

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:04:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080689.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_SRR3080689 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080689.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:04:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080689.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,037,567
Mapped reads	2,723,899 / 89.67%
Unmapped reads	313,668 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,288 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	146,206 / 4.81%
Duplication rate	4.47%
Clipped reads	798,337 / 26.28%

2.2. ACGT Content

Number/percentage of A's	58,855,277 / 30.55%
Number/percentage of C's	35,385,624 / 18.37%
Number/percentage of T's	60,297,243 / 31.3%
Number/percentage of G's	38,084,769 / 19.77%
Number/percentage of N's	2,901 / 0%
GC Percentage	38.14%

2.3. Coverage

Mean	0.0622

Standard Deviation	0.5632
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2.4. Mapping Quality

Mean Mapping Quality	48.29
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2.5. Mismatches and indels

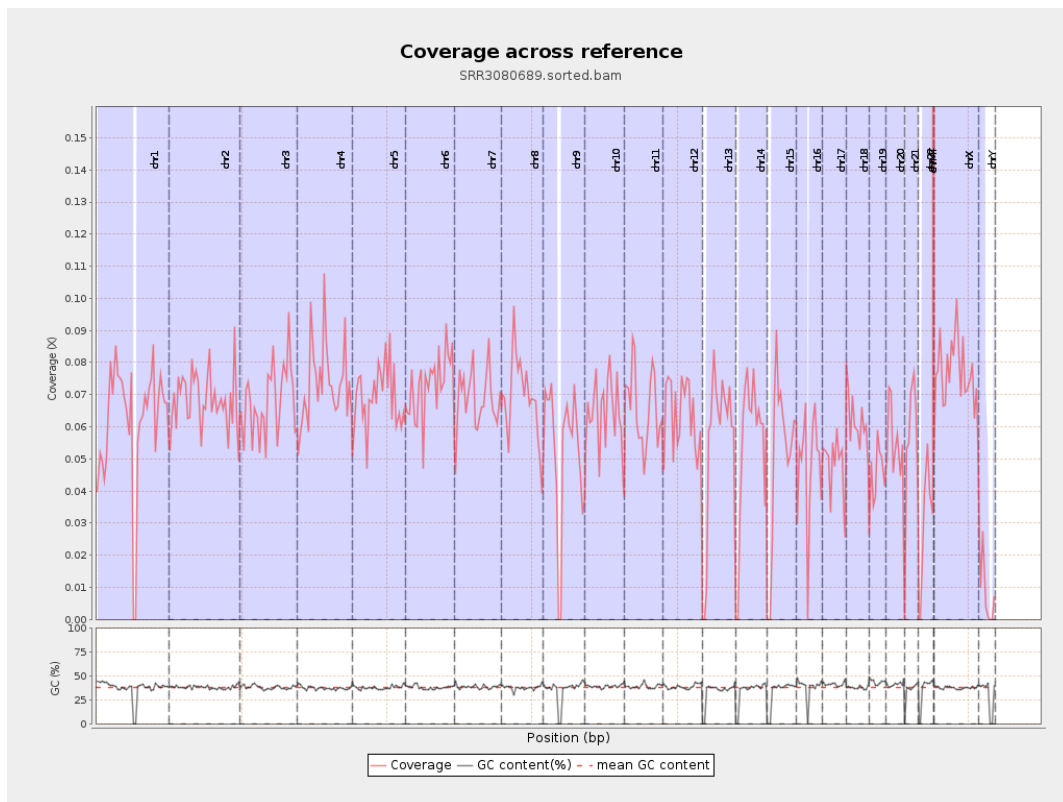
General error rate	0.81%
Mismatches	1,531,165
Insertions	15,130
Mapped reads with at least one insertion	0.55%
Deletions	40,255
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.76%

2.6. Chromosome stats

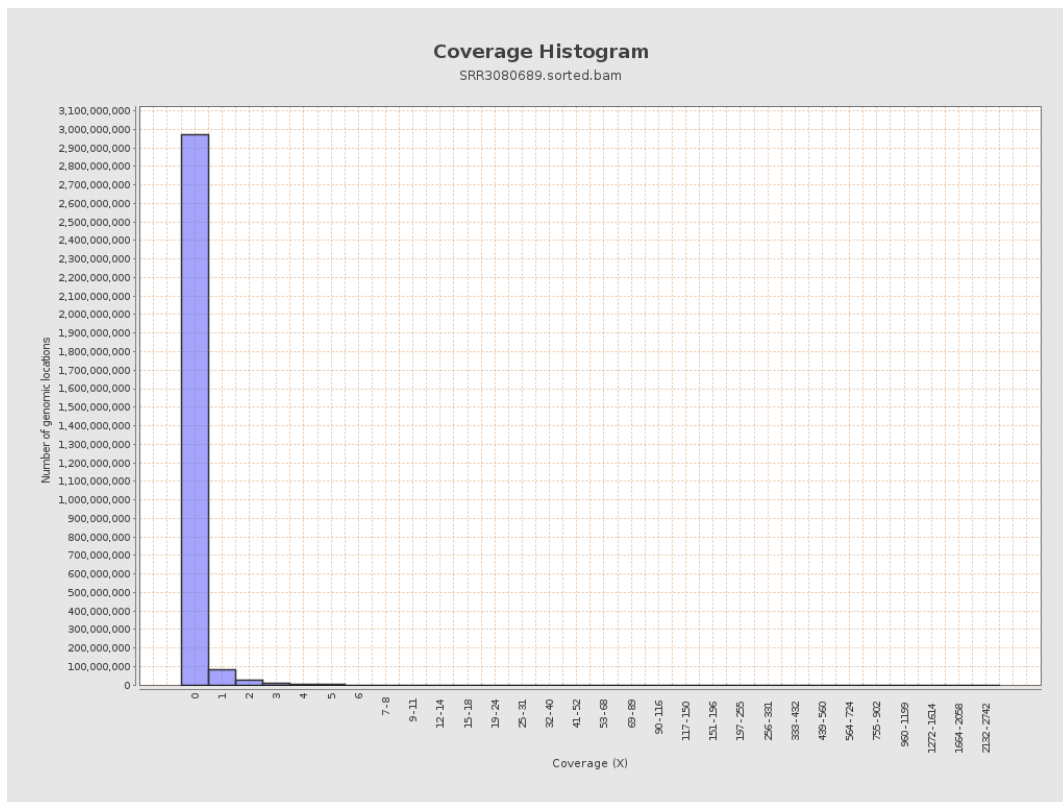
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15445764	0.062	0.571
chr2	243199373	16637979	0.0684	0.4523
chr3	198022430	13440786	0.0679	0.3729
chr4	191154276	13959016	0.073	0.422
chr5	180915260	12552269	0.0694	0.3785
chr6	171115067	12472395	0.0729	0.4192
chr7	159138663	10979553	0.069	0.5503

chr8	146364022	10052363	0.0687	1.7161
chr9	141213431	7493819	0.0531	0.3985
chr10	135534747	8788057	0.0648	0.4543
chr11	135006516	8831915	0.0654	0.3896
chr12	133851895	8447008	0.0631	0.3613
chr13	115169878	6331240	0.055	0.3386
chr14	107349540	5782515	0.0539	0.3477
chr15	102531392	5277202	0.0515	0.3203
chr16	90354753	4317452	0.0478	0.3328
chr17	81195210	3847769	0.0474	0.3248
chr18	78077248	4802176	0.0615	0.5955
chr19	59128983	2699851	0.0457	0.4362
chr20	63025520	3434241	0.0545	0.3414
chr21	48129895	2646080	0.055	0.3584
chr22	51304566	1514932	0.0295	0.2337
chrMT	16571	580594	35.0368	19.2771
chrX	155270560	11862771	0.0764	0.4045
chrY	59373566	501643	0.0084	0.2298

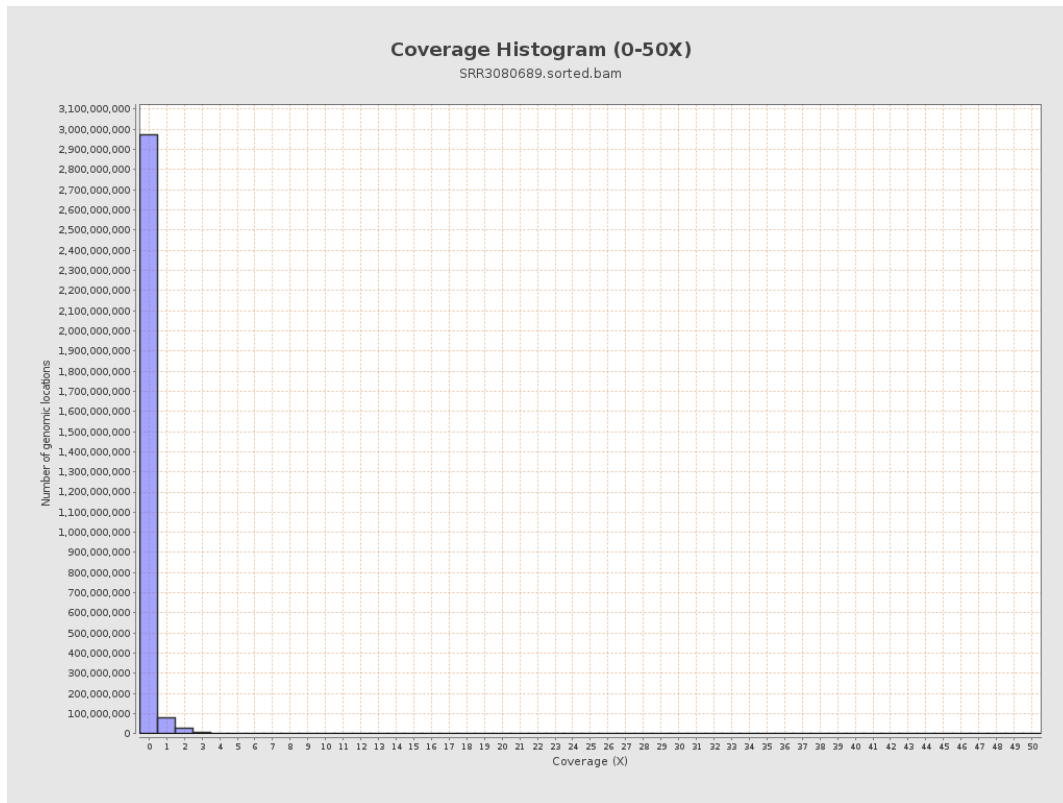
3. Results : Coverage across reference



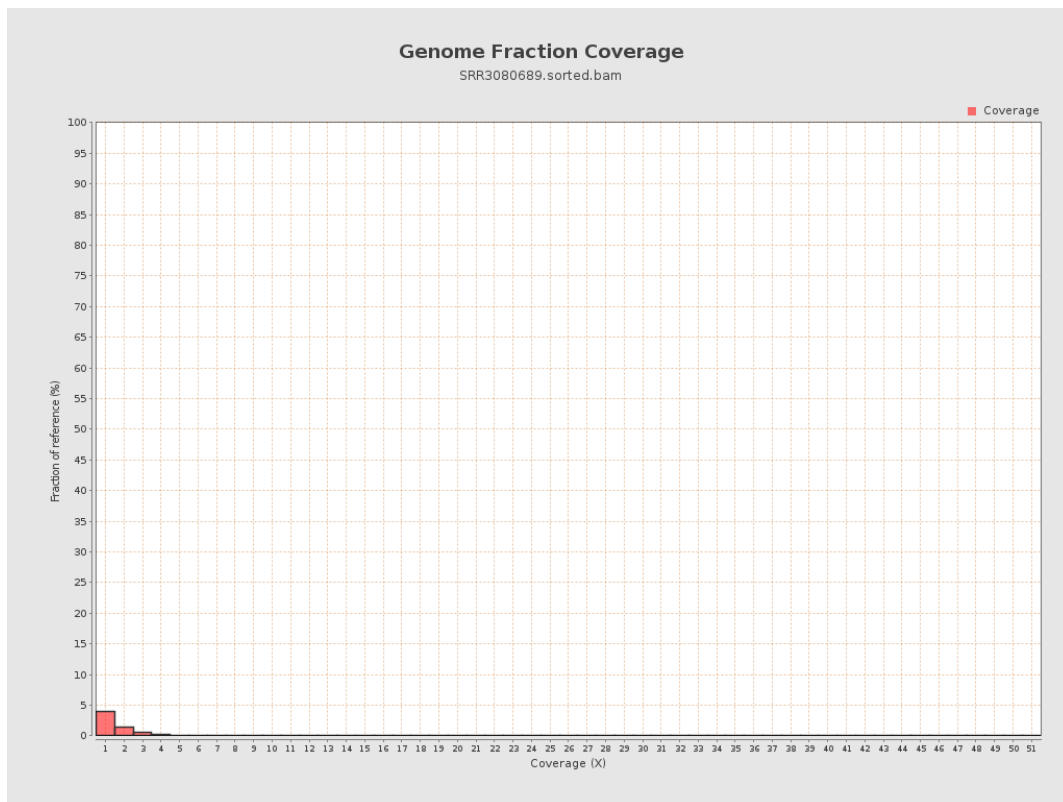
4. Results : Coverage Histogram



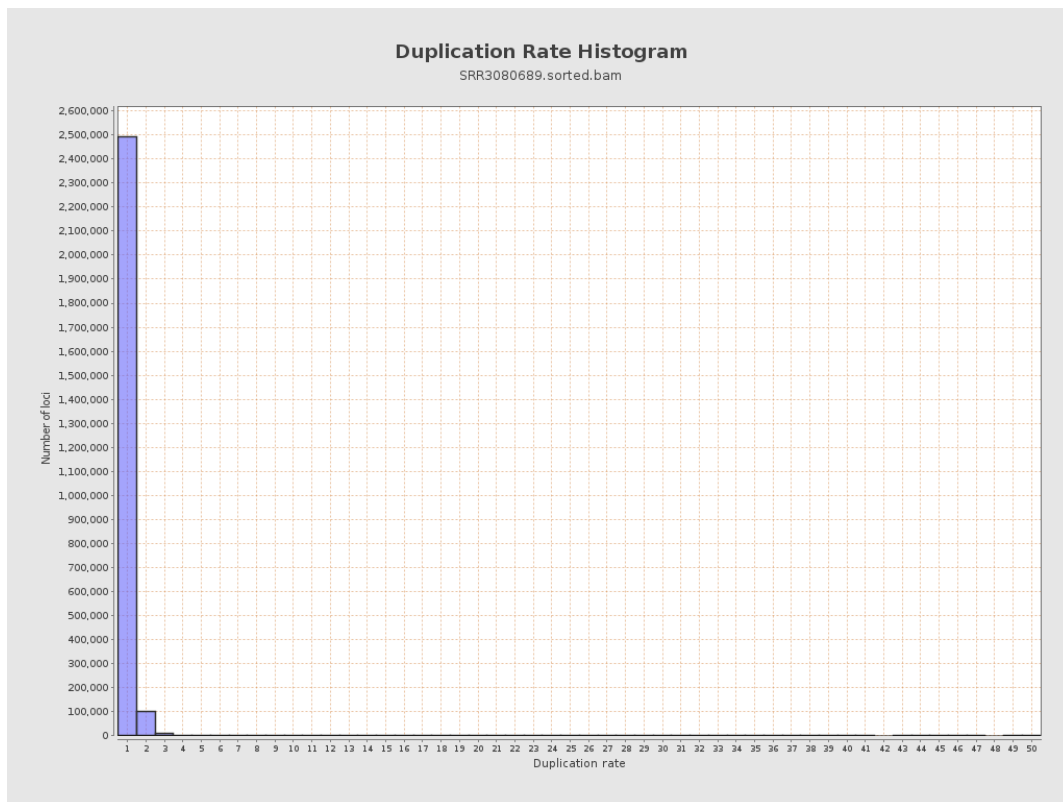
5. Results : Coverage Histogram (0-50X)



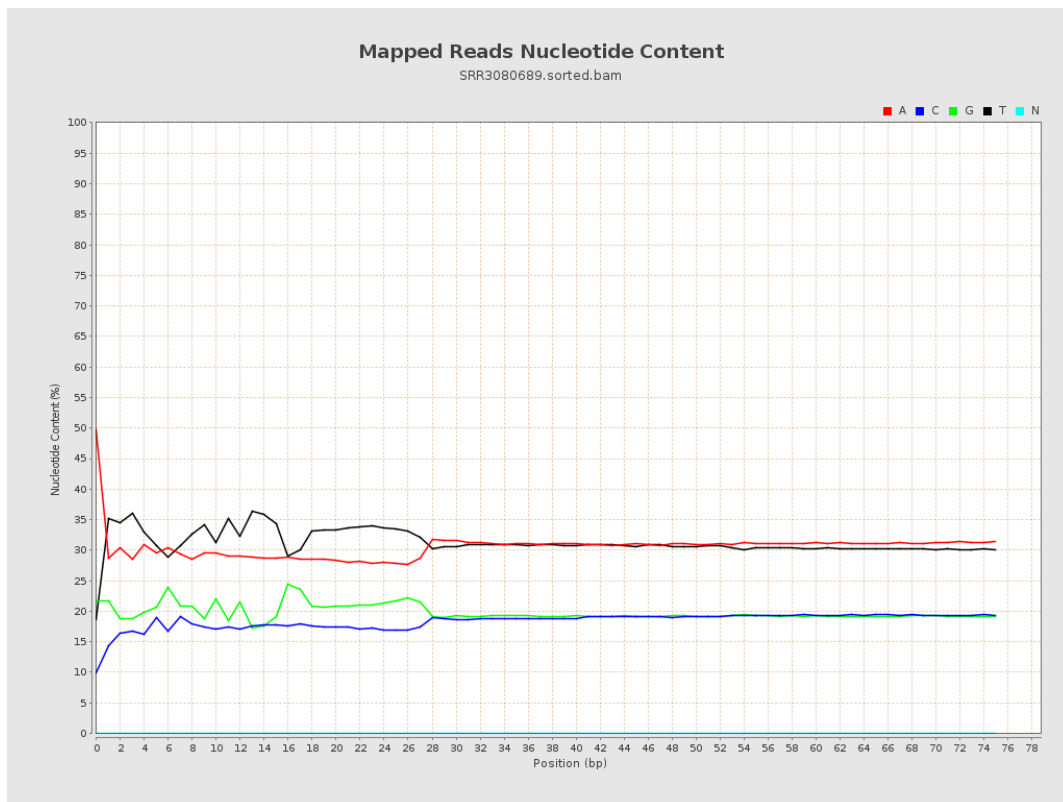
6. Results : Genome Fraction Coverage



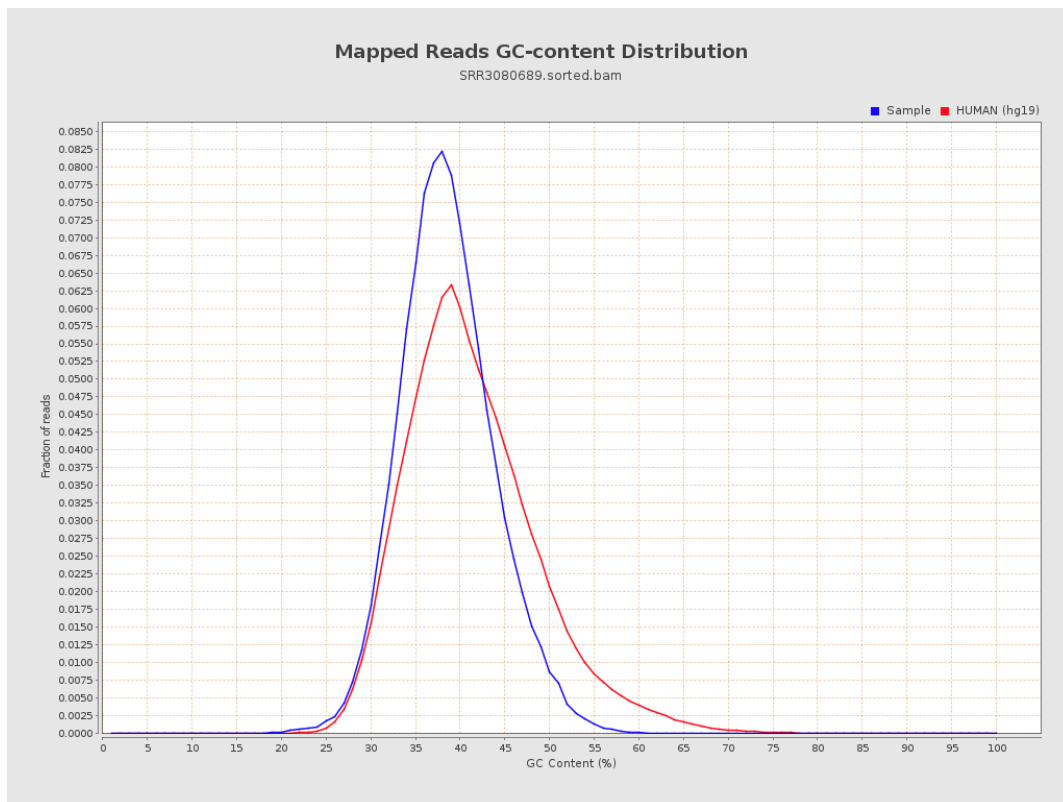
7. Results : Duplication Rate Histogram



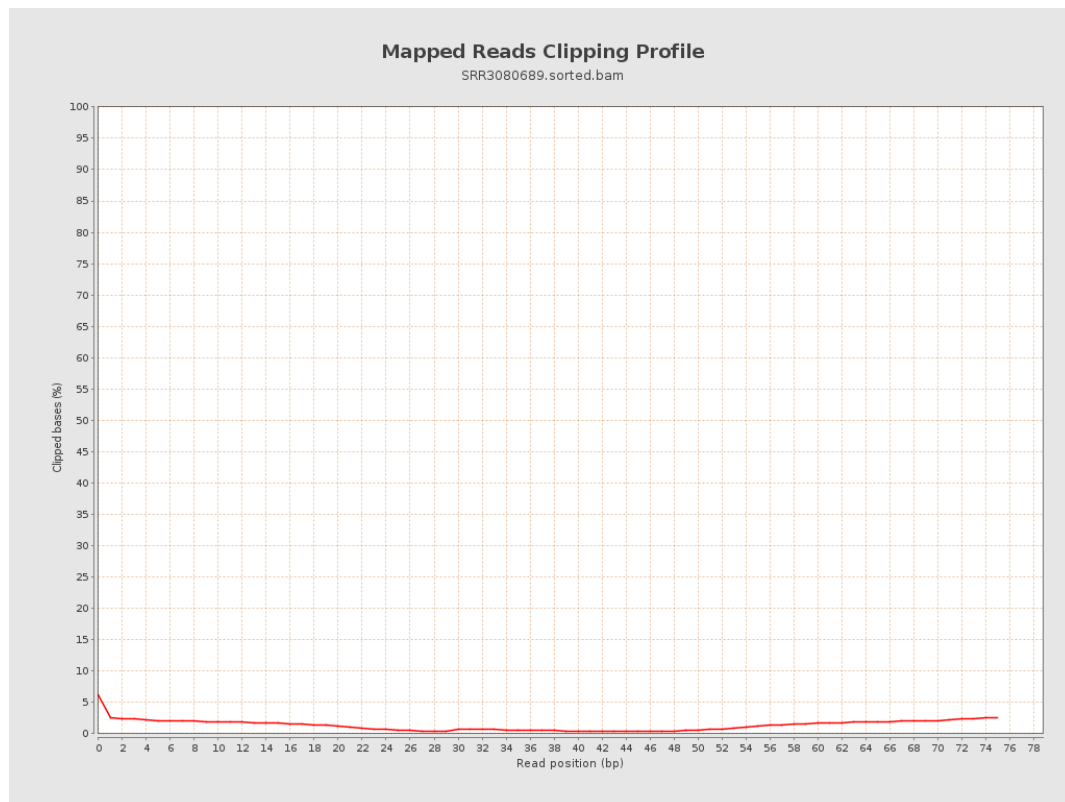
8. Results : Mapped Reads Nucleotide Content



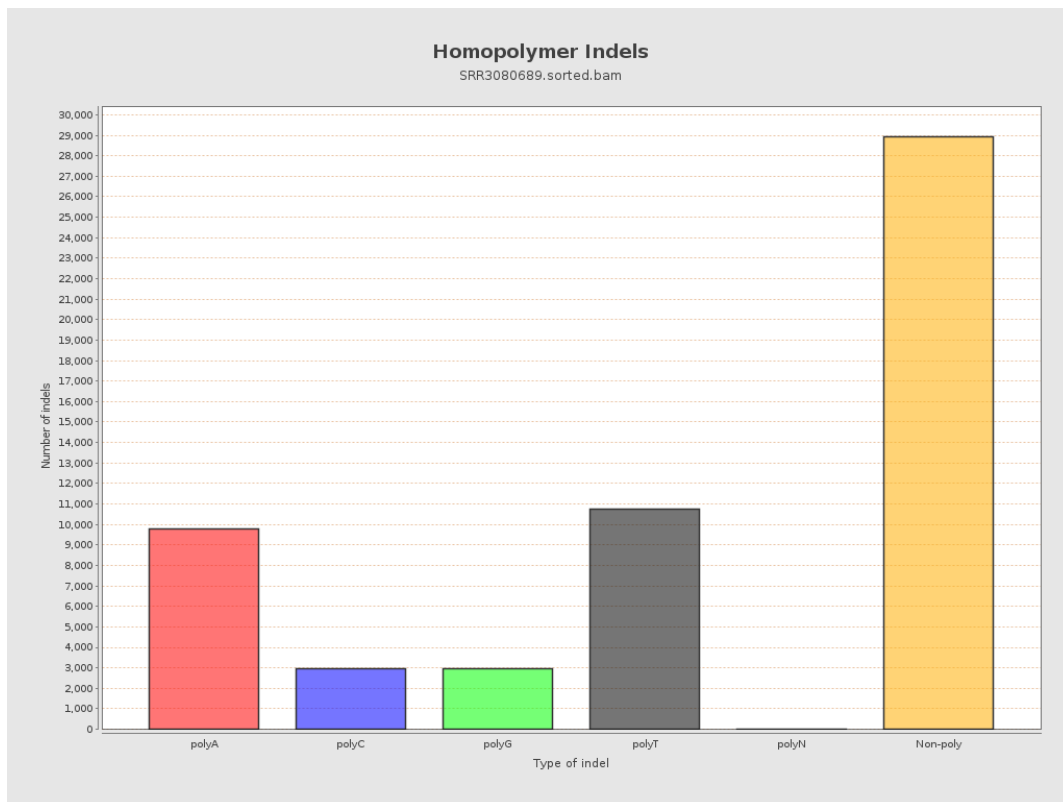
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

