Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:02:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080977.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_SRR3080977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080977.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:02:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,619,253
Mapped reads	5,023,630 / 89.4%
Unmapped reads	595,623 / 10.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,229 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	293,824 / 5.23%
Duplication rate	4.6%
Clipped reads	2,231,066 / 39.7%

2.2. ACGT Content

Number/percentage of A's	93,521,216 / 27.77%
Number/percentage of C's	59,074,466 / 17.54%
Number/percentage of T's	109,466,787 / 32.5%
Number/percentage of G's	74,065,475 / 21.99%
Number/percentage of N's	660,452 / 0.2%
GC Percentage	39.53%

2.3. Coverage

Mean	0.1088

Standard Deviation	0.7085

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

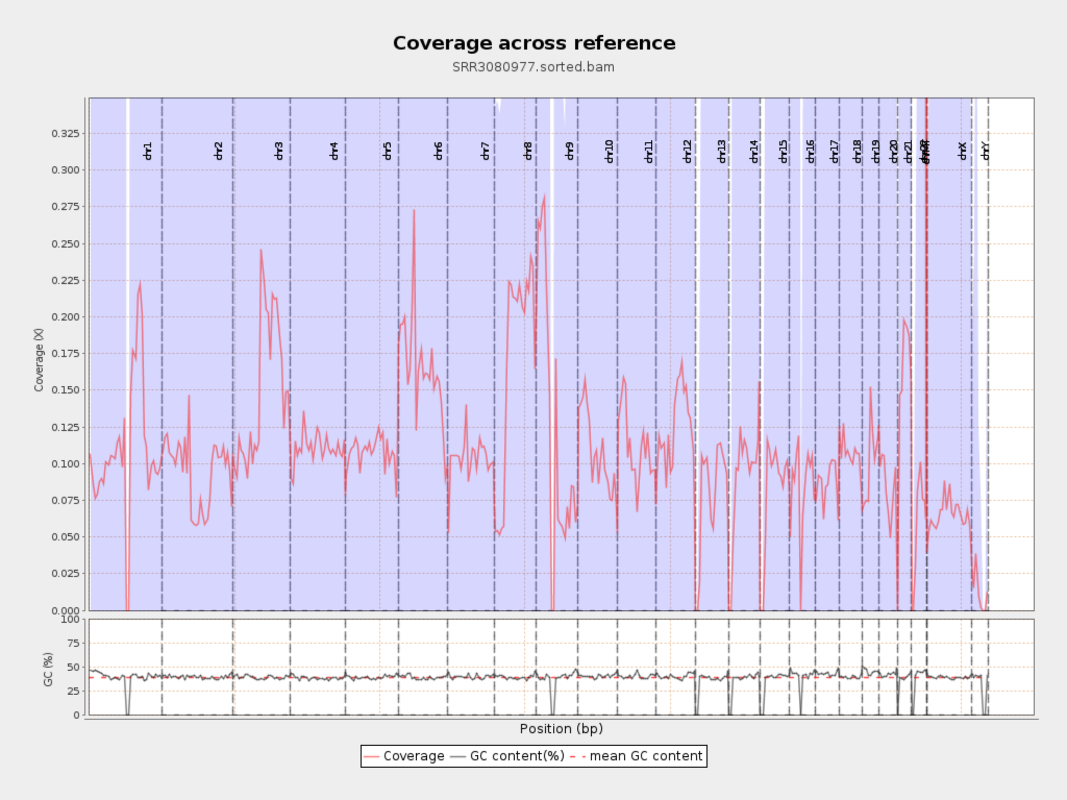
General error rate	0.99%
Mismatches	3,298,770
Insertions	27,036
Mapped reads with at least one insertion	0.53%
Deletions	75,157
Mapped reads with at least one deletion	1.48%
Homopolymer indels	49.23%

2.6. Chromosome stats

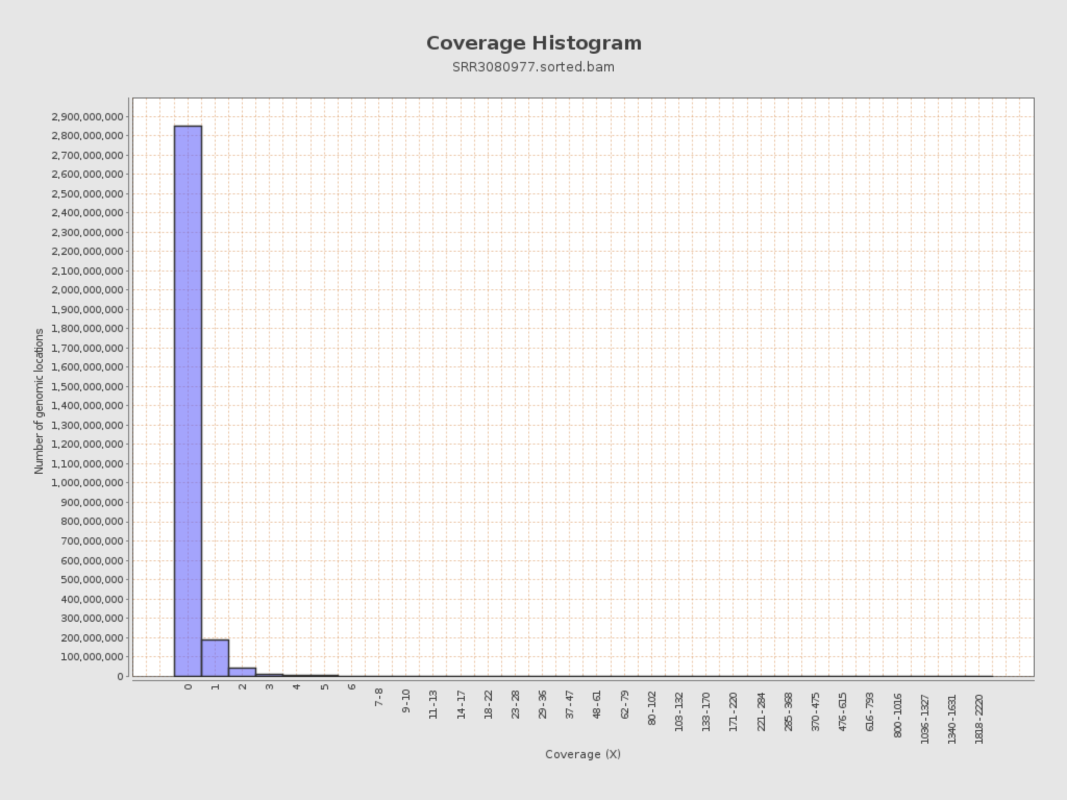
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27424481	0.11	0.89
chr2	243199373	23165461	0.0953	0.6929
chr3	198022430	29470843	0.1488	0.5027
chr4	191154276	21137726	0.1106	0.4658
chr5	180915260	19519441	0.1079	0.4274
chr6	171115067	28284342	0.1653	0.8187
chr7	159138663	16621359	0.1044	0.7238

chr8	146364022	24929320	0.1703	1.4407
chr9	141213431	17349476	0.1229	0.884
chr10	135534747	14856003	0.1096	0.5624
chr11	135006516	14916264	0.1105	0.5792
chr12	133851895	16680952	0.1246	0.481
chr13	115169878	8954030	0.0777	0.3593
chr14	107349540	9508861	0.0886	0.5134
chr15	102531392	8387401	0.0818	0.3745
chr16	90354753	7664524	0.0848	0.4711
chr17	81195210	7000670	0.0862	0.3955
chr18	78077248	8389881	0.1075	1.604
chr19	59128983	6008806	0.1016	0.6963
chr20	63025520	5245081	0.0832	0.419
chr21	48129895	7535800	0.1566	0.6354
chr22	51304566	2938796	0.0573	0.3025
chrMT	16571	122992	7.4221	4.4667
chrX	155270560	10091443	0.065	0.3729
chrY	59373566	708965	0.0119	0.2196

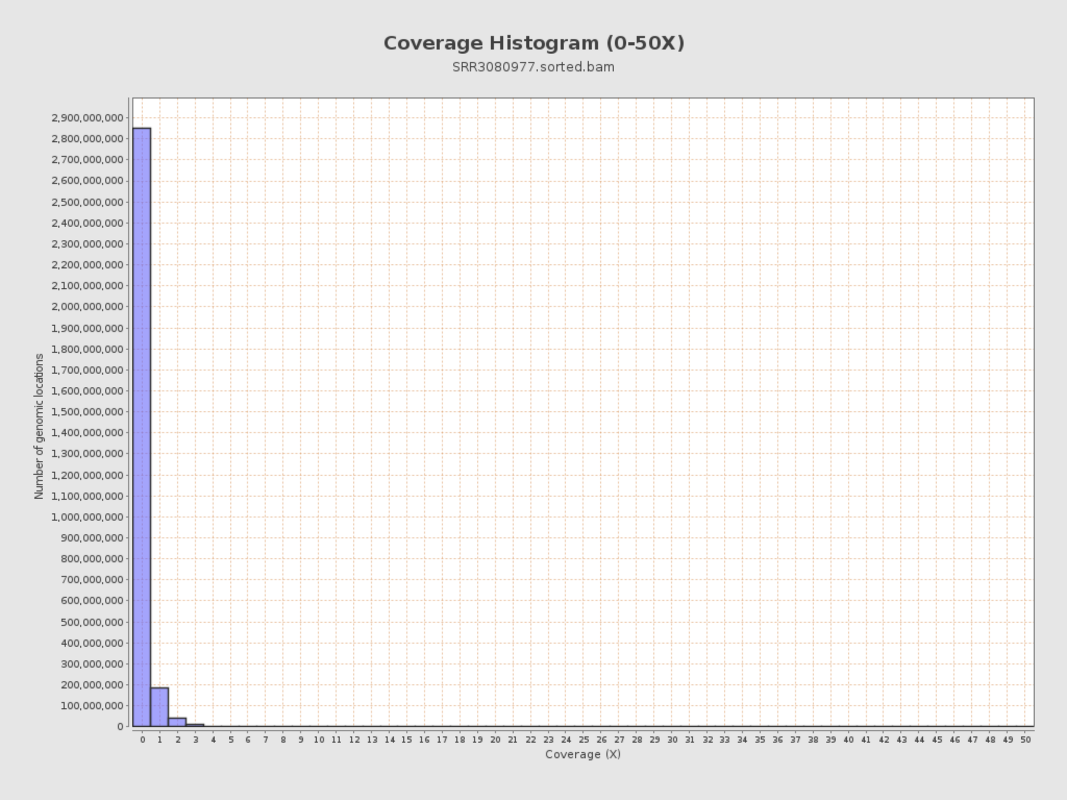
3. Results : Coverage across reference



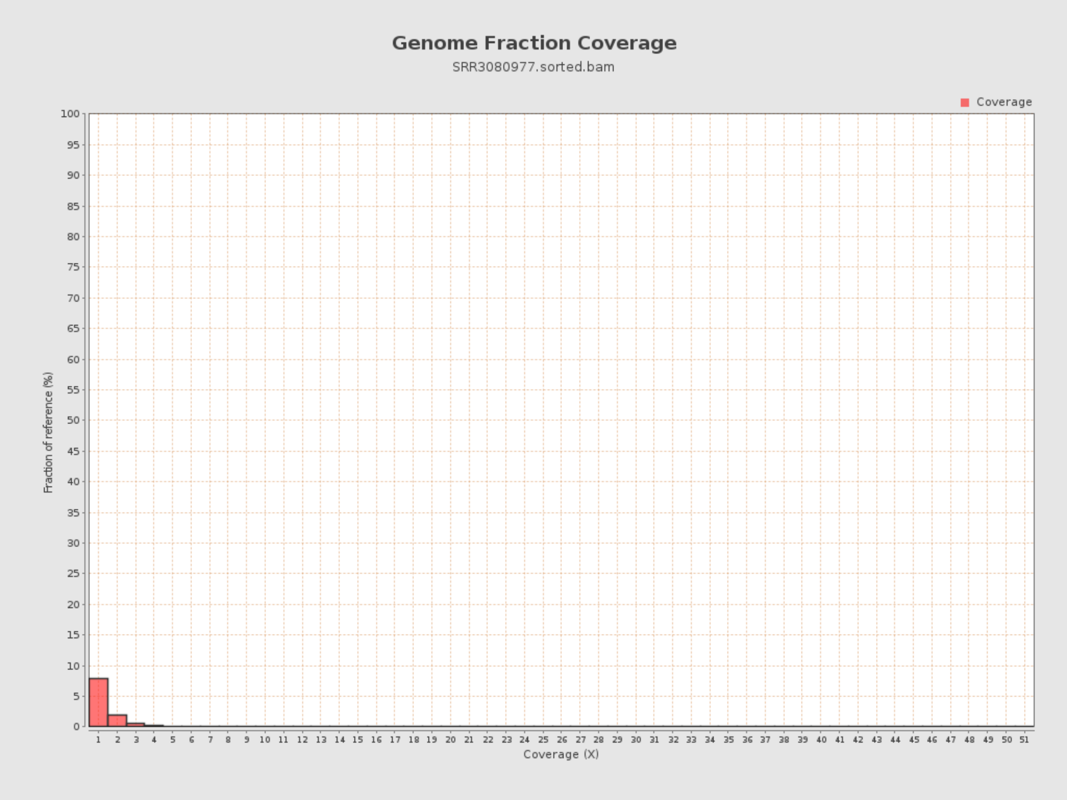
4. Results : Coverage Histogram



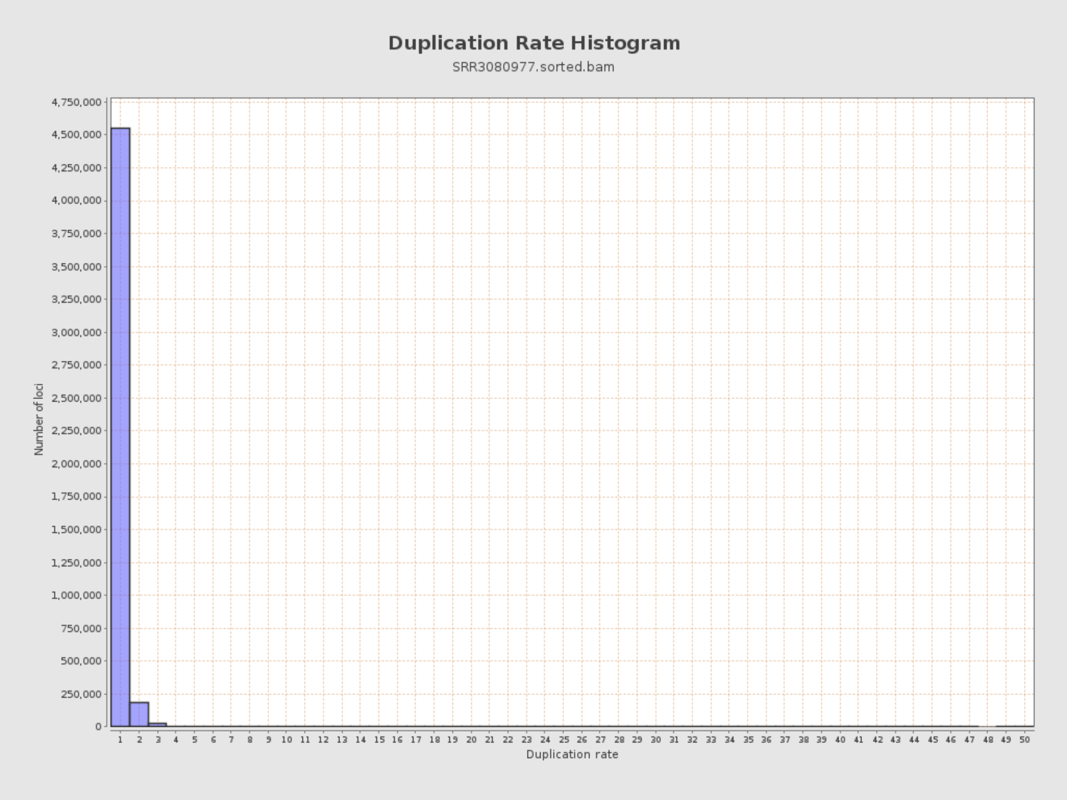
5. Results : Coverage Histogram (0-50X)



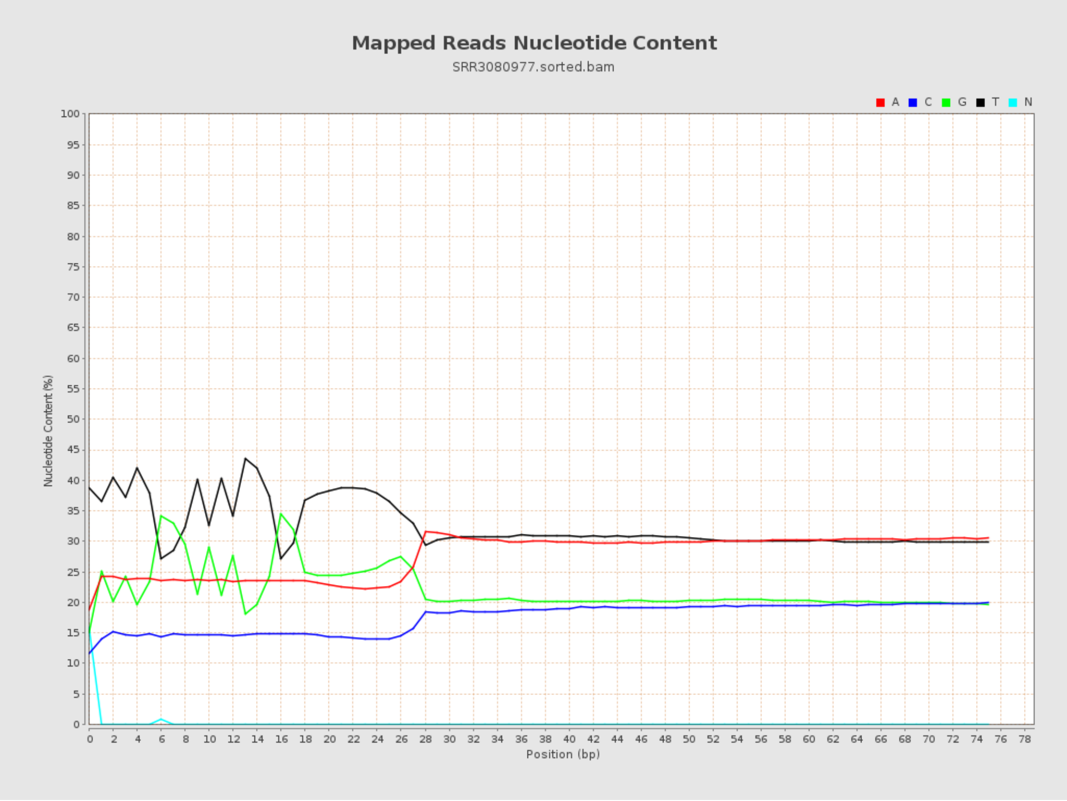
6. Results : Genome Fraction Coverage



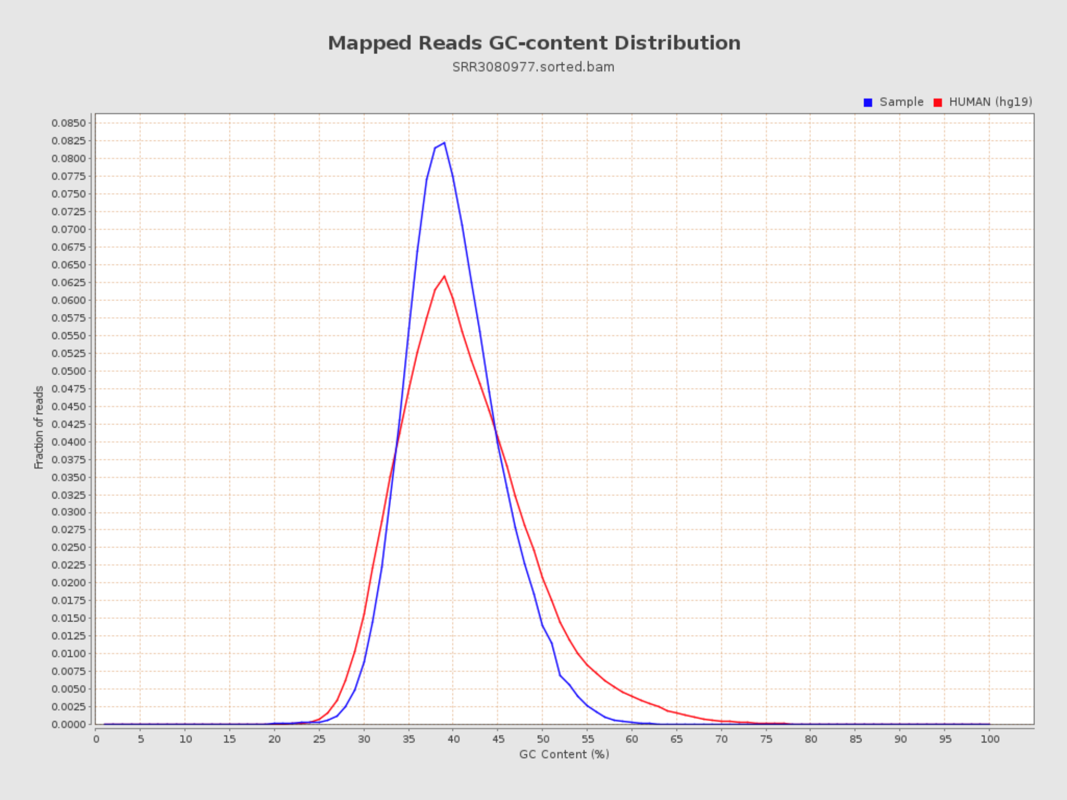
7. Results : Duplication Rate Histogram



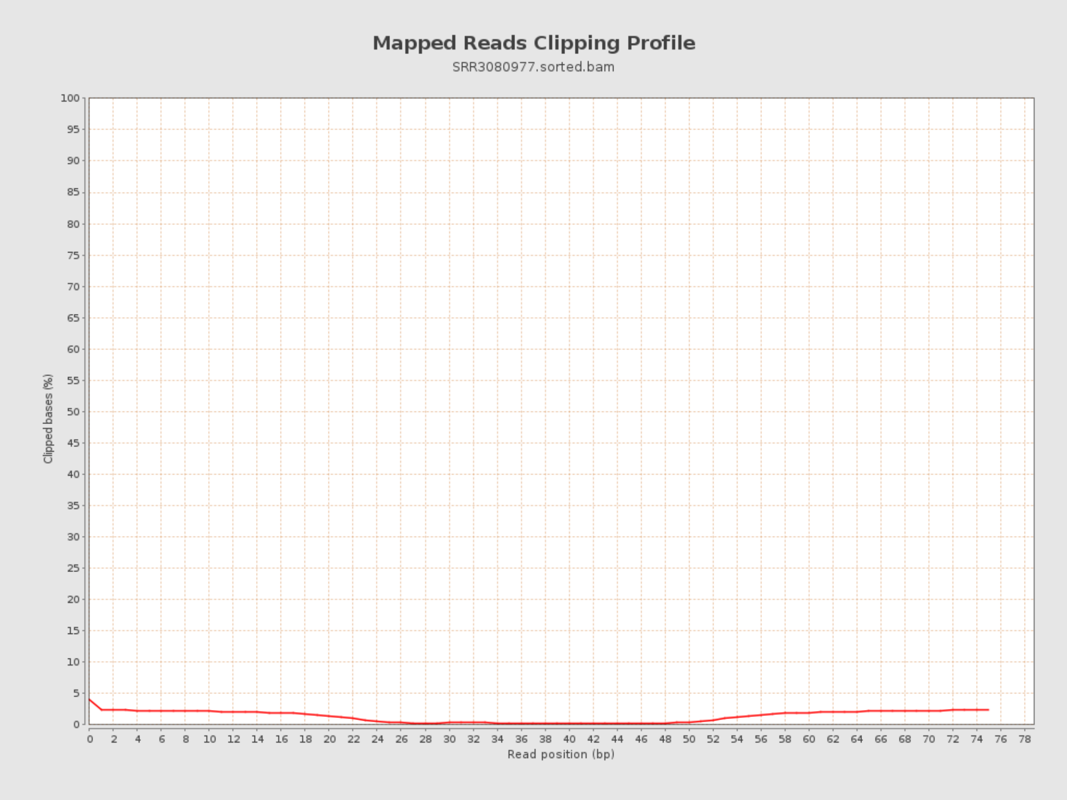
8. Results : Mapped Reads Nucleotide Content



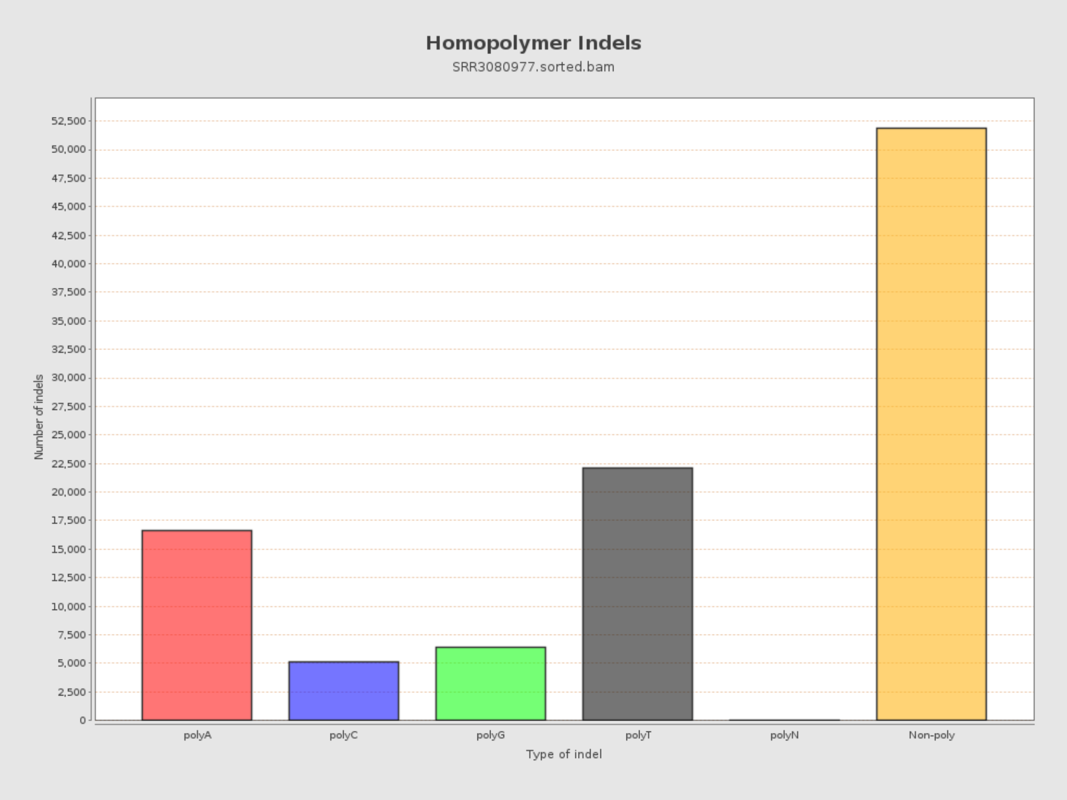
9. Results : Mapped Reads GC-content Distribution



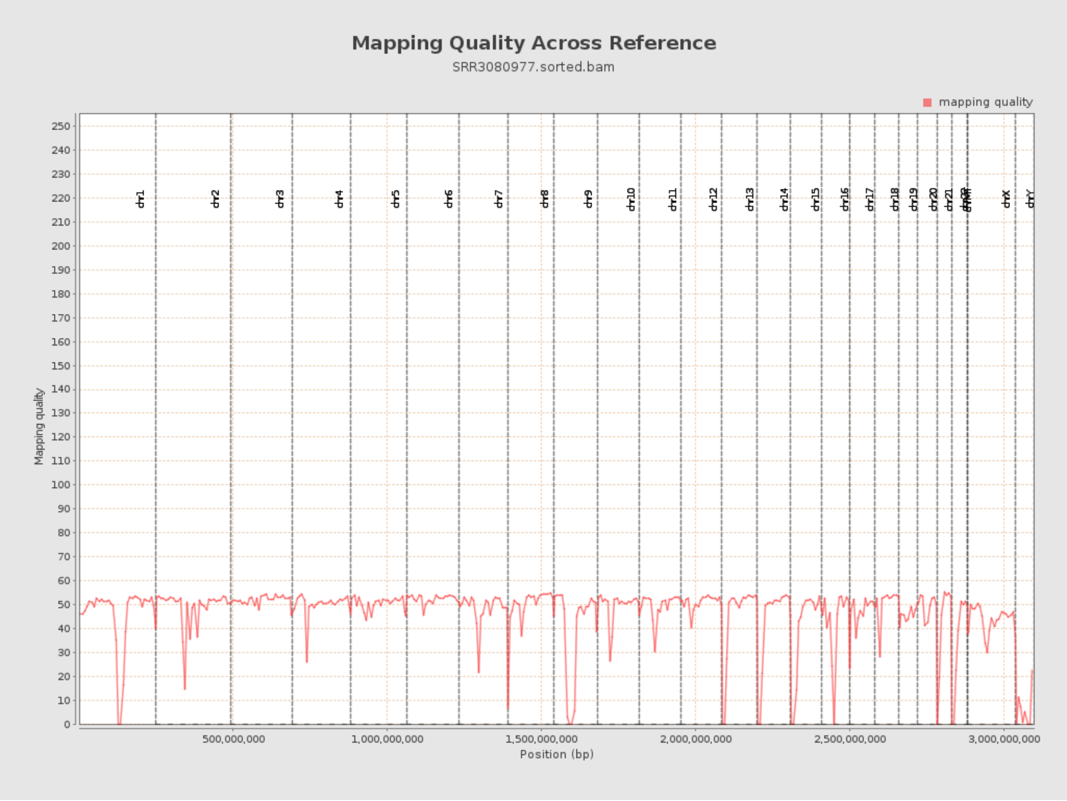
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram