Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/08/23 14:19:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080980.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_SRR3080980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:19:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,237,511
Mapped reads	3,550,445 / 83.79%
Unmapped reads	687,066 / 16.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,870 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	243,654 / 5.75%
Duplication rate	5.5%
Clipped reads	1,421,215 / 33.54%

2.2. ACGT Content

Number/percentage of A's	67,562,336 / 28.2%
Number/percentage of C's	42,233,714 / 17.63%
Number/percentage of T's	78,203,513 / 32.64%
Number/percentage of G's	51,106,936 / 21.33%
Number/percentage of N's	477,842 / 0.2%
GC Percentage	38.96%

2.3. Coverage

Mean	0.0774

Standard Deviation	0.5871

2.4. Mapping Quality

Mean Mapping Quality	47.32

2.5. Mismatches and indels

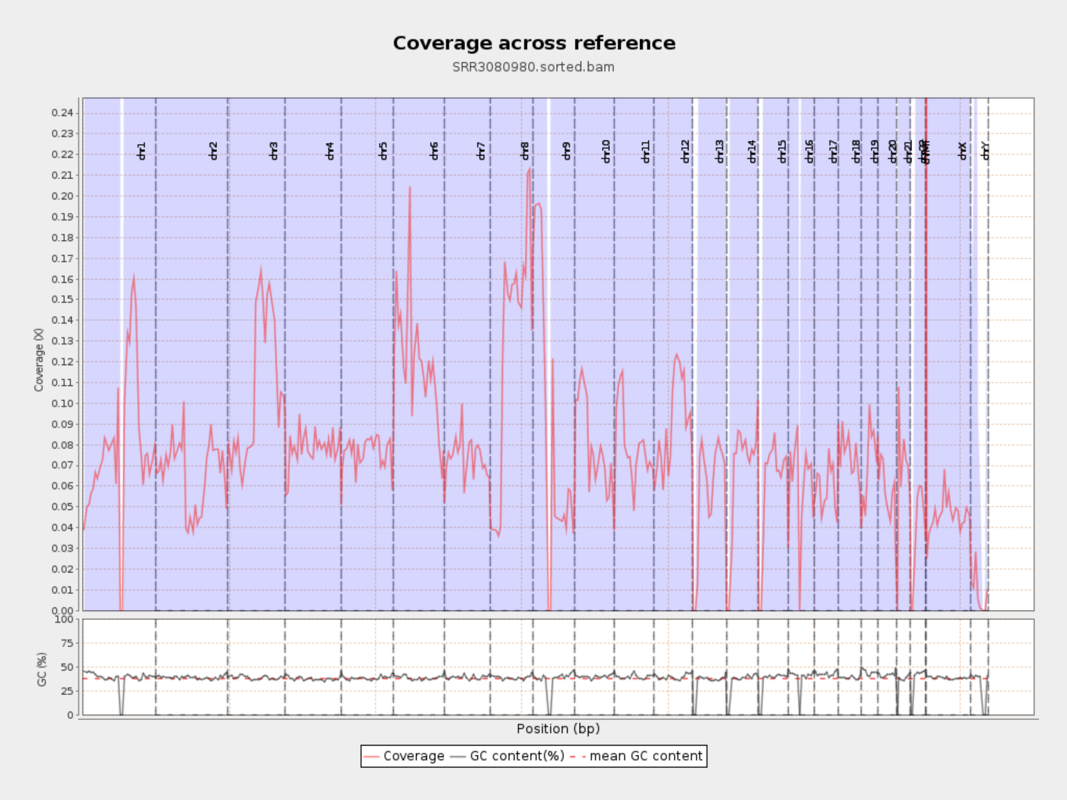
General error rate	0.99%
Mismatches	2,335,586
Insertions	18,107
Mapped reads with at least one insertion	0.51%
Deletions	48,911
Mapped reads with at least one deletion	1.36%
Homopolymer indels	49.52%

2.6. Chromosome stats

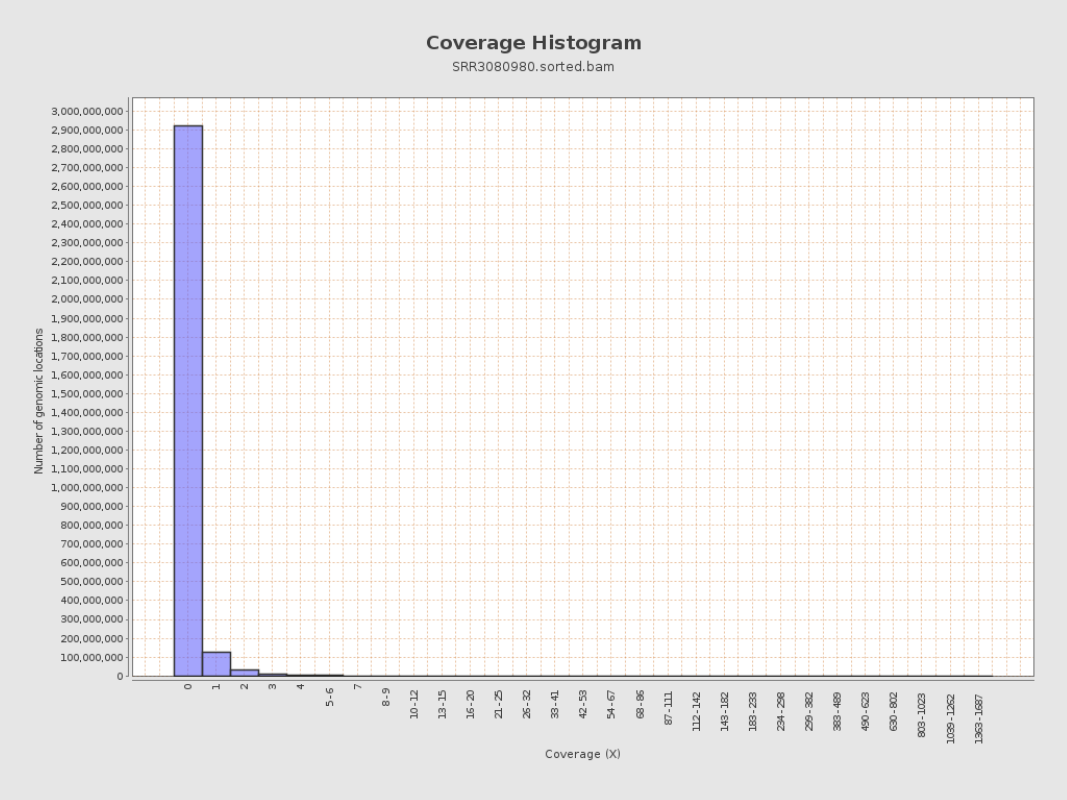
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19609650	0.0787	0.895
chr2	243199373	16207364	0.0666	0.5133
chr3	198022430	21010796	0.1061	0.4281
chr4	191154276	15009997	0.0785	0.388
chr5	180915260	13846092	0.0765	0.3634
chr6	171115067	20649341	0.1207	0.698
chr7	159138663	11762389	0.0739	0.5943

chr8	146364022	18826191	0.1286	1.1279
chr9	141213431	12366131	0.0876	0.7087
chr10	135534747	10920376	0.0806	0.508
chr11	135006516	10775384	0.0798	0.4743
chr12	133851895	12112523	0.0905	0.4137
chr13	115169878	6602055	0.0573	0.31
chr14	107349540	7020050	0.0654	0.4066
chr15	102531392	6069546	0.0592	0.3146
chr16	90354753	5371781	0.0595	0.3894
chr17	81195210	4835990	0.0596	0.328
chr18	78077248	5896610	0.0755	1.1484
chr19	59128983	4232542	0.0716	0.6661
chr20	63025520	3671197	0.0582	0.3376
chr21	48129895	3302881	0.0686	0.4325
chr22	51304566	1957894	0.0382	0.2485
chrMT	16571	31082	1.8757	1.5963
chrX	155270560	7074248	0.0456	0.3181
chrY	59373566	508369	0.0086	0.1856

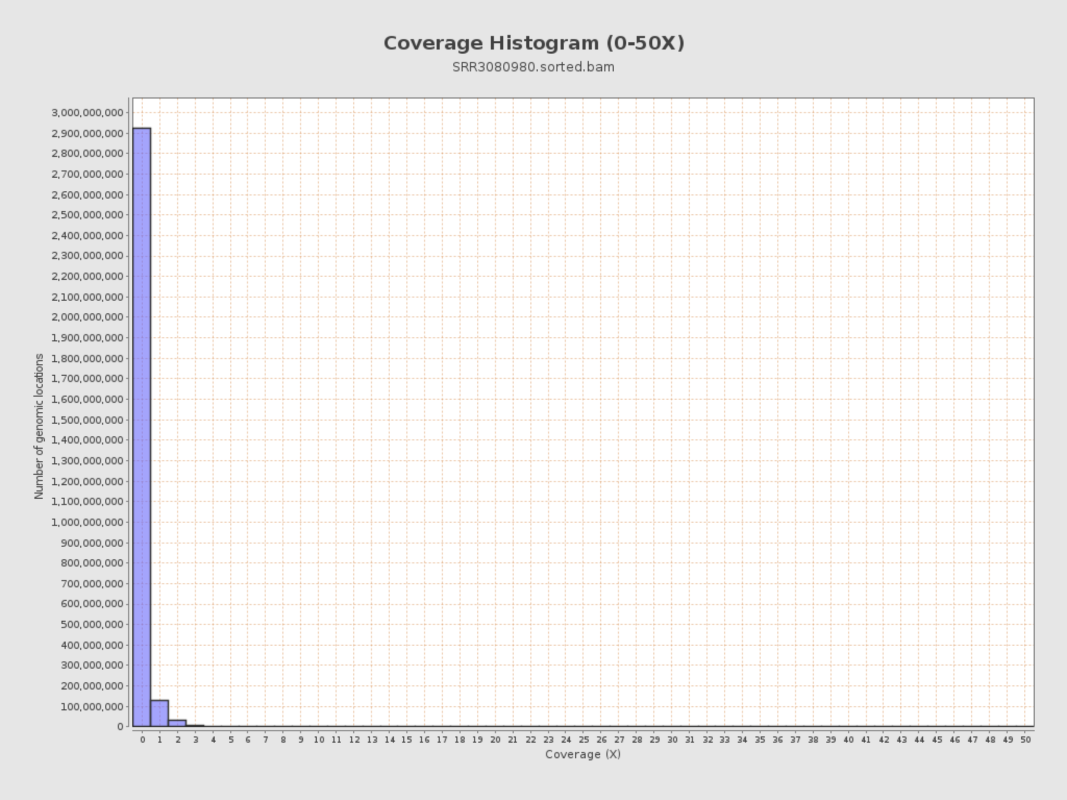
3. Results : Coverage across reference



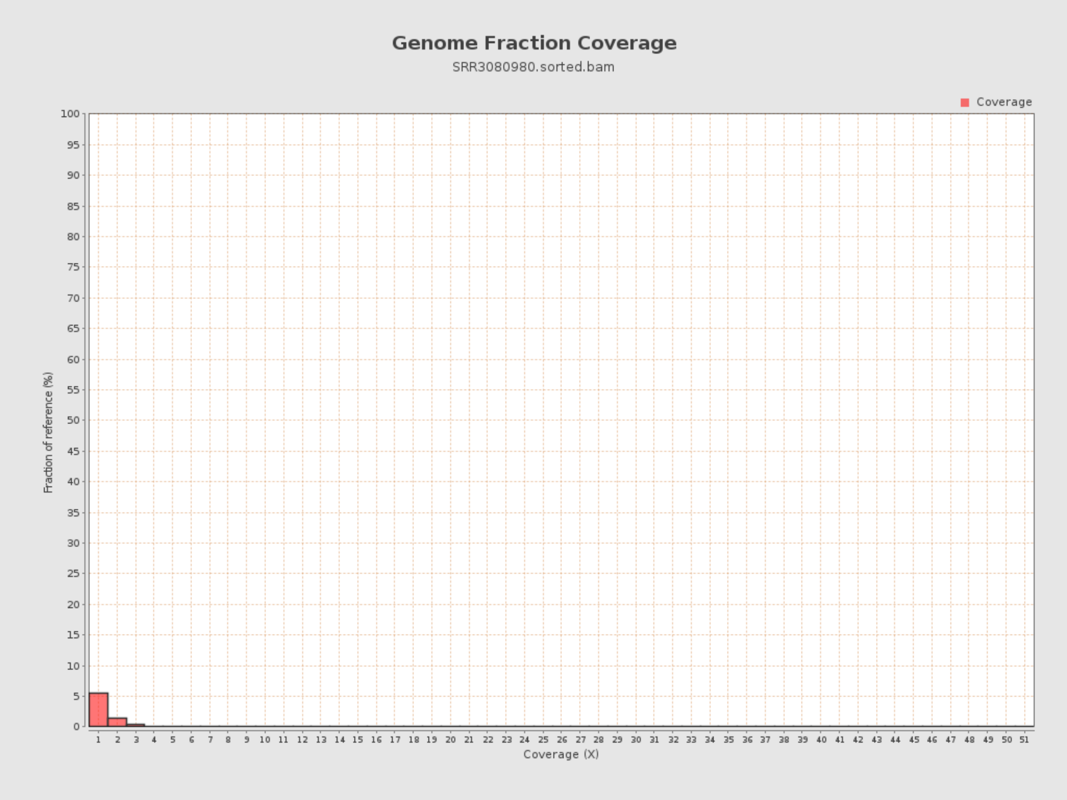
4. Results : Coverage Histogram



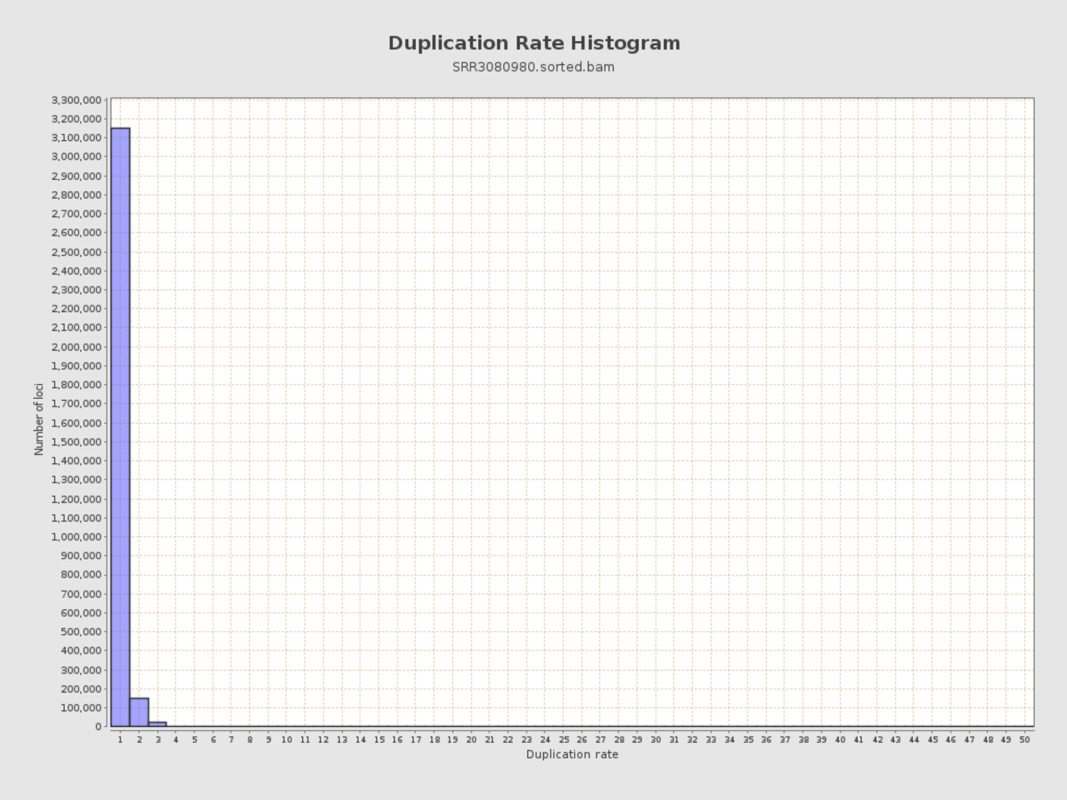
5. Results : Coverage Histogram (0-50X)



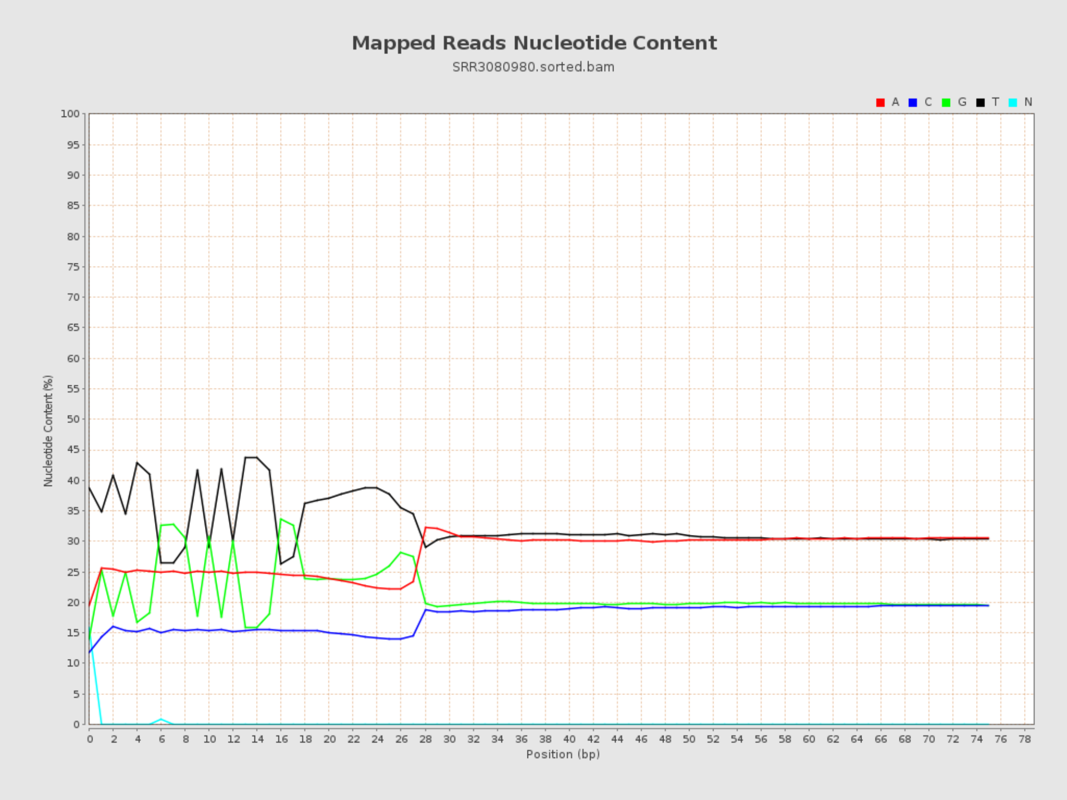
6. Results : Genome Fraction Coverage



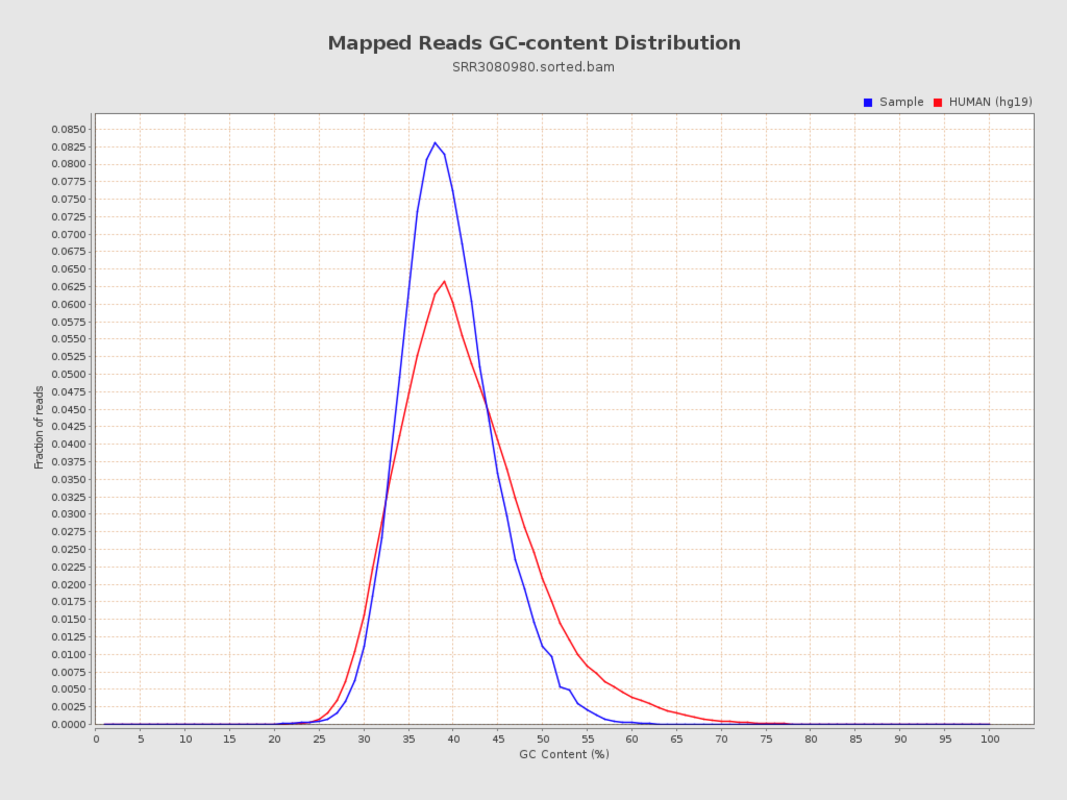
7. Results : Duplication Rate Histogram



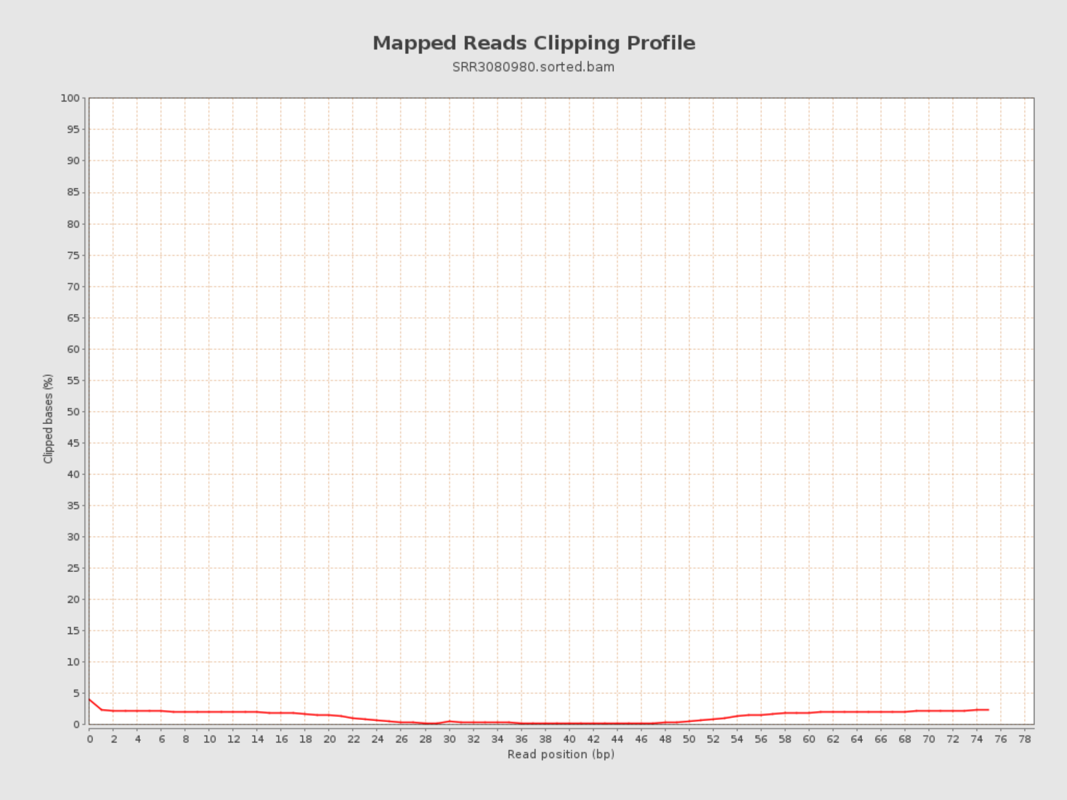
8. Results : Mapped Reads Nucleotide Content



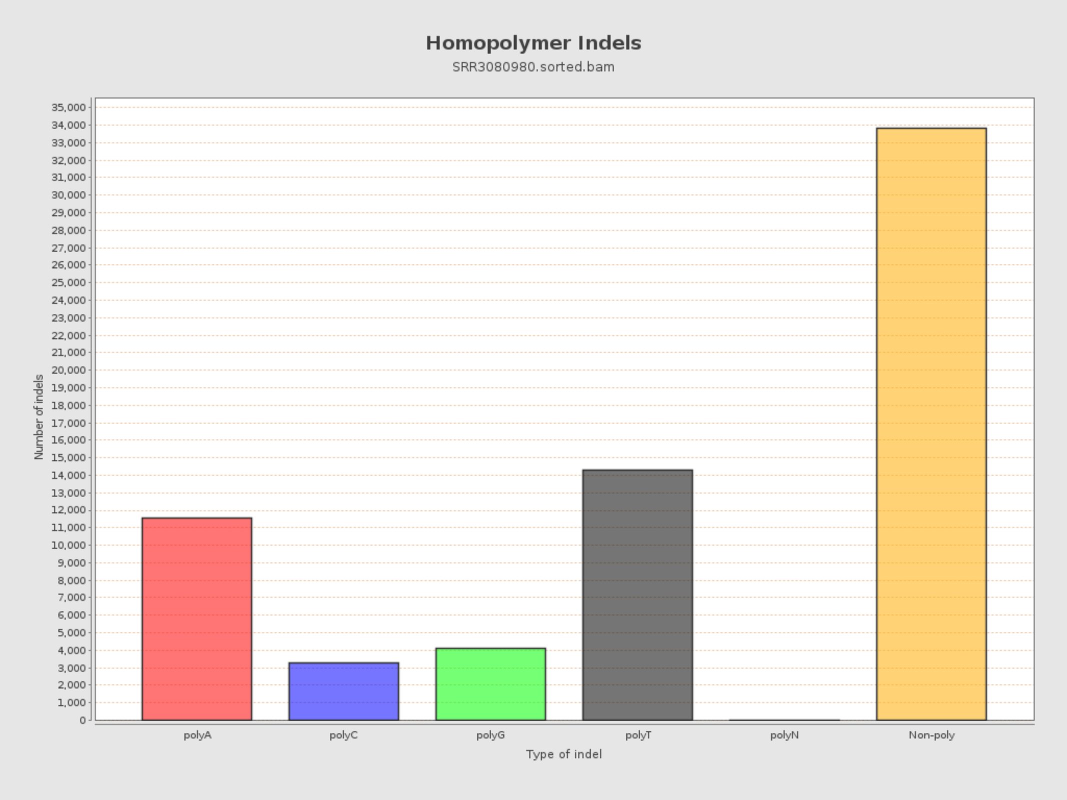
9. Results : Mapped Reads GC-content Distribution



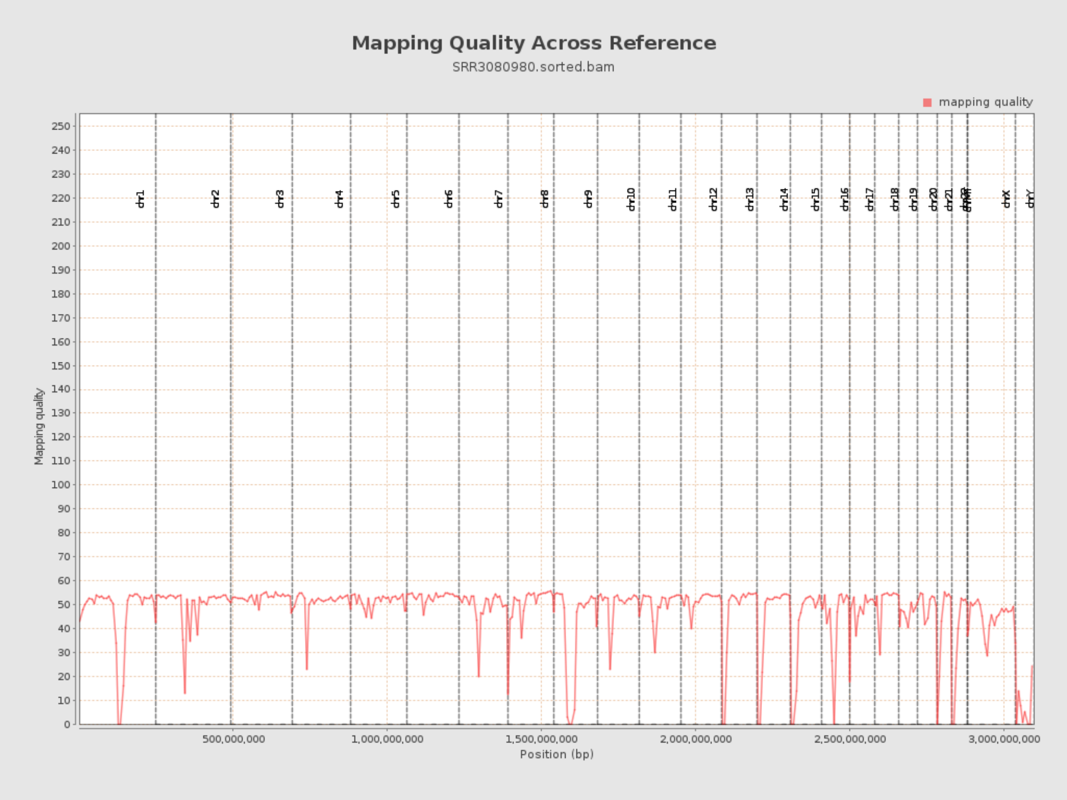
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram