

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:47:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013287.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_SRR6013287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013287.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:46:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,956,498
Mapped reads	1,702,947 / 87.04%
Unmapped reads	253,551 / 12.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,137 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	131,446 / 6.72%
Duplication rate	6.29%
Clipped reads	840,951 / 42.98%

2.2. ACGT Content

Number/percentage of A's	30,383,132 / 27.27%
Number/percentage of C's	20,068,758 / 18.01%
Number/percentage of T's	36,031,358 / 32.33%
Number/percentage of G's	24,950,228 / 22.39%
Number/percentage of N's	1,481 / 0%
GC Percentage	40.4%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3716
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2.4. Mapping Quality

Mean Mapping Quality	45.31
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2.5. Mismatches and indels

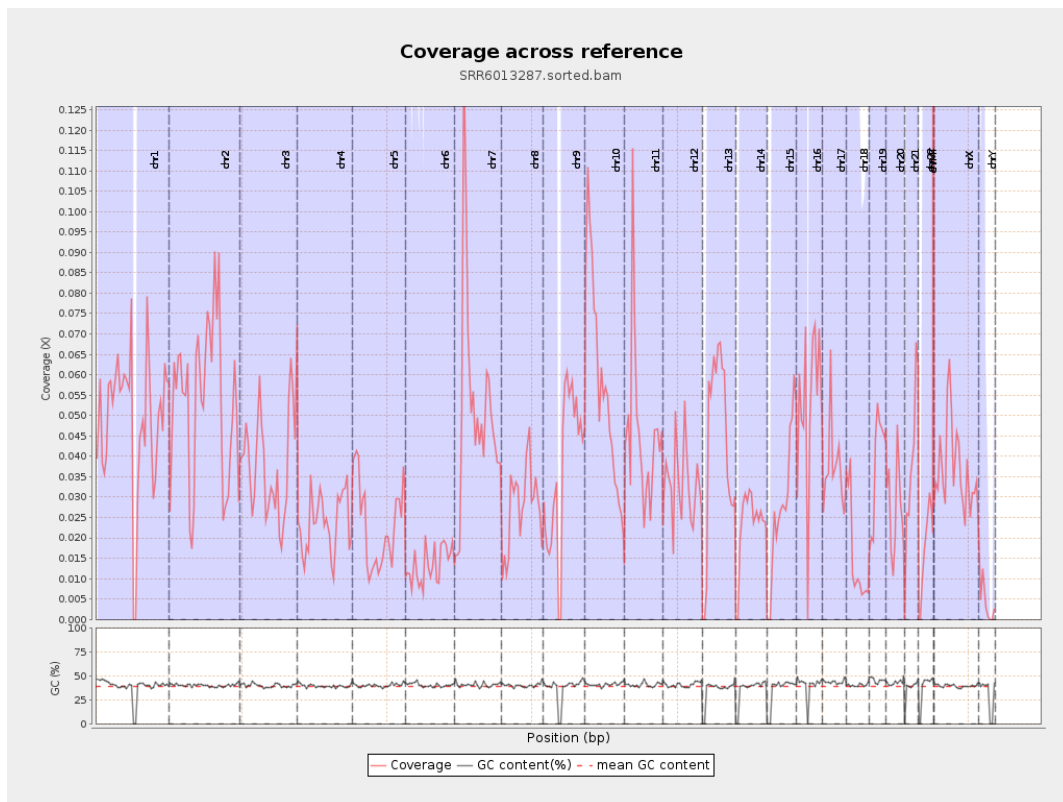
General error rate	0.75%
Mismatches	825,917
Insertions	7,993
Mapped reads with at least one insertion	0.47%
Deletions	33,891
Mapped reads with at least one deletion	1.97%
Homopolymer indels	46.18%

2.6. Chromosome stats

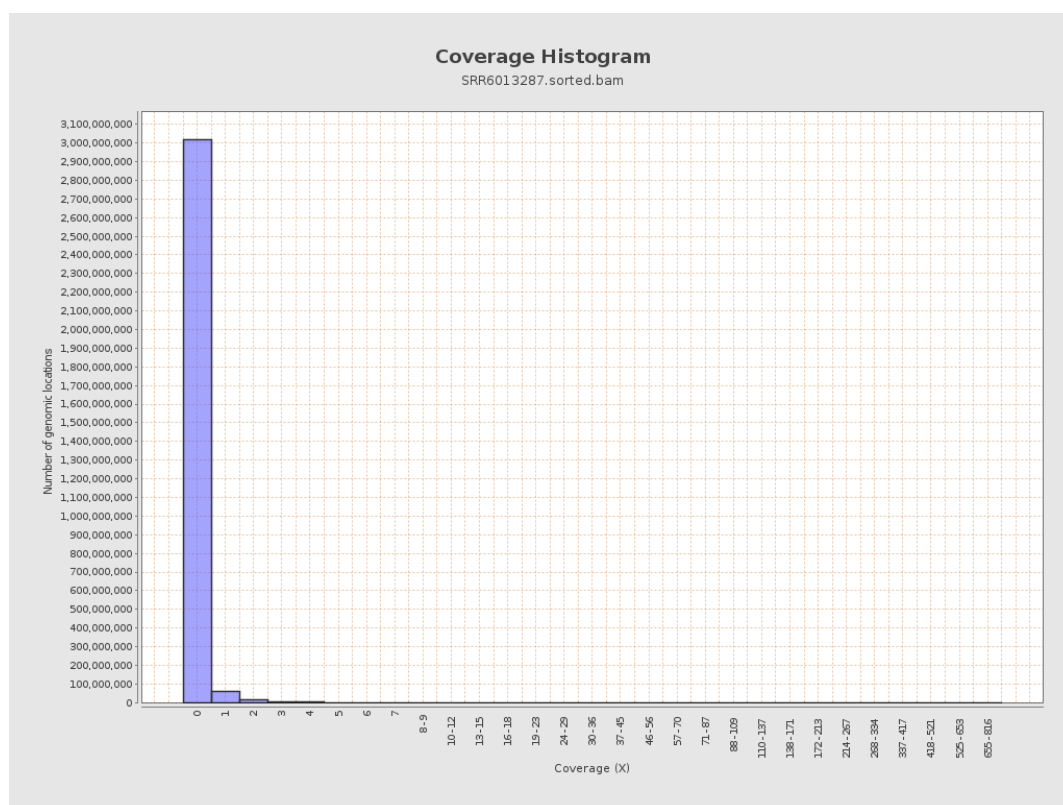
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12198780	0.0489	0.7404
chr2	243199373	13042781	0.0536	0.4524
chr3	198022430	7543034	0.0381	0.2571
chr4	191154276	4494076	0.0235	0.2279
chr5	180915260	4147258	0.0229	0.2001
chr6	171115067	2269722	0.0133	0.1702
chr7	159138663	8300691	0.0522	0.4056

chr8	146364022	3977167	0.0272	0.3671
chr9	141213431	5157975	0.0365	0.3335
chr10	135534747	7921483	0.0584	0.3924
chr11	135006516	6063317	0.0449	0.3959
chr12	133851895	4459752	0.0333	0.2434
chr13	115169878	4898334	0.0425	0.2736
chr14	107349540	2493223	0.0232	0.207
chr15	102531392	2896036	0.0282	0.2233
chr16	90354753	4789286	0.053	0.3104
chr17	81195210	2994659	0.0369	0.2923
chr18	78077248	1168342	0.015	0.5514
chr19	59128983	2286021	0.0387	0.5007
chr20	63025520	1670085	0.0265	0.2195
chr21	48129895	1841069	0.0383	0.2747
chr22	51304566	892597	0.0174	0.1657
chrMT	16571	12698	0.7663	1.1909
chrX	155270560	5724842	0.0369	0.282
chrY	59373566	250051	0.0042	0.1179

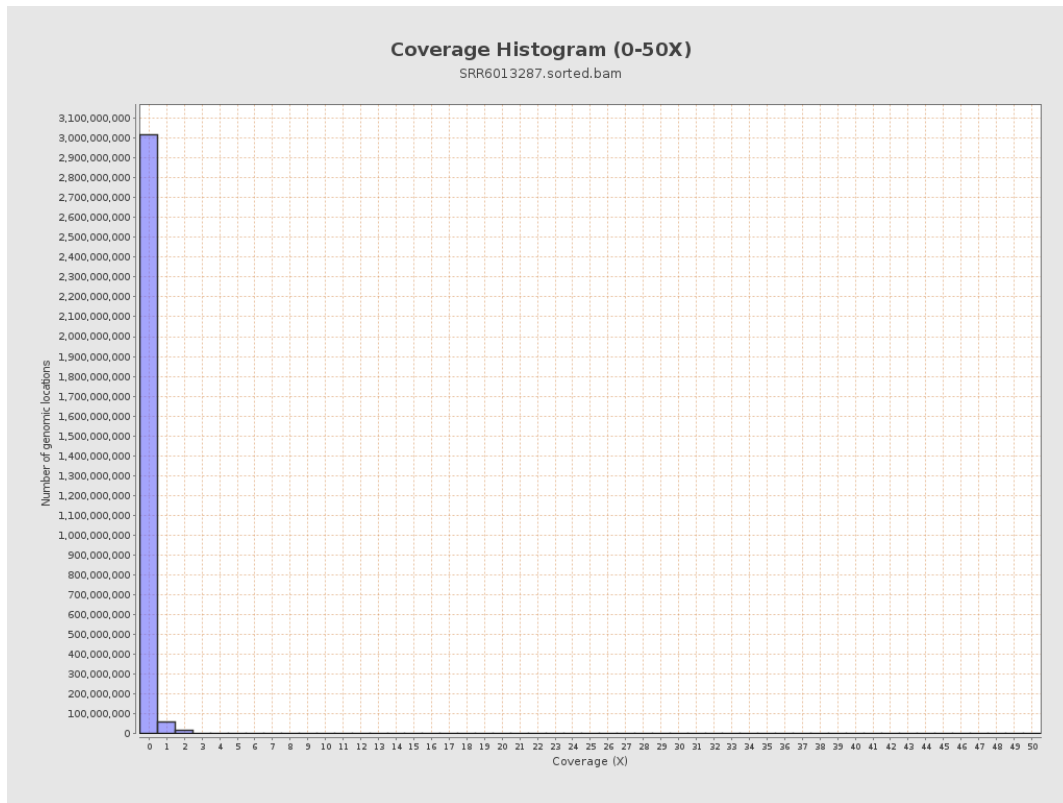
3. Results : Coverage across reference



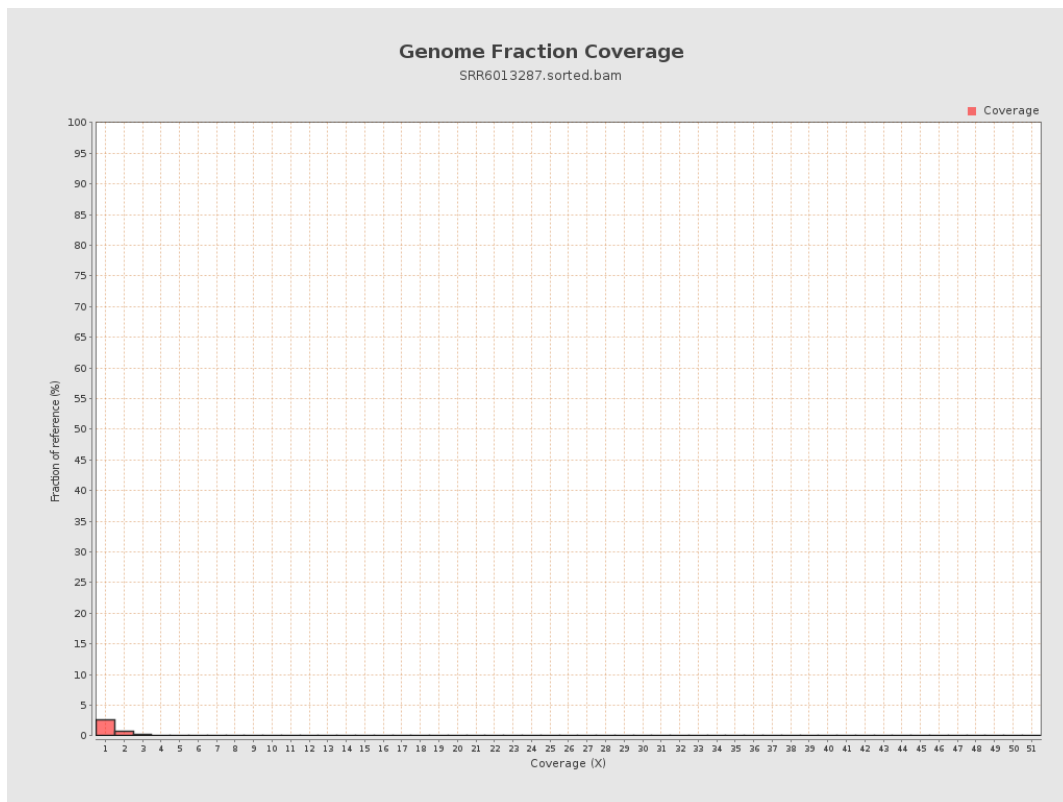
4. Results : Coverage Histogram



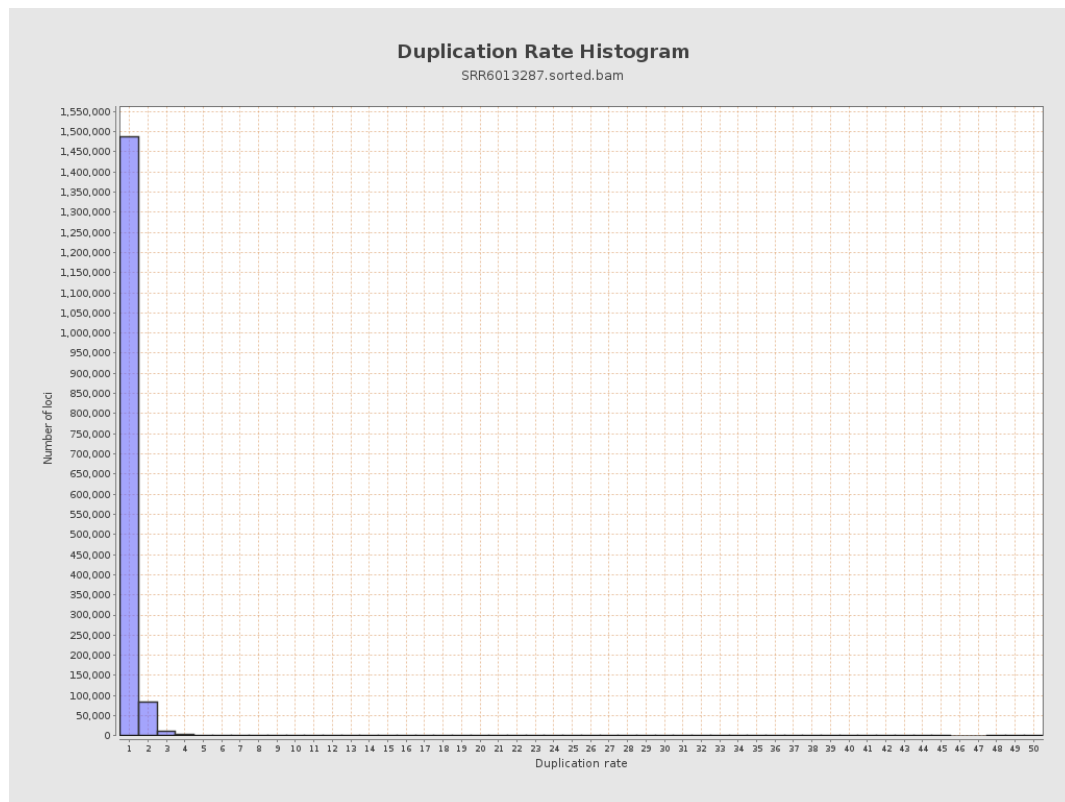
5. Results : Coverage Histogram (0-50X)



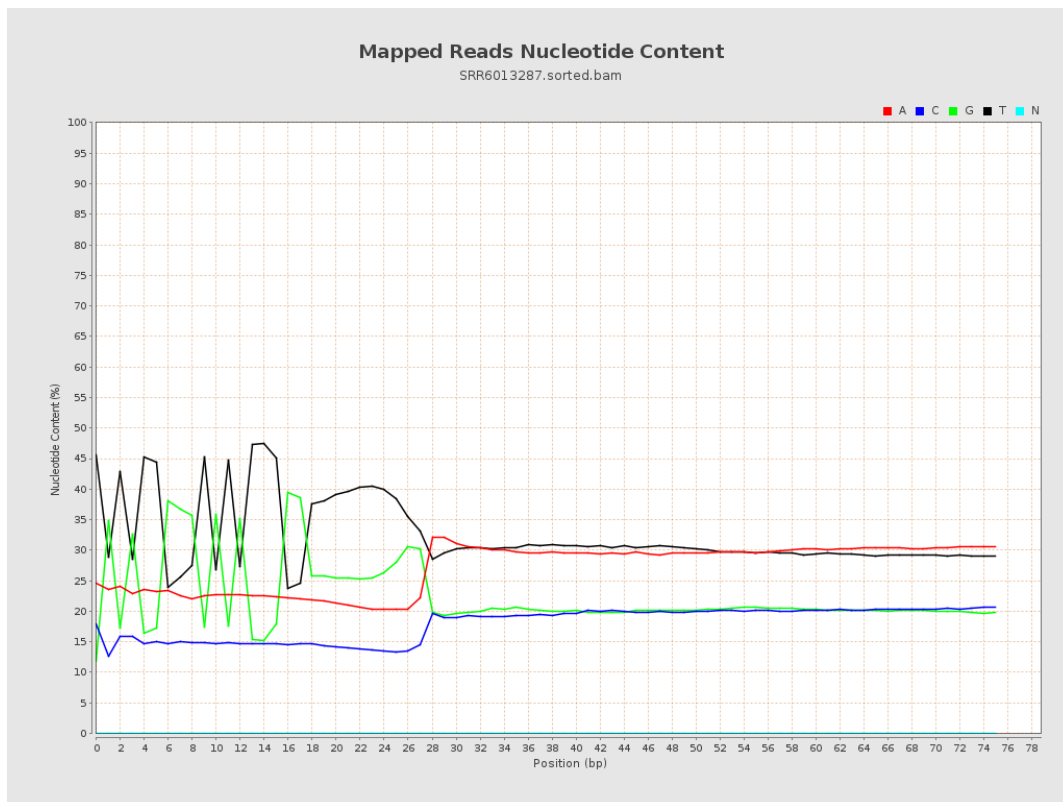
6. Results : Genome Fraction Coverage



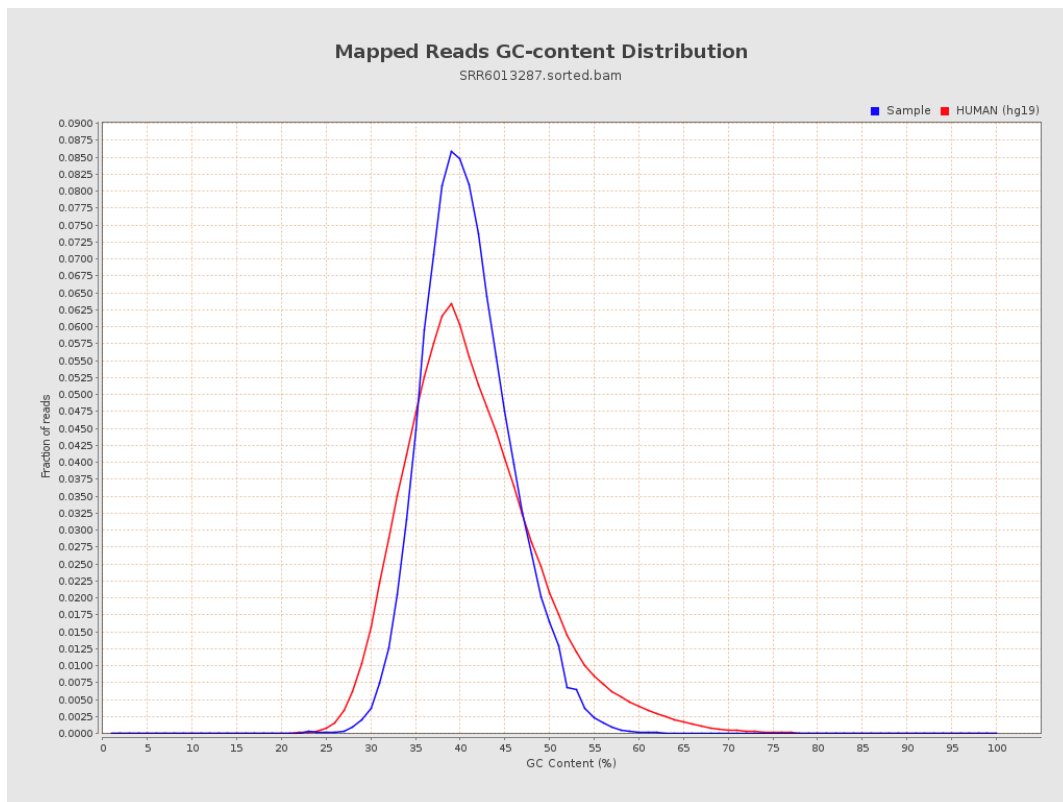
7. Results : Duplication Rate Histogram



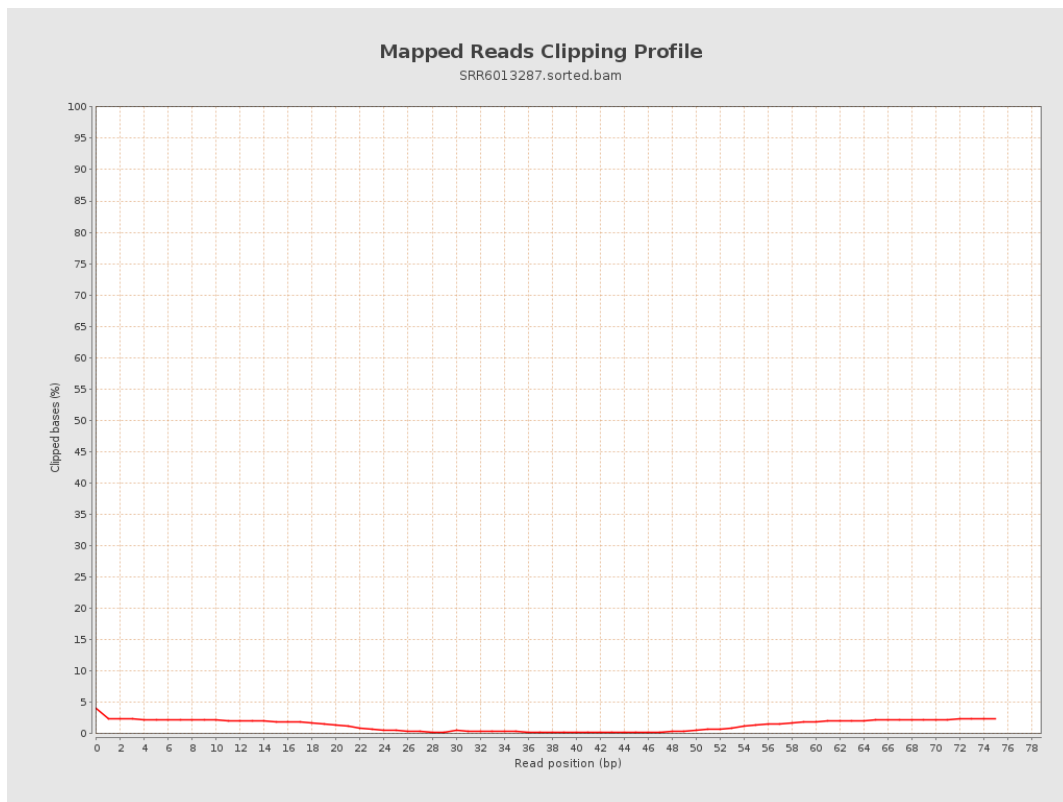
8. Results : Mapped Reads Nucleotide Content



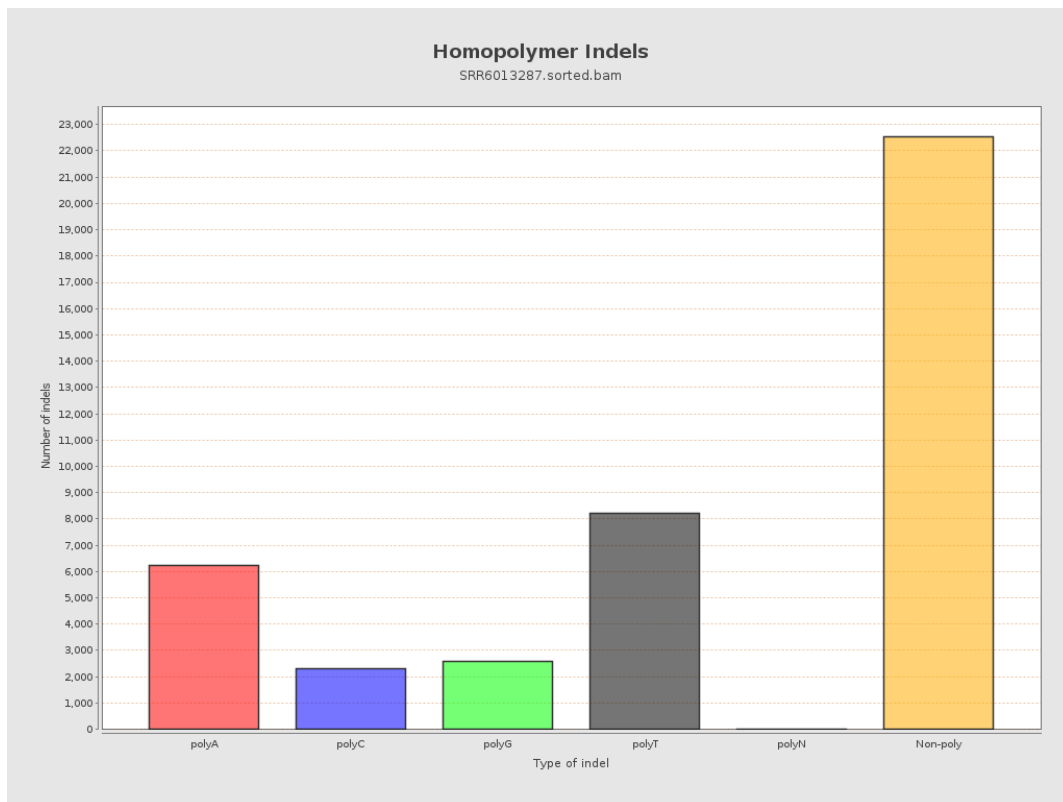
9. Results : Mapped Reads GC-content Distribution



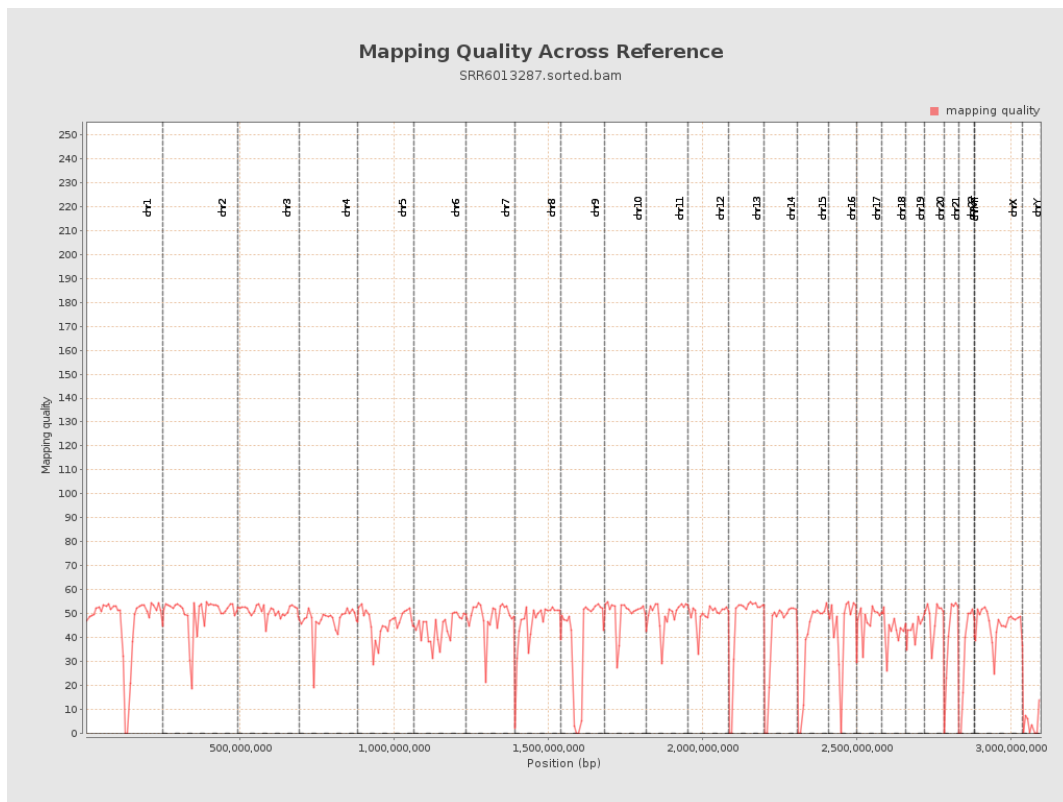
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

