

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:45:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080989.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_SRR3080989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:45:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,435,522
Mapped reads	2,362,938 / 68.78%
Unmapped reads	1,072,584 / 31.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,064 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	97,372 / 2.83%
Duplication rate	3.3%
Clipped reads	1,414,470 / 41.17%

2.2. ACGT Content

Number/percentage of A's	41,700,378 / 28.07%
Number/percentage of C's	30,877,588 / 20.79%
Number/percentage of T's	42,536,918 / 28.64%
Number/percentage of G's	33,420,187 / 22.5%
Number/percentage of N's	1,973 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.048

Standard Deviation	0.3437
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2.4. Mapping Quality

Mean Mapping Quality	43.8
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2.5. Mismatches and indels

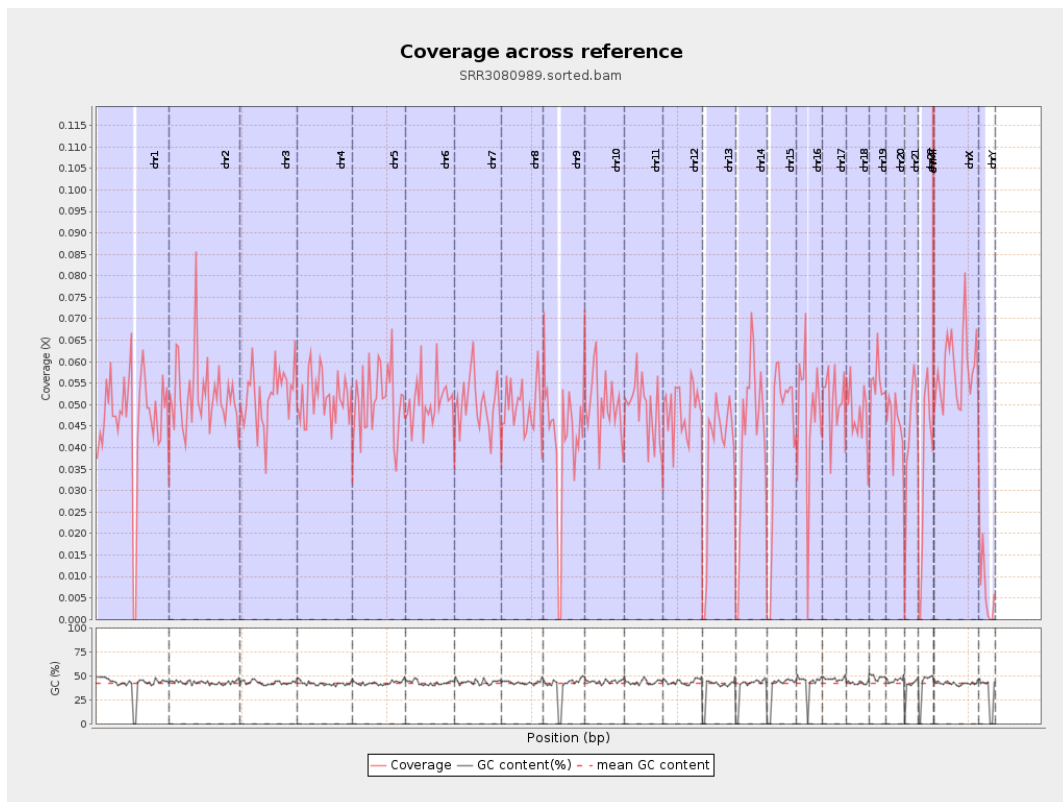
General error rate	0.78%
Mismatches	1,130,798
Insertions	11,142
Mapped reads with at least one insertion	0.47%
Deletions	30,799
Mapped reads with at least one deletion	1.29%
Homopolymer indels	44.94%

2.6. Chromosome stats

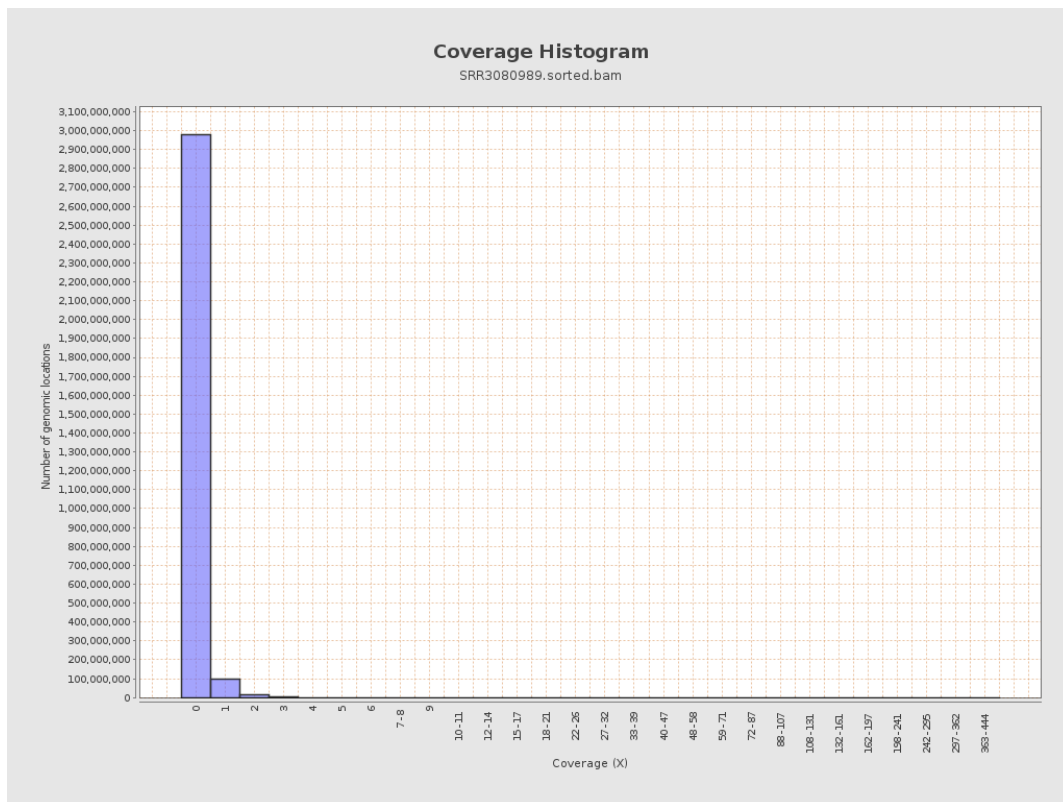
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11599031	0.0465	0.449
chr2	243199373	12762109	0.0525	0.4141
chr3	198022430	10336349	0.0522	0.2759
chr4	191154276	9893894	0.0518	0.2904
chr5	180915260	9240585	0.0511	0.2741
chr6	171115067	8654796	0.0506	0.3119
chr7	159138663	7994689	0.0502	0.427

chr8	146364022	7218250	0.0493	0.3585
chr9	141213431	5751965	0.0407	0.3491
chr10	135534747	6769715	0.0499	0.3408
chr11	135006516	6587066	0.0488	0.3643
chr12	133851895	6560262	0.049	0.2722
chr13	115169878	4380219	0.038	0.2355
chr14	107349540	4657220	0.0434	0.2751
chr15	102531392	4404331	0.043	0.269
chr16	90354753	4327650	0.0479	0.2931
chr17	81195210	4121973	0.0508	0.2928
chr18	78077248	3743815	0.048	0.5968
chr19	59128983	3240428	0.0548	0.3927
chr20	63025520	2843790	0.0451	0.2662
chr21	48129895	2054339	0.0427	0.2714
chr22	51304566	1758768	0.0343	0.2238
chrMT	16571	147827	8.9208	5.8567
chrX	155270560	9130130	0.0588	0.3228
chrY	59373566	412013	0.0069	0.1463

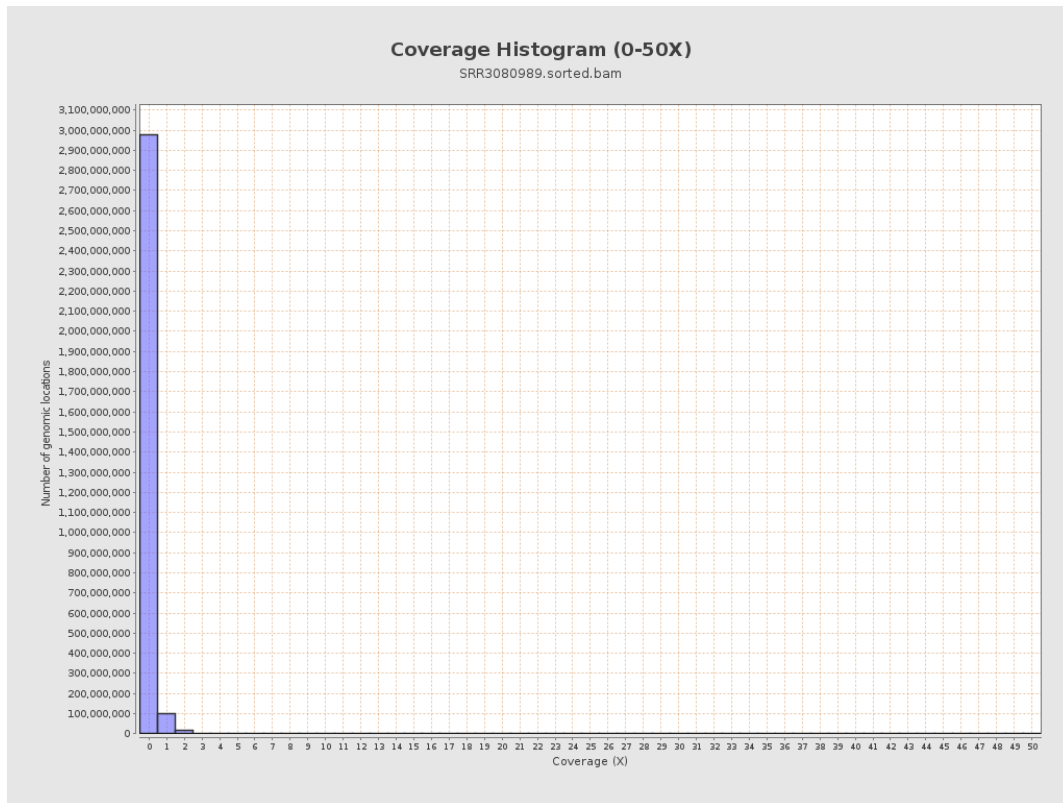
3. Results : Coverage across reference



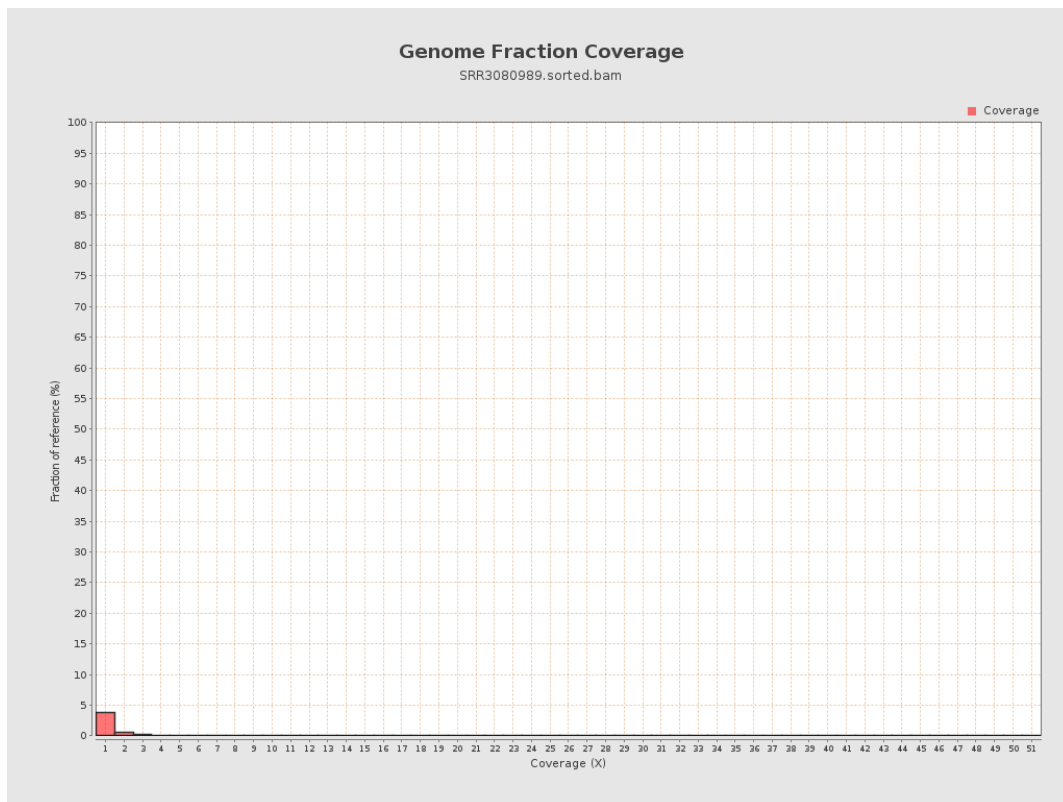
4. Results : Coverage Histogram



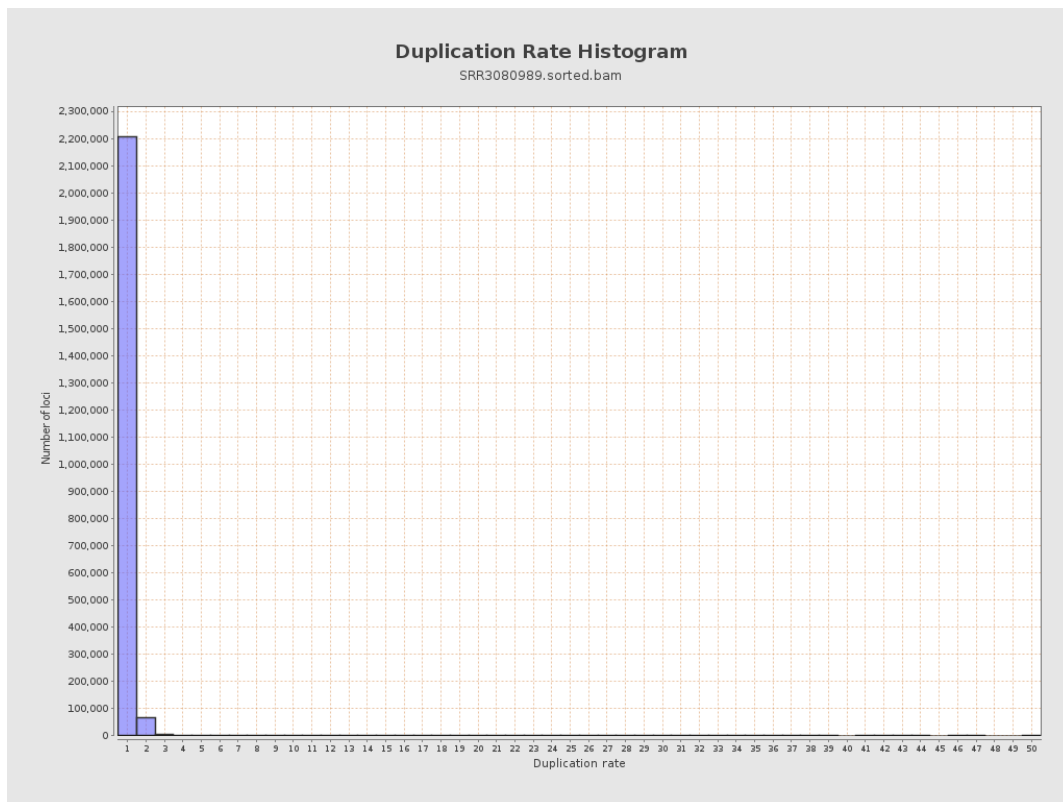
5. Results : Coverage Histogram (0-50X)



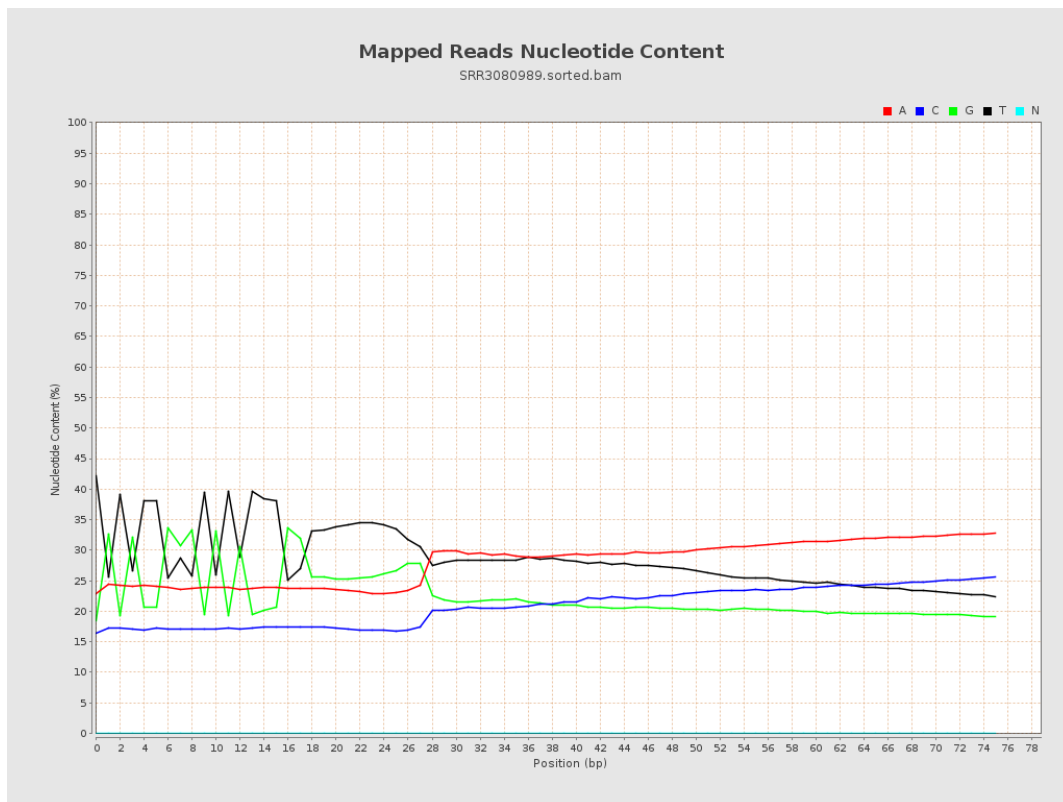
6. Results : Genome Fraction Coverage



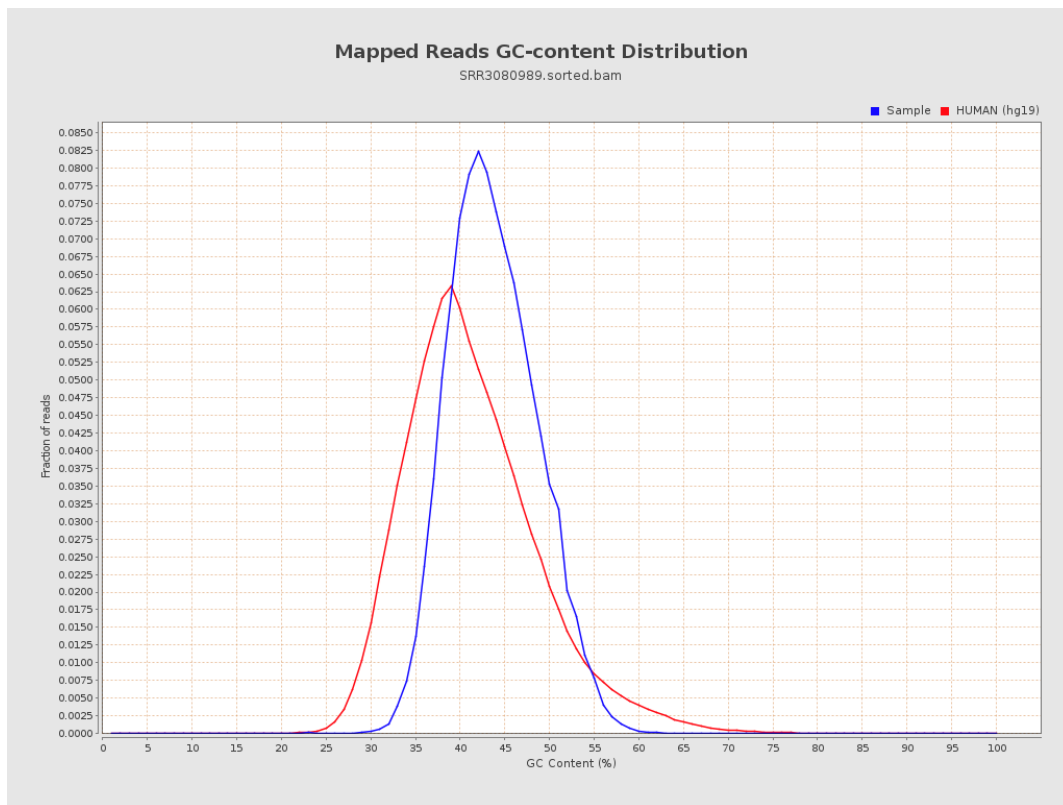
7. Results : Duplication Rate Histogram



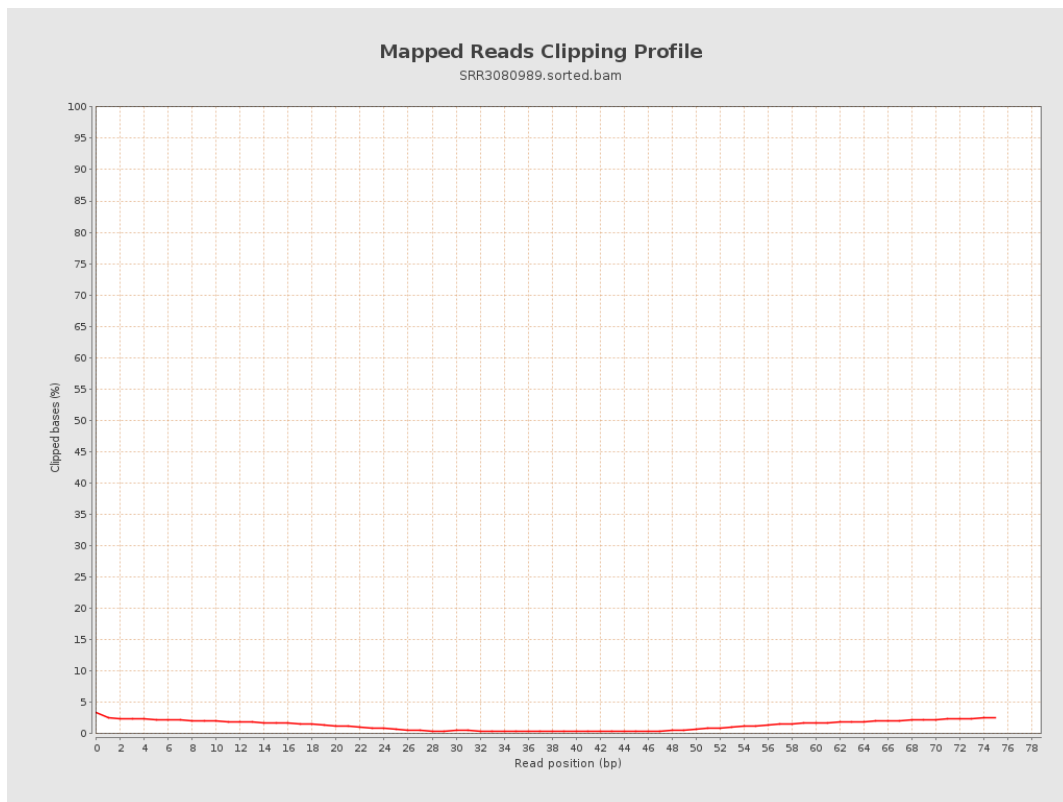
8. Results : Mapped Reads Nucleotide Content



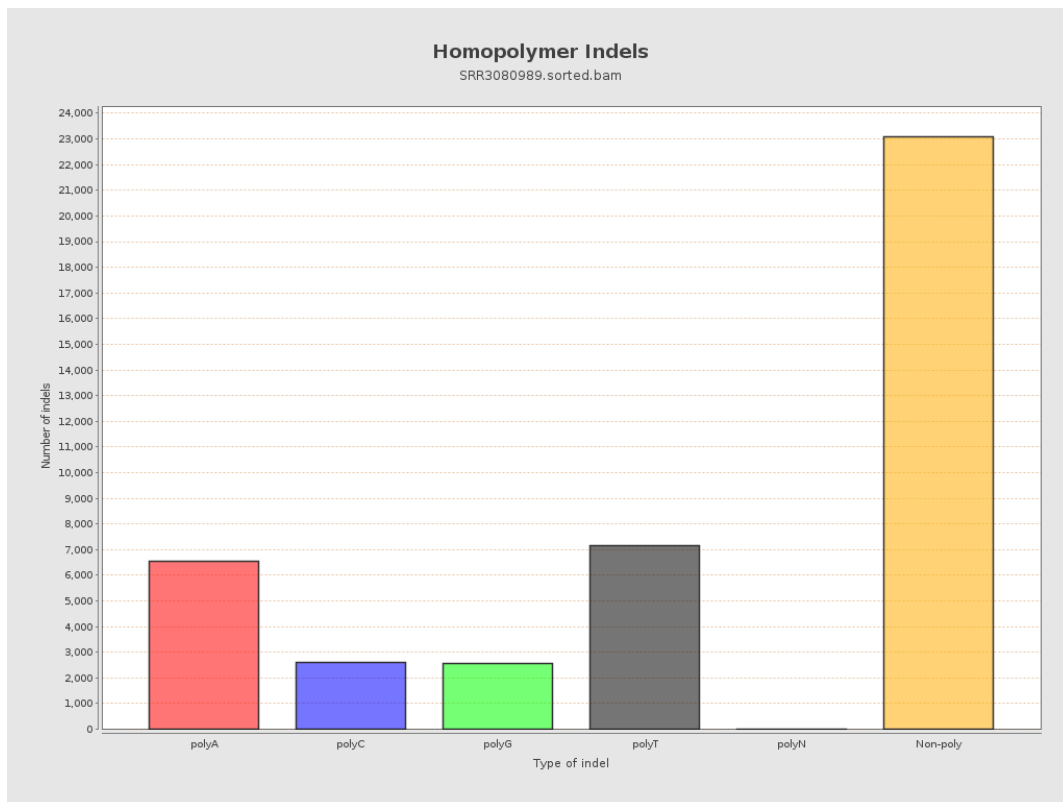
9. Results : Mapped Reads GC-content Distribution



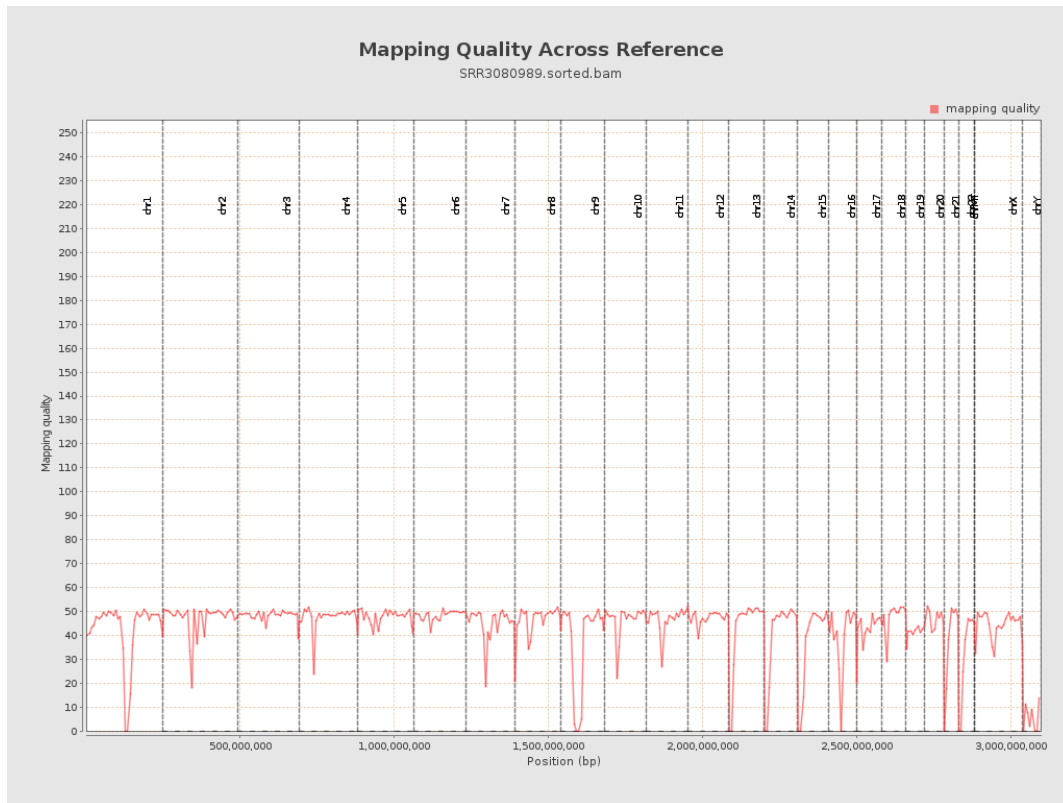
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

