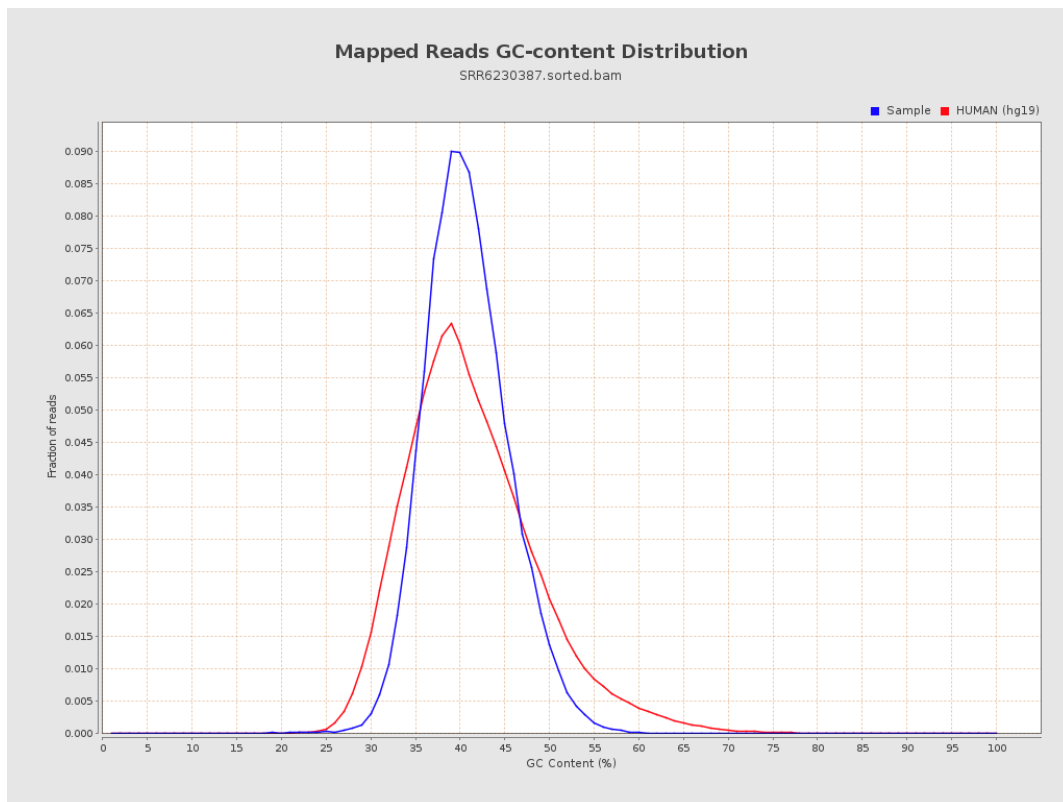
7. Results : Duplication Rate Histogram



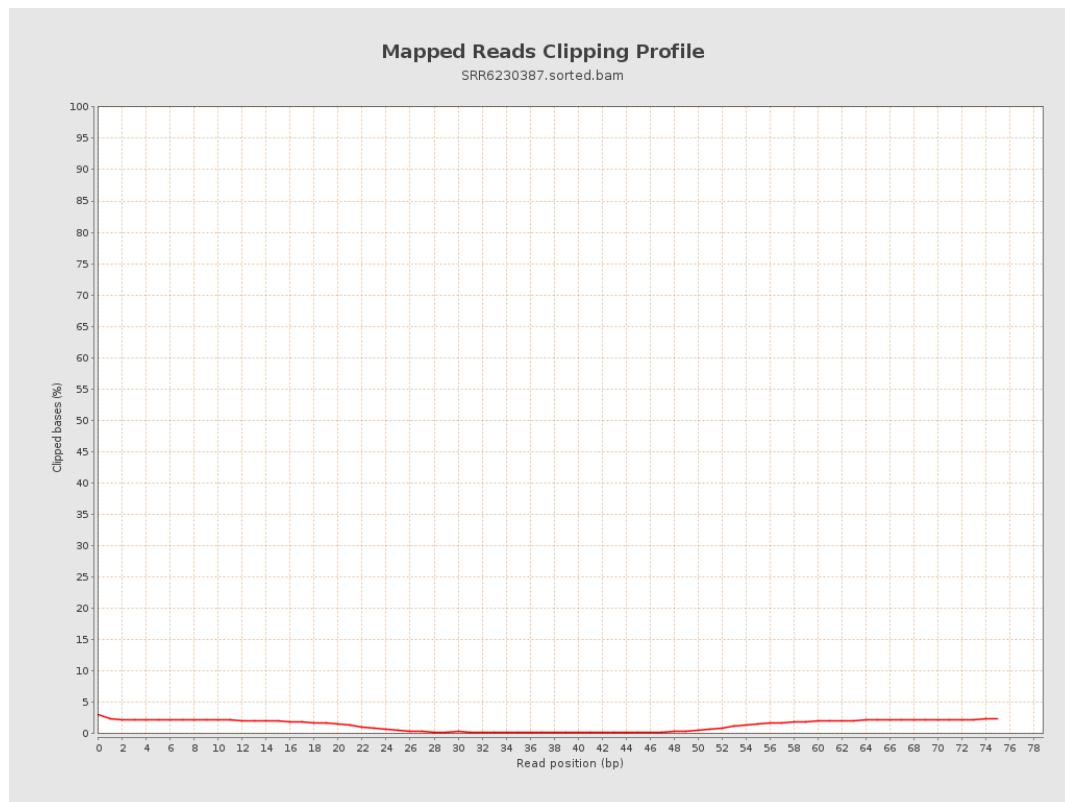
8. Results : Mapped Reads Nucleotide Content



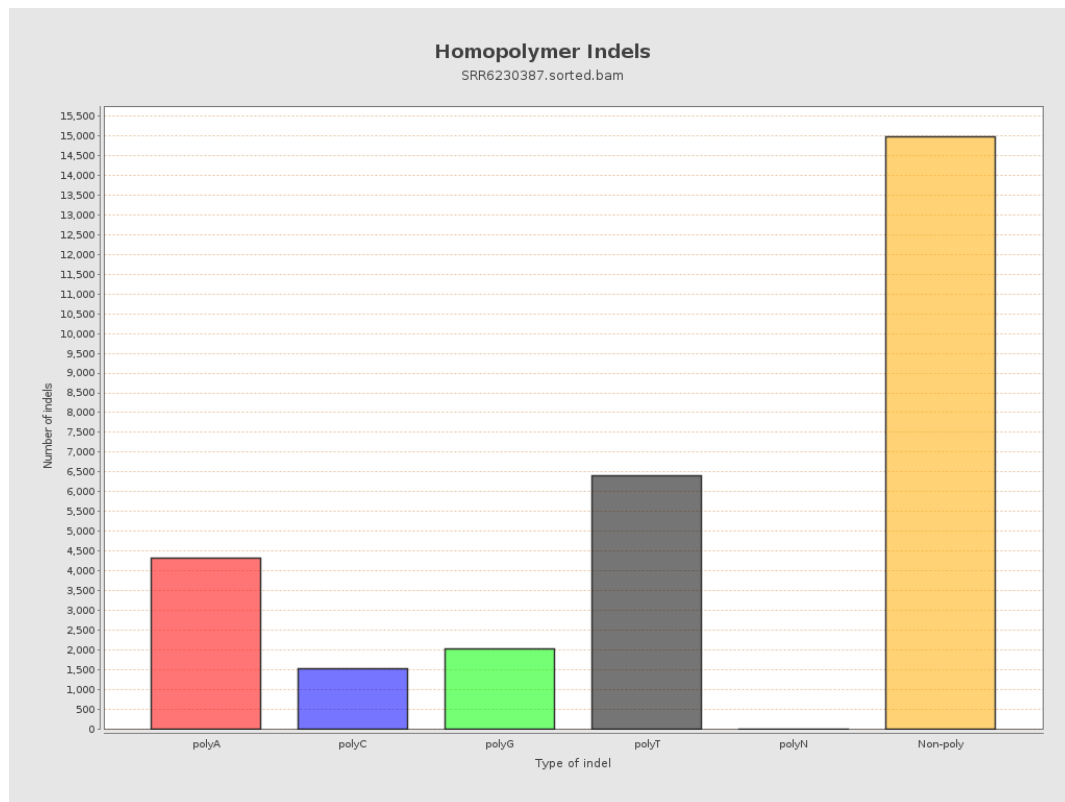
9. Results : Mapped Reads GC-content Distribution



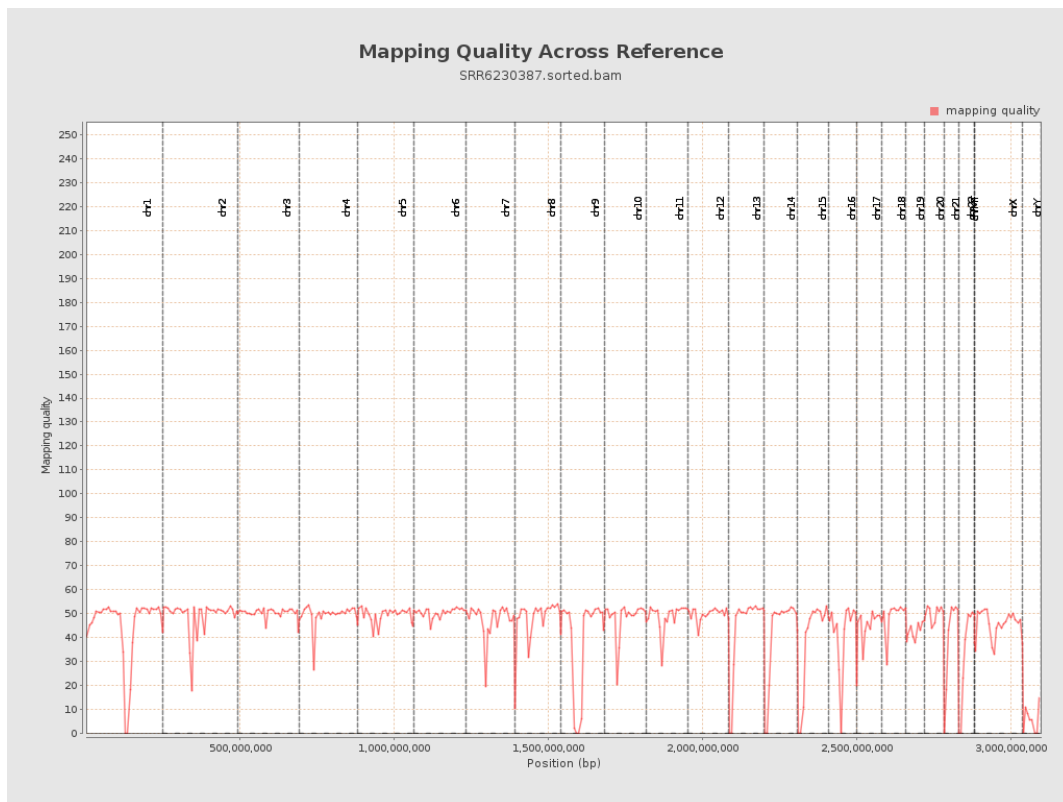
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

