Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:20:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068073.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_SRR6068073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:20:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,511,107
Mapped reads	3,123,697 / 88.97%
Unmapped reads	387,410 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,455 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	463,303 / 13.2%
Duplication rate	12.16%
Clipped reads	1,698,578 / 48.38%

2.2. ACGT Content

Number/percentage of A's	51,911,821 / 25.92%
Number/percentage of C's	36,378,066 / 18.16%
Number/percentage of T's	64,815,880 / 32.36%
Number/percentage of G's	47,151,356 / 23.54%
Number/percentage of N's	23,005 / 0.01%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0647

Standard Deviation	0.6713

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

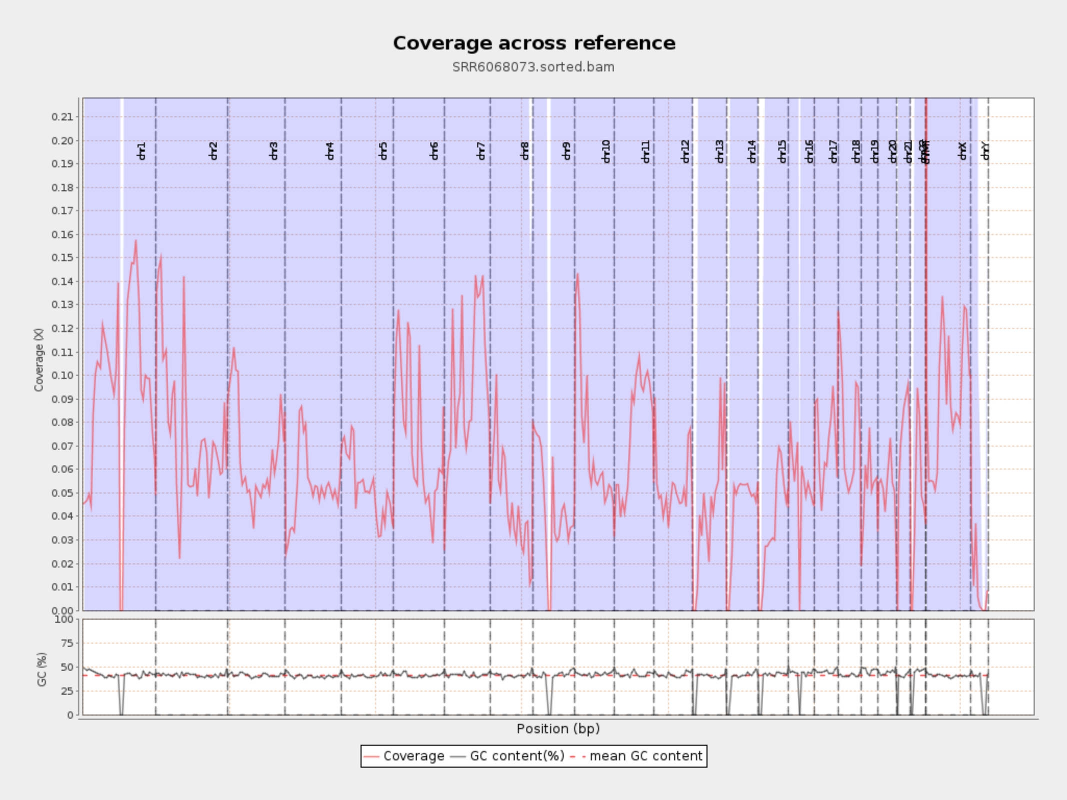
General error rate	0.56%
Mismatches	1,094,483
Insertions	13,347
Mapped reads with at least one insertion	0.42%
Deletions	43,993
Mapped reads with at least one deletion	1.39%
Homopolymer indels	44.19%

2.6. Chromosome stats

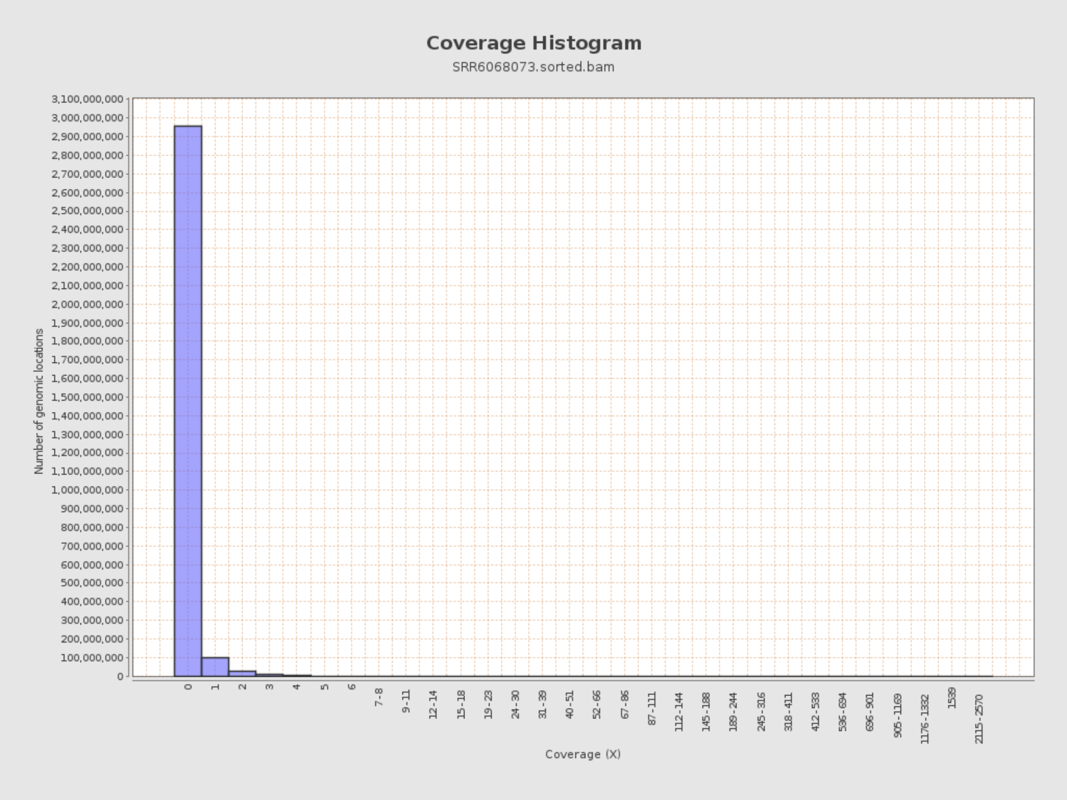
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23479637	0.0942	1.1704
chr2	243199373	18808659	0.0773	1.2435
chr3	198022430	13220554	0.0668	0.3541
chr4	191154276	10061492	0.0526	0.359
chr5	180915260	9528715	0.0527	0.3183
chr6	171115067	12707487	0.0743	0.5083
chr7	159138663	15250943	0.0958	0.8822

chr8	146364022	6585574	0.045	0.7674
chr9	141213431	6126195	0.0434	0.4929
chr10	135534747	9855385	0.0727	0.5029
chr11	135006516	10334420	0.0765	0.5179
chr12	133851895	7100691	0.053	0.3399
chr13	115169878	5077433	0.0441	0.326
chr14	107349540	4610714	0.043	0.3285
chr15	102531392	3626071	0.0354	0.2836
chr16	90354753	4778412	0.0529	0.3428
chr17	81195210	5867906	0.0723	0.4041
chr18	78077248	6097949	0.0781	0.9689
chr19	59128983	3137851	0.0531	0.7989
chr20	63025520	3390515	0.0538	0.3492
chr21	48129895	3415051	0.071	0.3879
chr22	51304566	2383884	0.0465	0.2893
chrMT	16571	235001	14.1815	9.8688
chrX	155270560	14013406	0.0903	0.479
chrY	59373566	663137	0.0112	0.3567

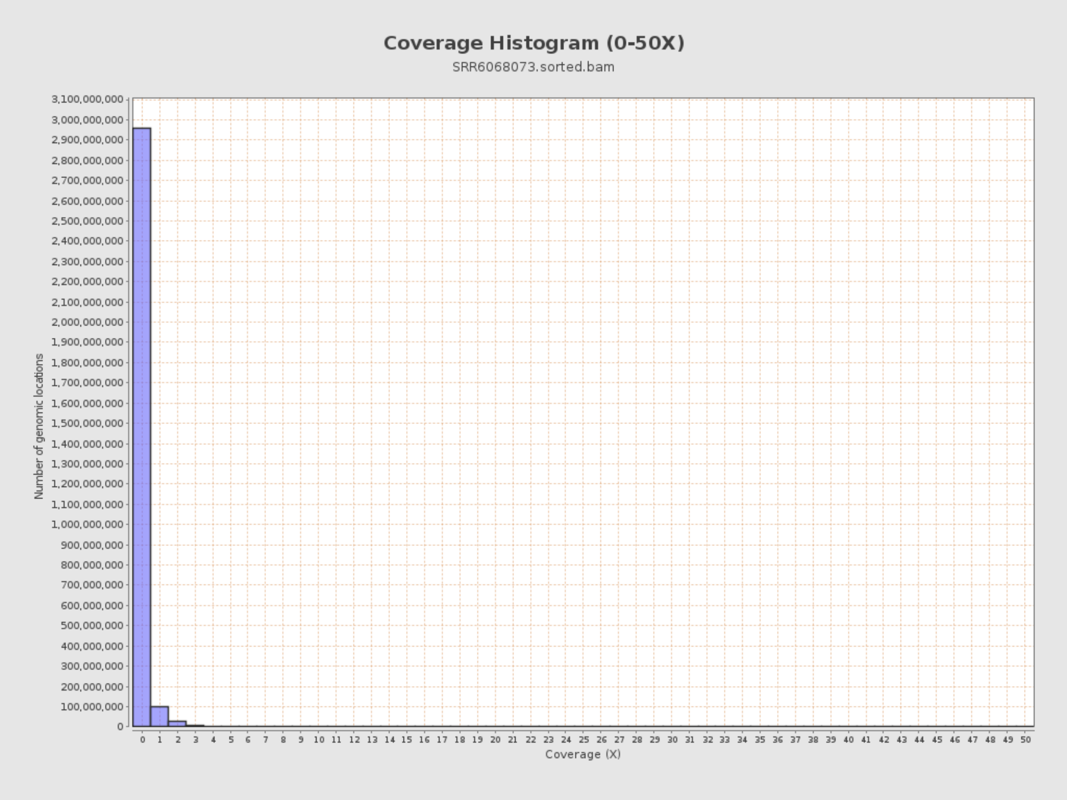
3. Results : Coverage across reference



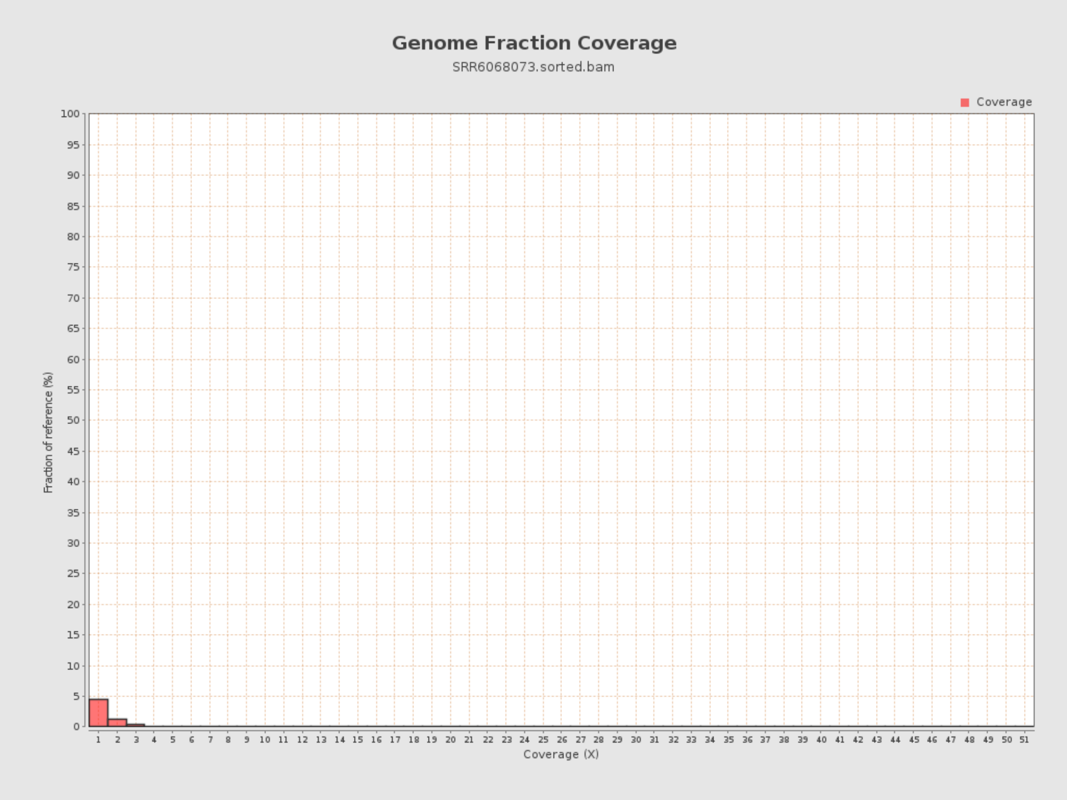
4. Results : Coverage Histogram



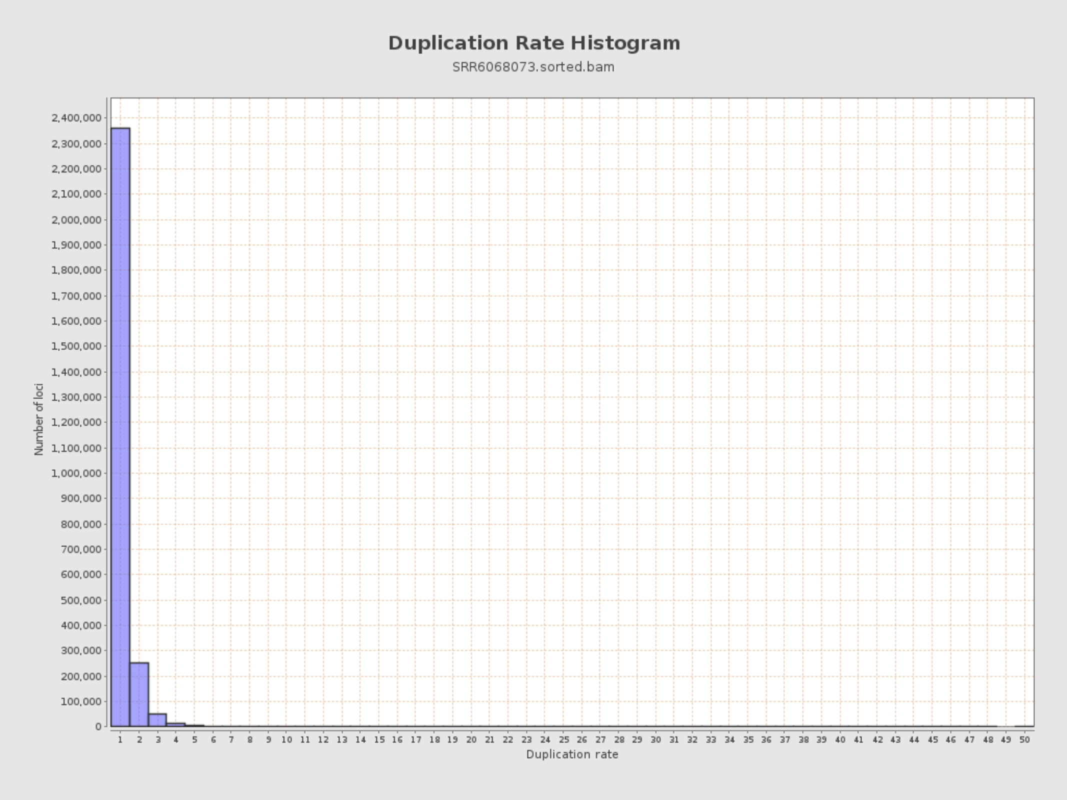
5. Results : Coverage Histogram (0-50X)



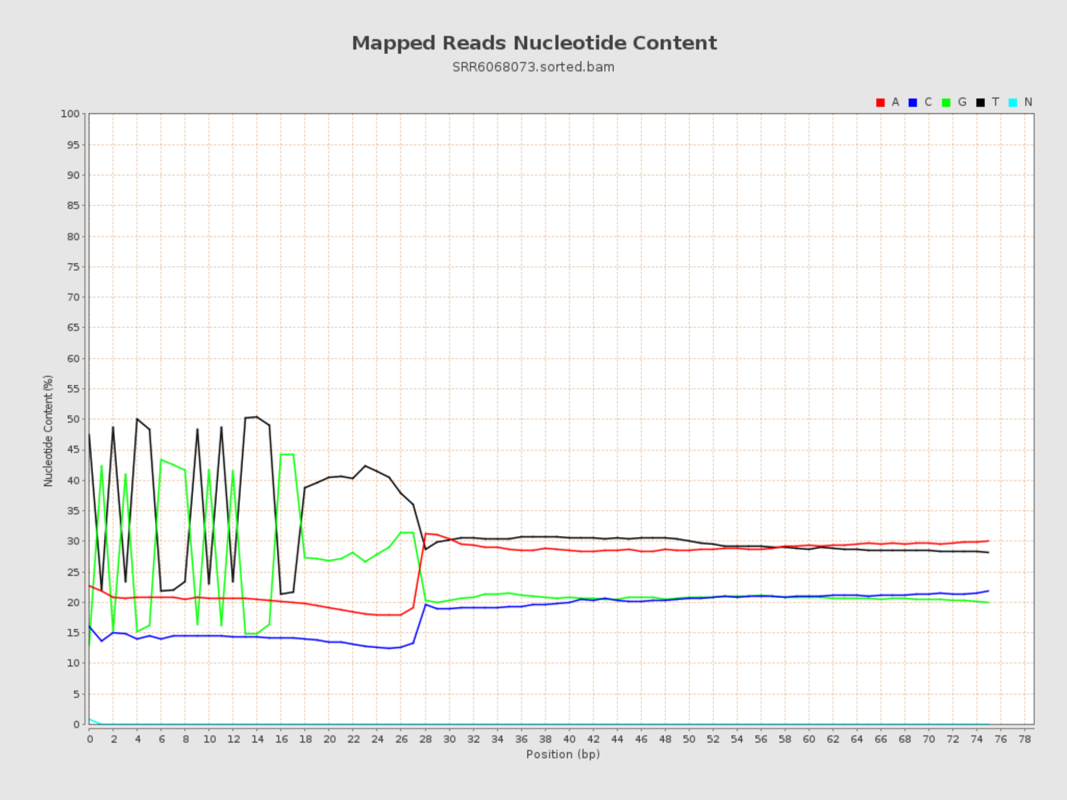
6. Results : Genome Fraction Coverage



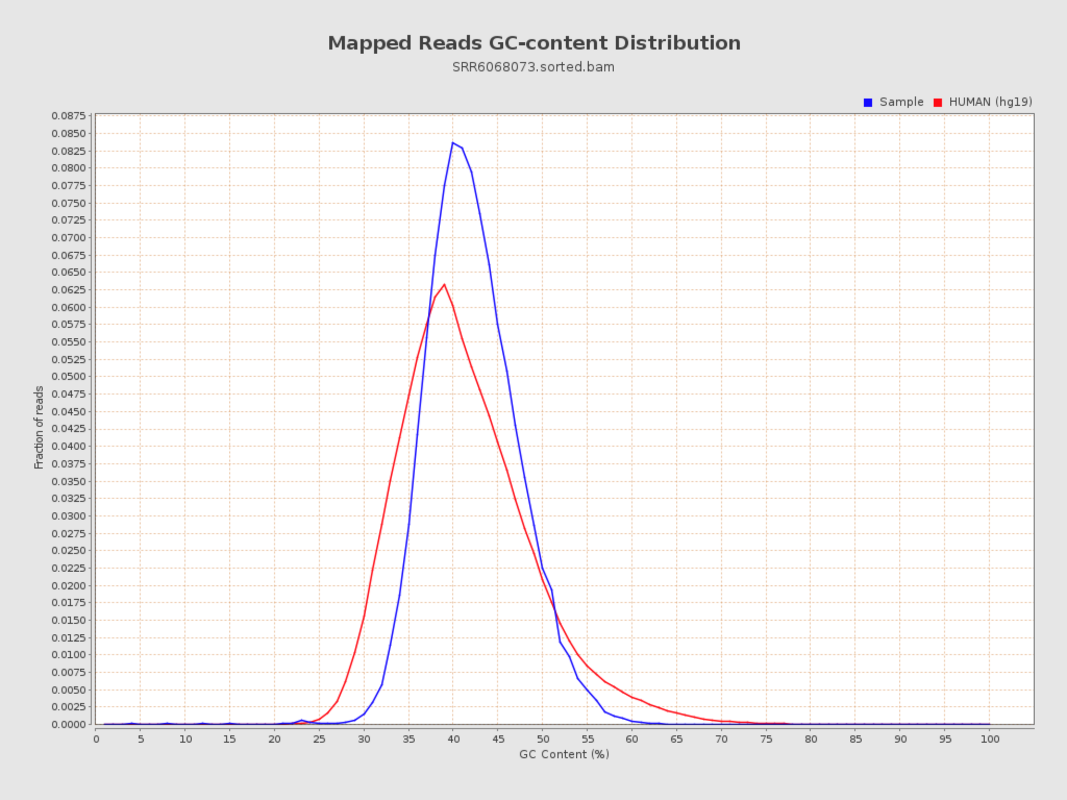
7. Results : Duplication Rate Histogram



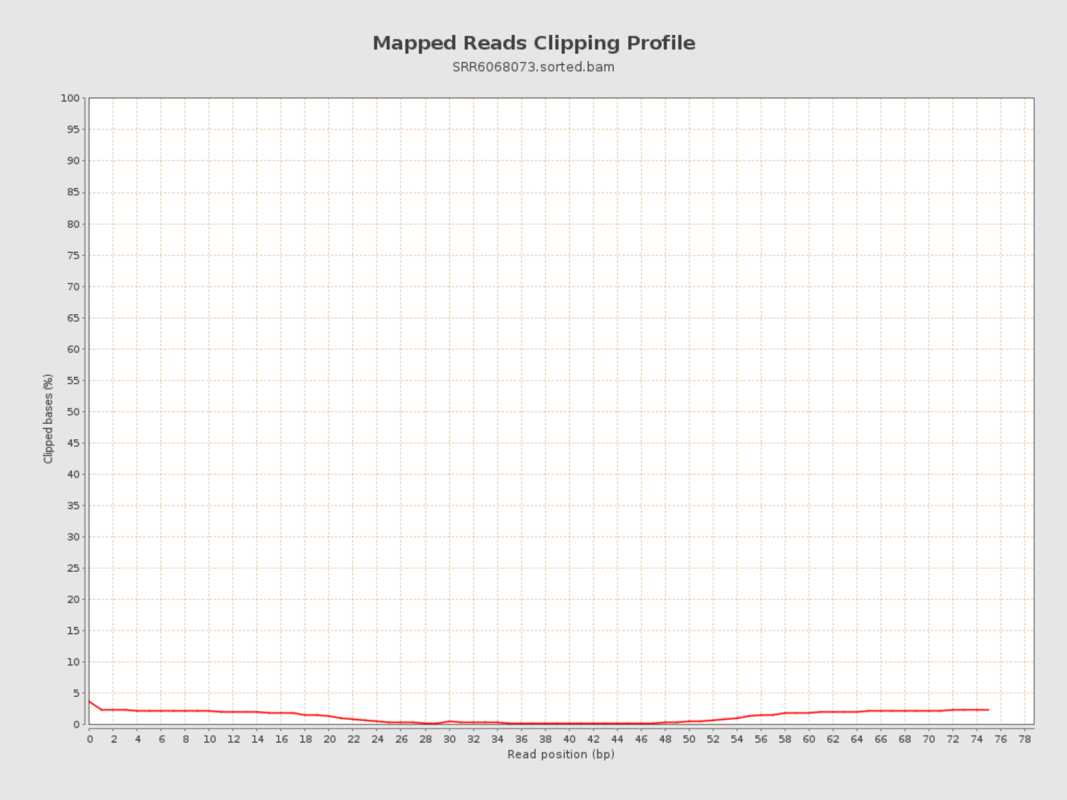
8. Results : Mapped Reads Nucleotide Content



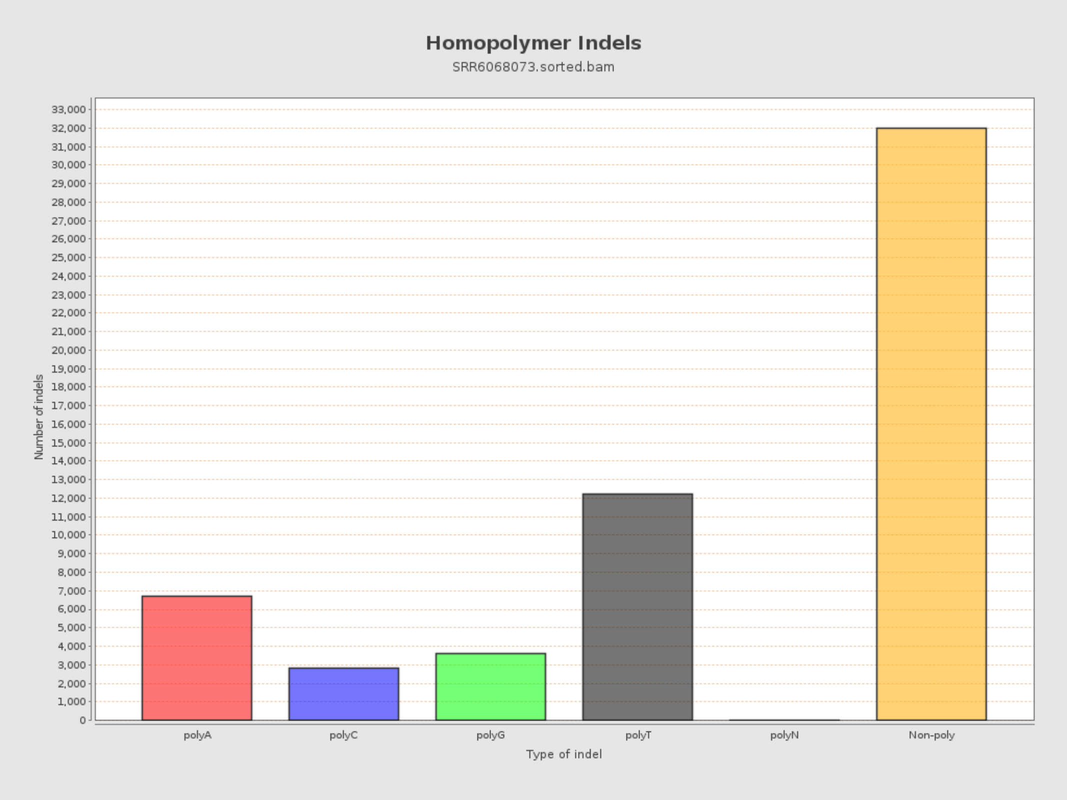
9. Results : Mapped Reads GC-content Distribution



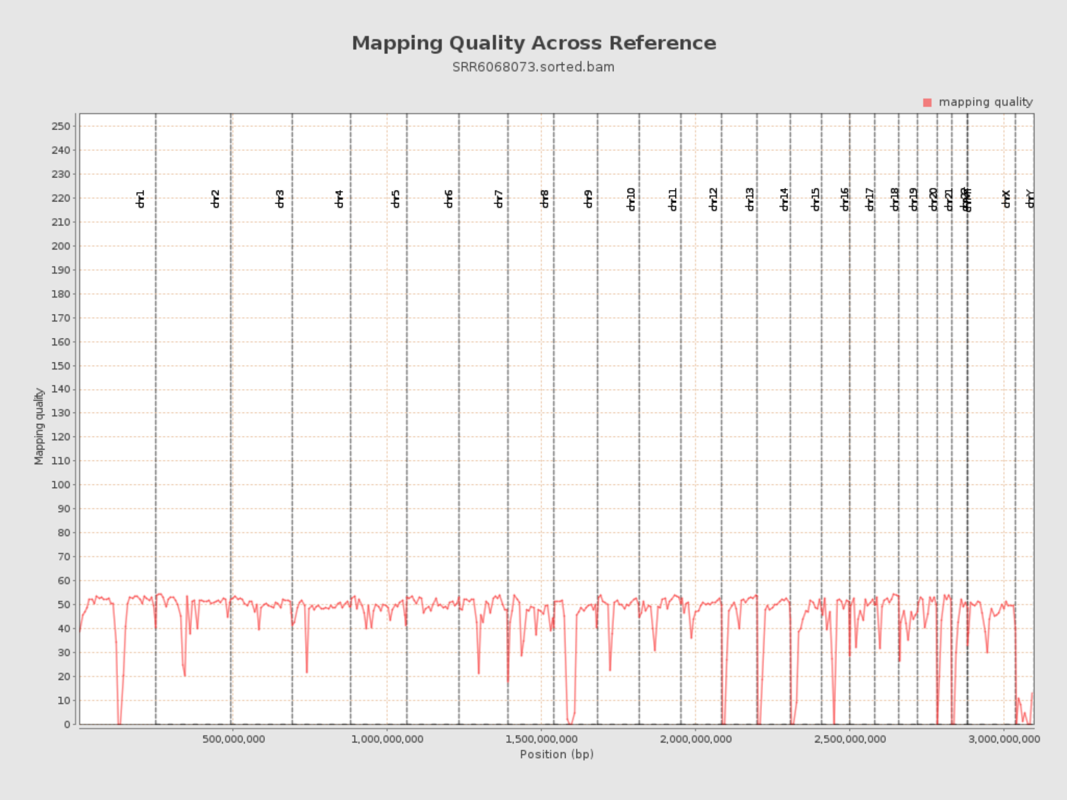
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram