Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:32:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080642.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_SRR3080642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080642.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:32:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080642.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,662,902
Mapped reads	3,098,749 / 84.6%
Unmapped reads	564,153 / 15.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,938 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	154,153 / 4.21%
Duplication rate	4.08%
Clipped reads	1,634,402 / 44.62%

2.2. ACGT Content

Number/percentage of A's	54,349,368 / 26.78%
Number/percentage of C's	35,337,486 / 17.42%
Number/percentage of T's	66,594,420 / 32.82%
Number/percentage of G's	46,470,035 / 22.9%
Number/percentage of N's	159,105 / 0.08%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0656

Standard Deviation	0.4802

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

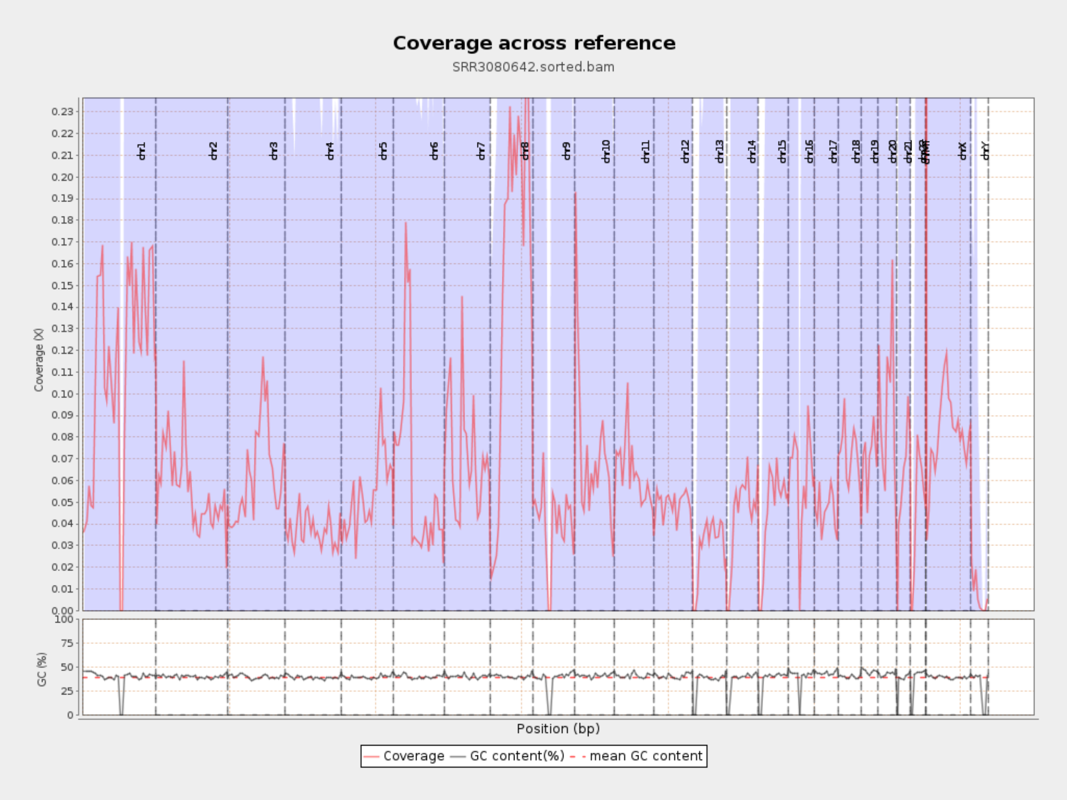
General error rate	0.89%
Mismatches	1,780,003
Insertions	17,796
Mapped reads with at least one insertion	0.57%
Deletions	50,992
Mapped reads with at least one deletion	1.63%
Homopolymer indels	47.38%

2.6. Chromosome stats

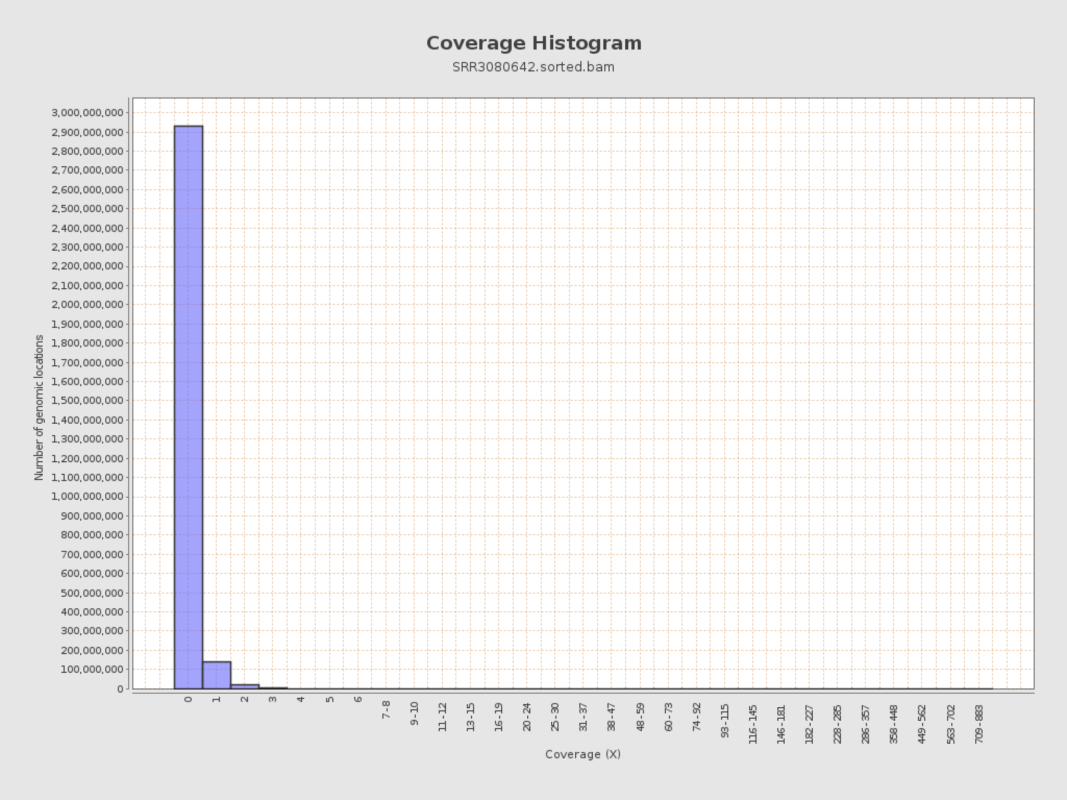
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27631963	0.1109	0.778
chr2	243199373	13737627	0.0565	0.5075
chr3	198022430	12494363	0.0631	0.2895
chr4	191154276	7089267	0.0371	0.233
chr5	180915260	9758395	0.0539	0.2669
chr6	171115067	10835617	0.0633	0.4466
chr7	159138663	11511573	0.0723	1.0251

chr8	146364022	23022443	0.1573	0.6632
chr9	141213431	5702007	0.0404	0.3746
chr10	135534747	9967718	0.0735	0.4287
chr11	135006516	8510844	0.063	0.3576
chr12	133851895	6597806	0.0493	0.2589
chr13	115169878	3390870	0.0294	0.1951
chr14	107349540	4681475	0.0436	0.2592
chr15	102531392	4501124	0.0439	0.2415
chr16	90354753	5413593	0.0599	0.3032
chr17	81195210	3779586	0.0465	0.2893
chr18	78077248	5730723	0.0734	0.6146
chr19	59128983	4144707	0.0701	0.5021
chr20	63025520	5912309	0.0938	0.3661
chr21	48129895	2894292	0.0601	0.2962
chr22	51304566	2370247	0.0462	0.246
chrMT	16571	195964	11.8257	8.1534
chrX	155270560	12693968	0.0818	0.3921
chrY	59373566	424742	0.0072	0.1402

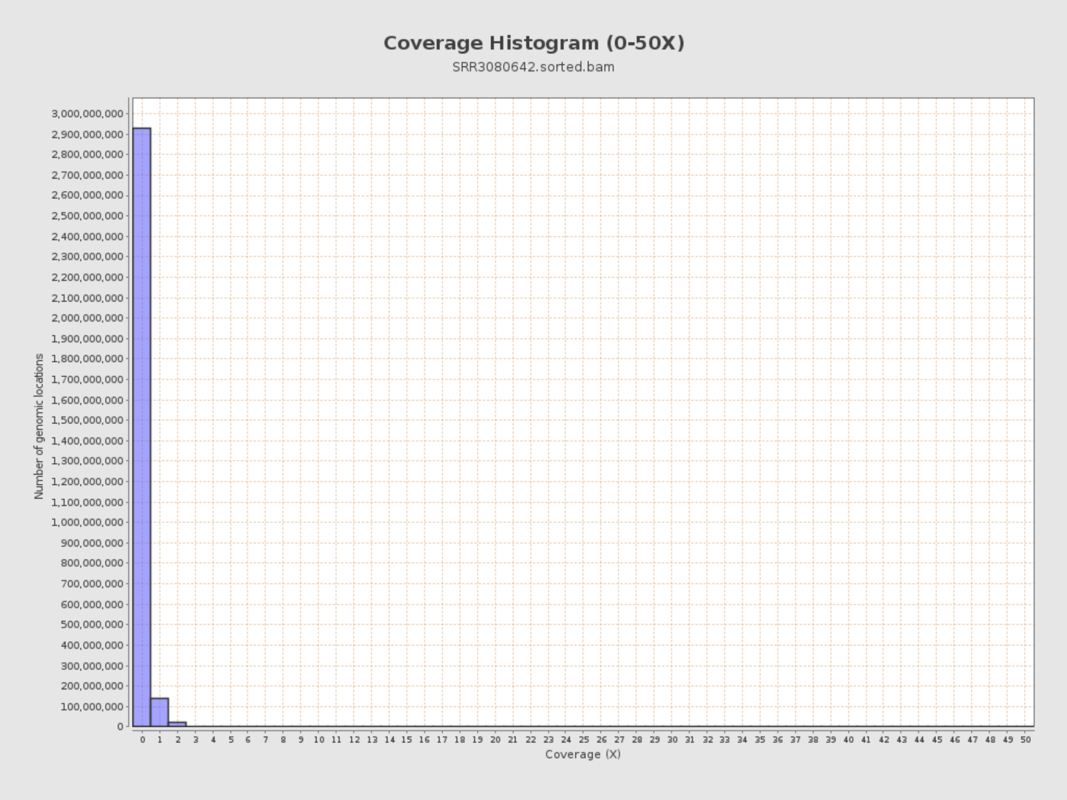
3. Results : Coverage across reference



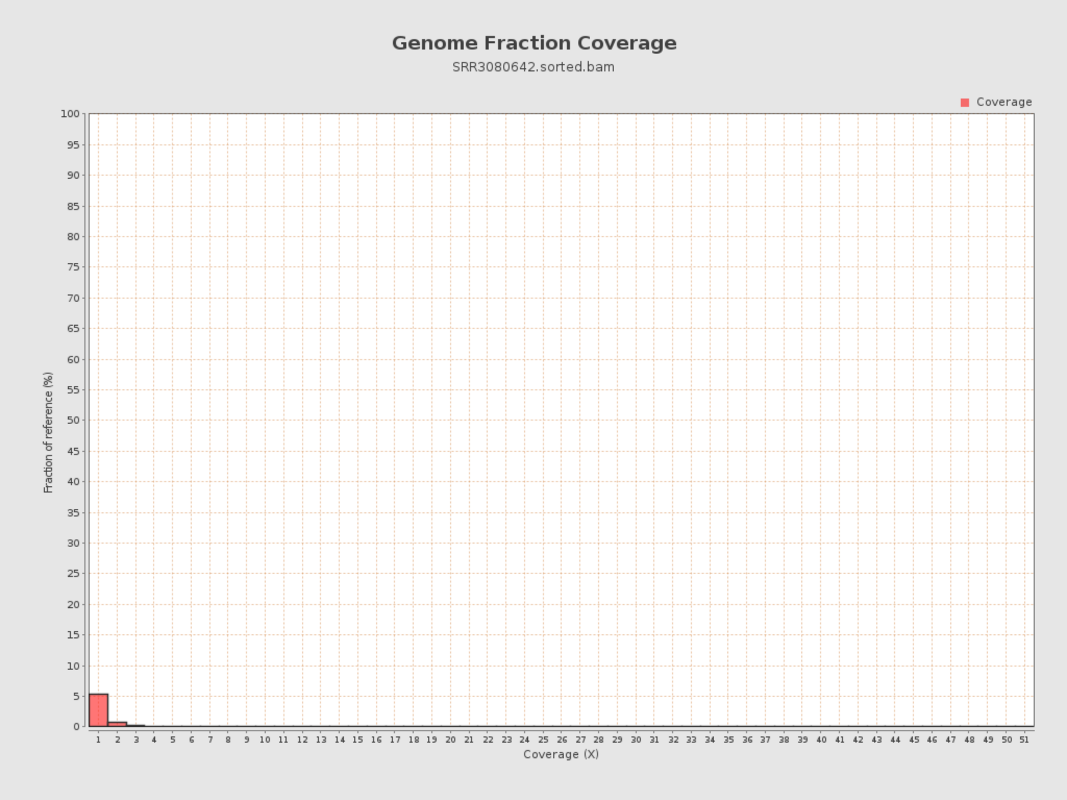
4. Results : Coverage Histogram



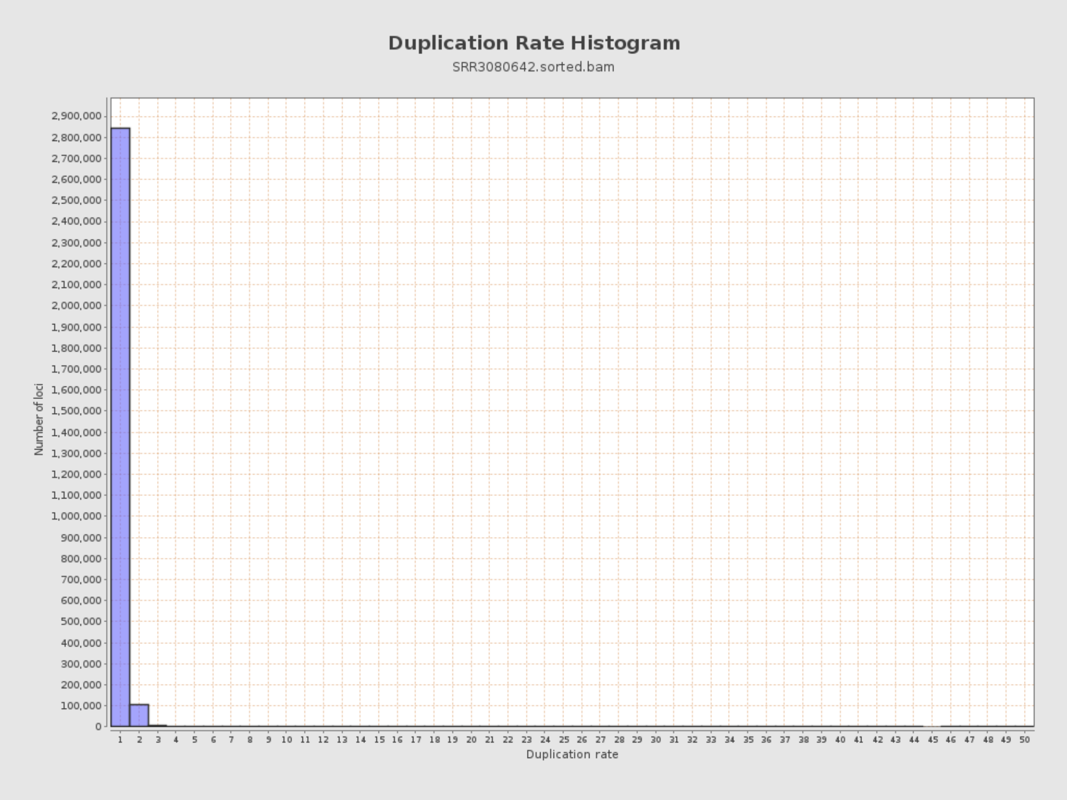
5. Results : Coverage Histogram (0-50X)



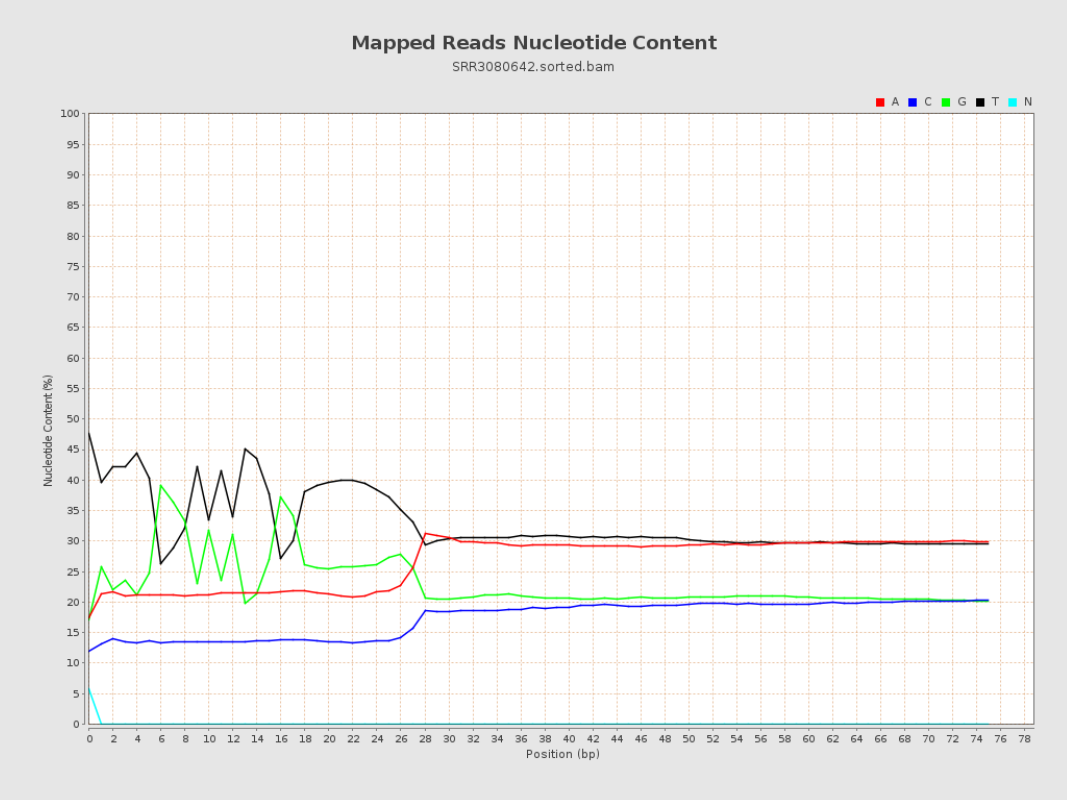
6. Results : Genome Fraction Coverage



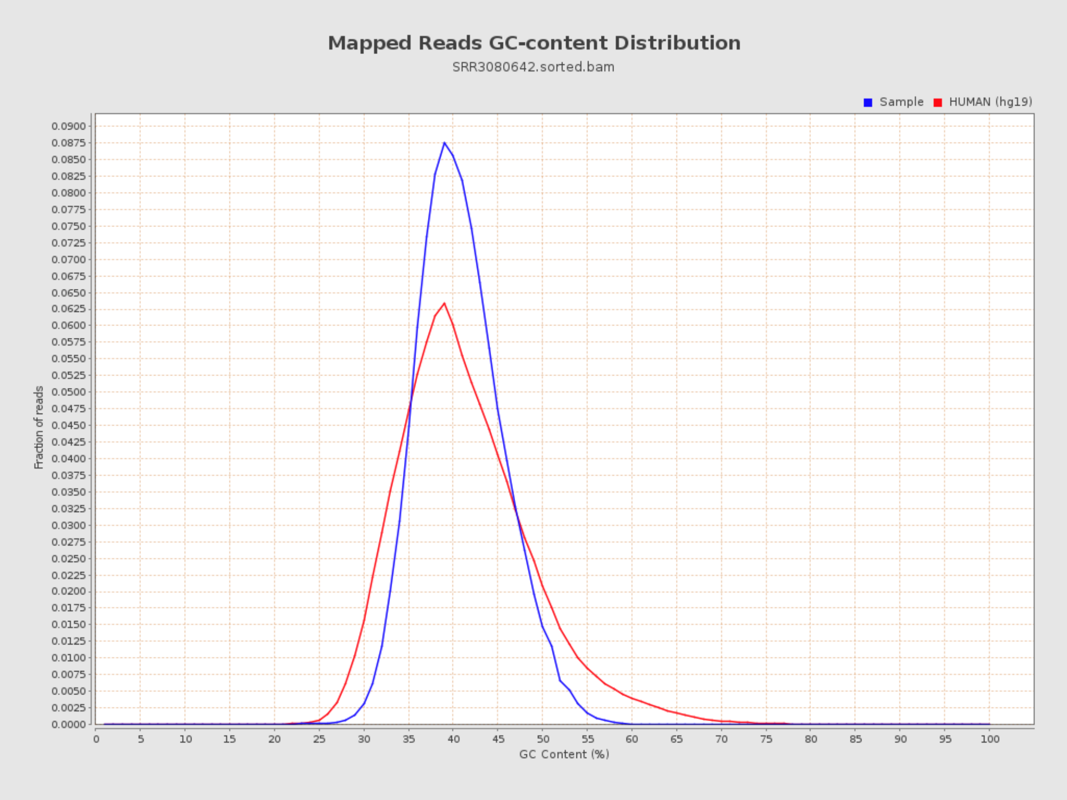
7. Results : Duplication Rate Histogram



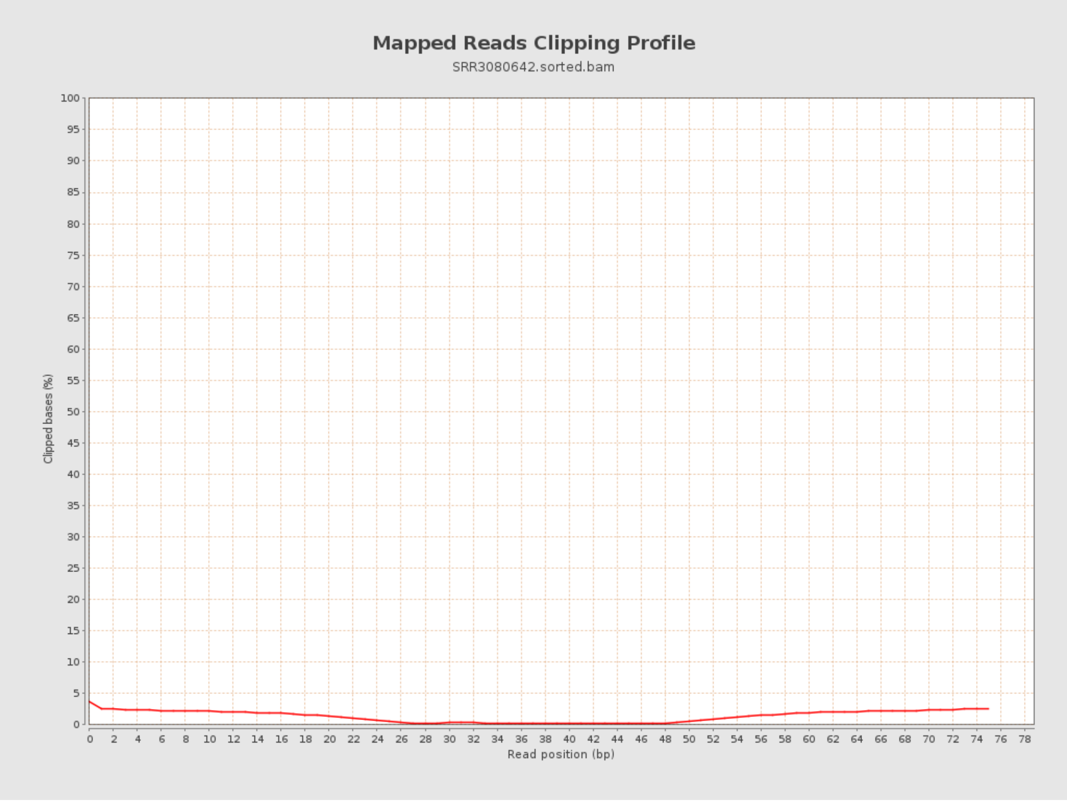
8. Results : Mapped Reads Nucleotide Content



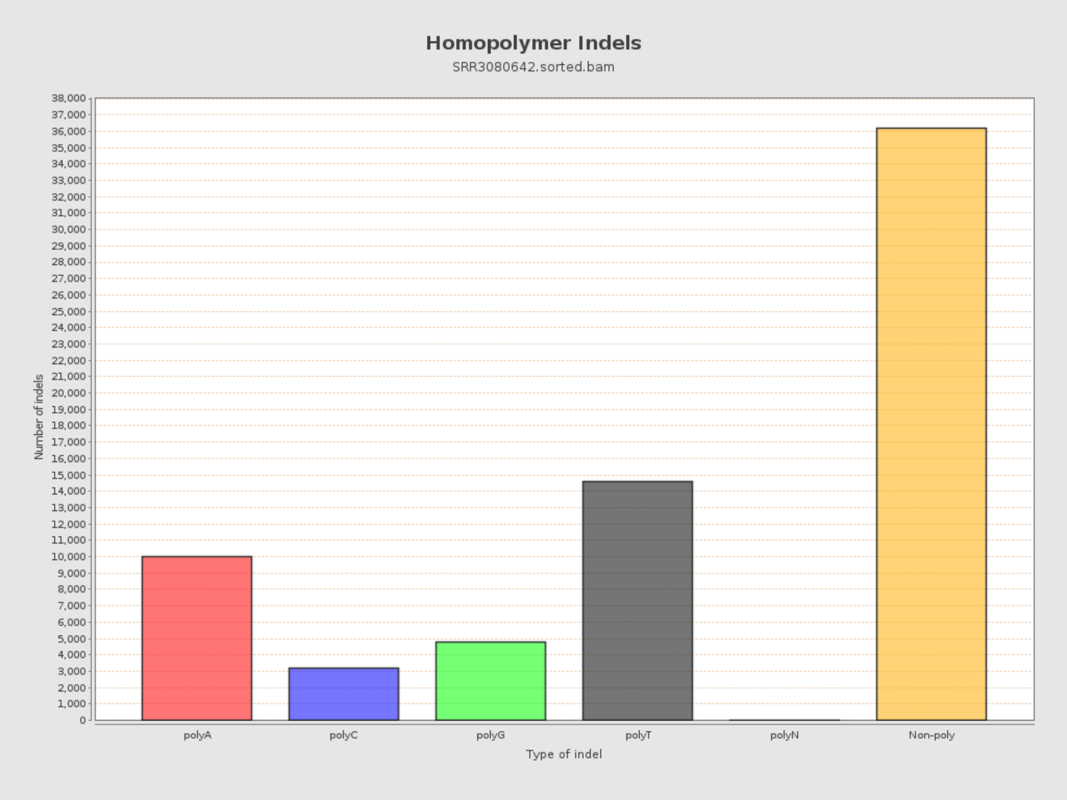
9. Results : Mapped Reads GC-content Distribution



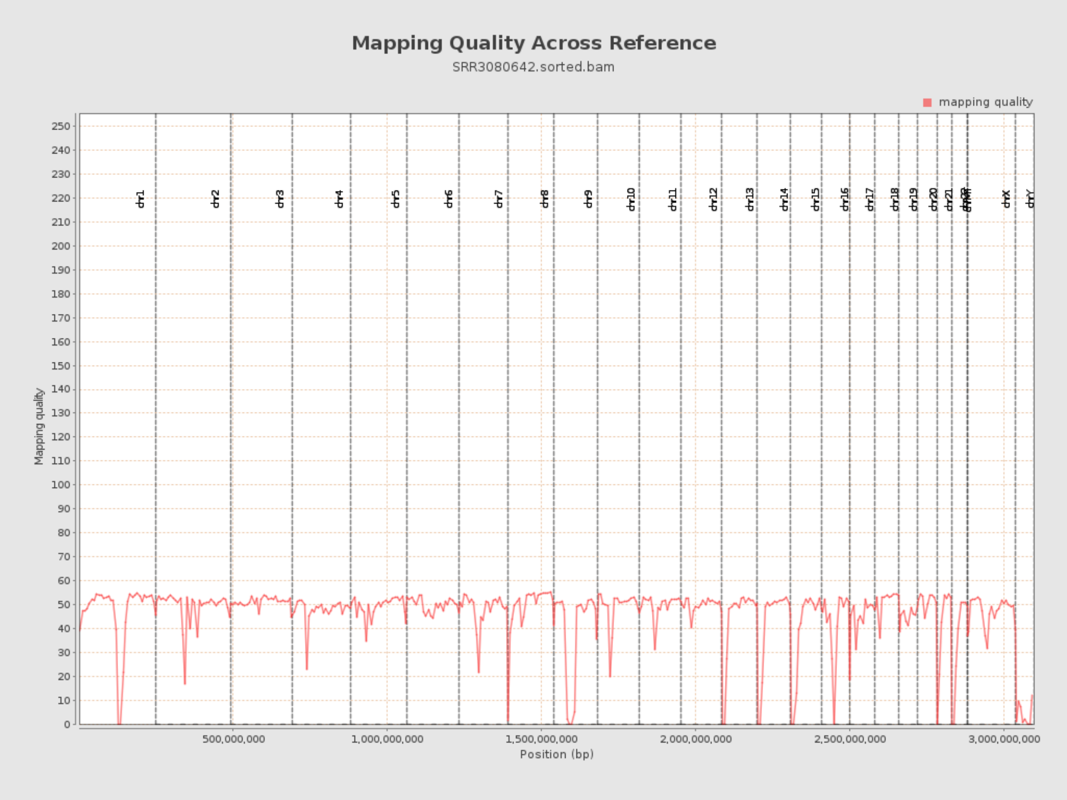
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram