Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:47:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080688.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_SRR3080688 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080688.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080688.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,588,398
Mapped reads	2,283,988 / 88.24%
Unmapped reads	304,410 / 11.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,930 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	109,286 / 4.22%
Duplication rate	4.05%
Clipped reads	627,872 / 24.26%

2.2. ACGT Content

Number/percentage of A's	49,608,681 / 30.53%
Number/percentage of C's	29,967,589 / 18.44%
Number/percentage of T's	50,534,069 / 31.1%
Number/percentage of G's	32,360,651 / 19.92%
Number/percentage of N's	2,477 / 0%
GC Percentage	38.36%

2.3. Coverage

Mean	0.0525

Standard Deviation	0.4639

2.4. Mapping Quality

Mean Mapping Quality	48.26

2.5. Mismatches and indels

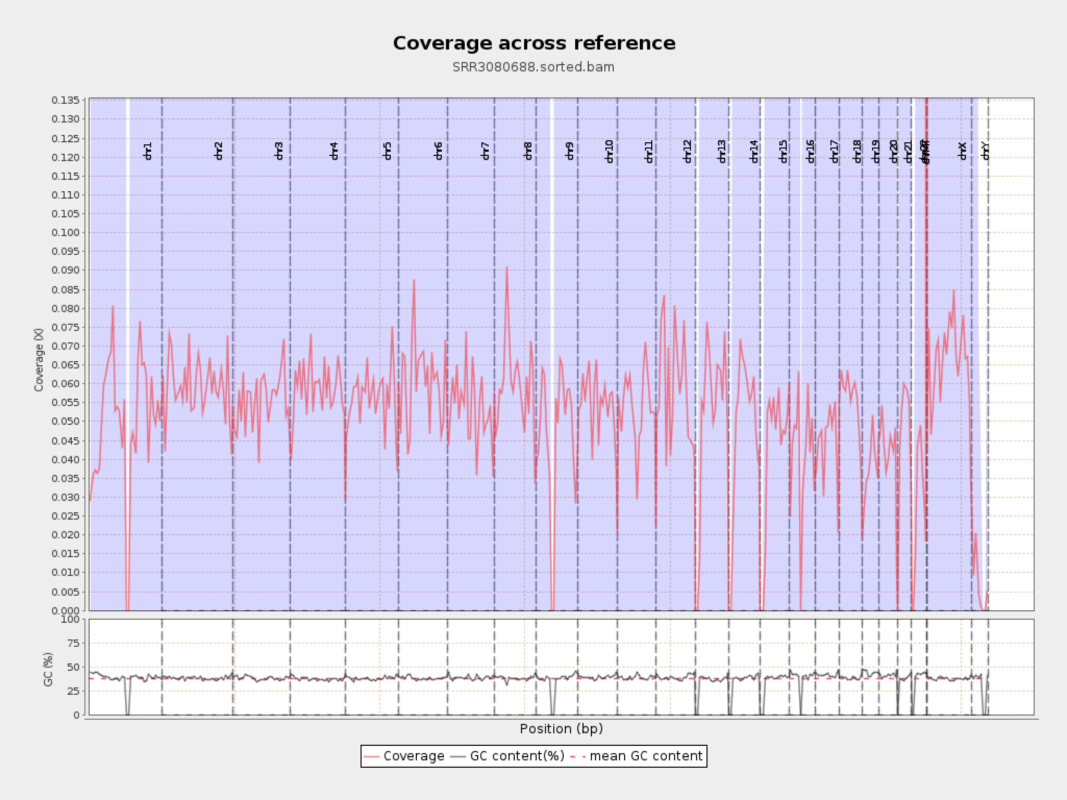
General error rate	0.81%
Mismatches	1,290,105
Insertions	12,518
Mapped reads with at least one insertion	0.54%
Deletions	33,683
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.4%

2.6. Chromosome stats

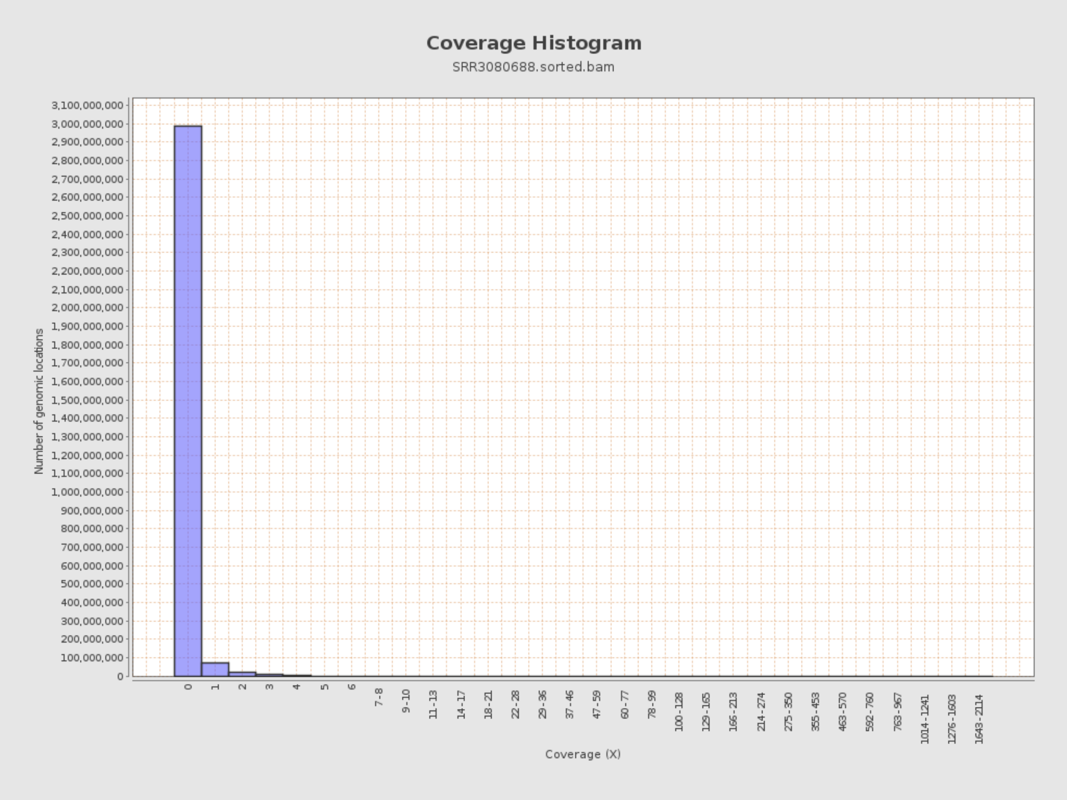
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12469114	0.05	0.4216
chr2	243199373	14469189	0.0595	0.4164
chr3	198022430	11021695	0.0557	0.3334
chr4	191154276	11298279	0.0591	0.3569
chr5	180915260	10204586	0.0564	0.3372
chr6	171115067	10384201	0.0607	0.3794
chr7	159138663	8548718	0.0537	0.4438

chr8	146364022	8743271	0.0597	1.3596
chr9	141213431	6502942	0.0461	0.3754
chr10	135534747	7480357	0.0552	0.3904
chr11	135006516	7225601	0.0535	0.3803
chr12	133851895	7866075	0.0588	0.3438
chr13	115169878	5854871	0.0508	0.3201
chr14	107349540	5150091	0.048	0.3211
chr15	102531392	4246335	0.0414	0.2833
chr16	90354753	3731653	0.0413	0.2924
chr17	81195210	3569215	0.044	0.2993
chr18	78077248	4425398	0.0567	0.4975
chr19	59128983	2222263	0.0376	0.3384
chr20	63025520	2711785	0.043	0.2941
chr21	48129895	2240617	0.0466	0.3164
chr22	51304566	1344714	0.0262	0.2188
chrMT	16571	164648	9.9359	6.6421
chrX	155270560	10255561	0.066	0.3693
chrY	59373566	403392	0.0068	0.1608

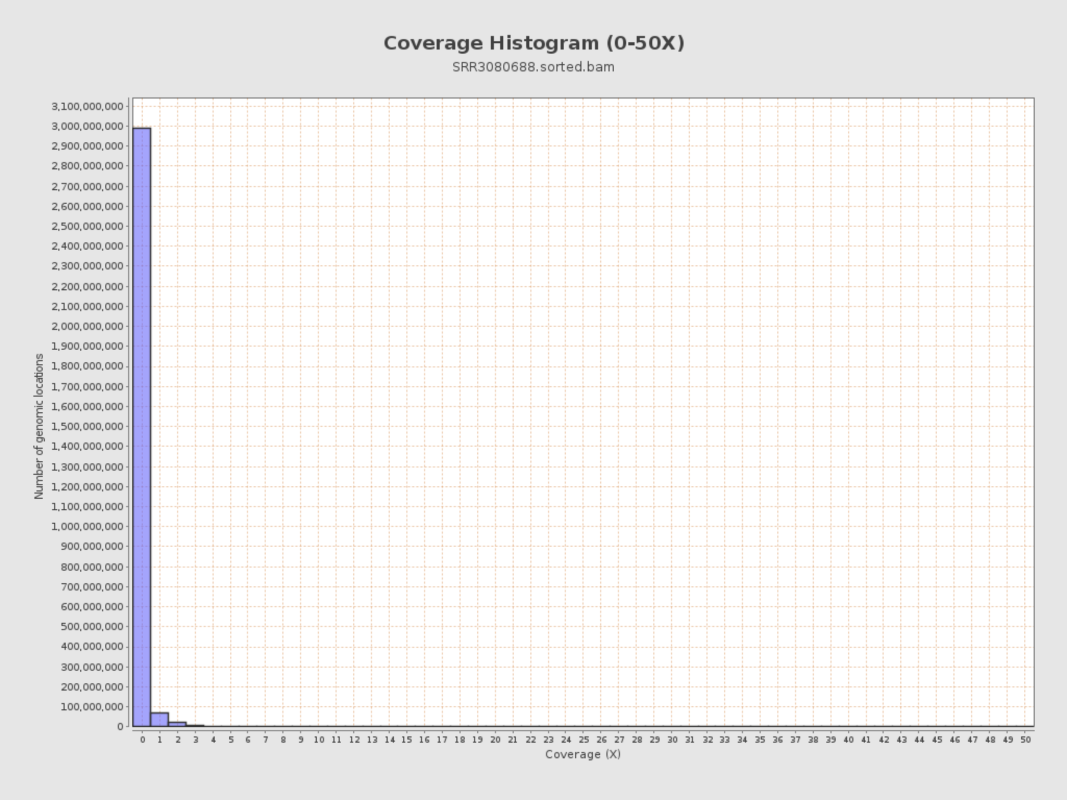
3. Results : Coverage across reference



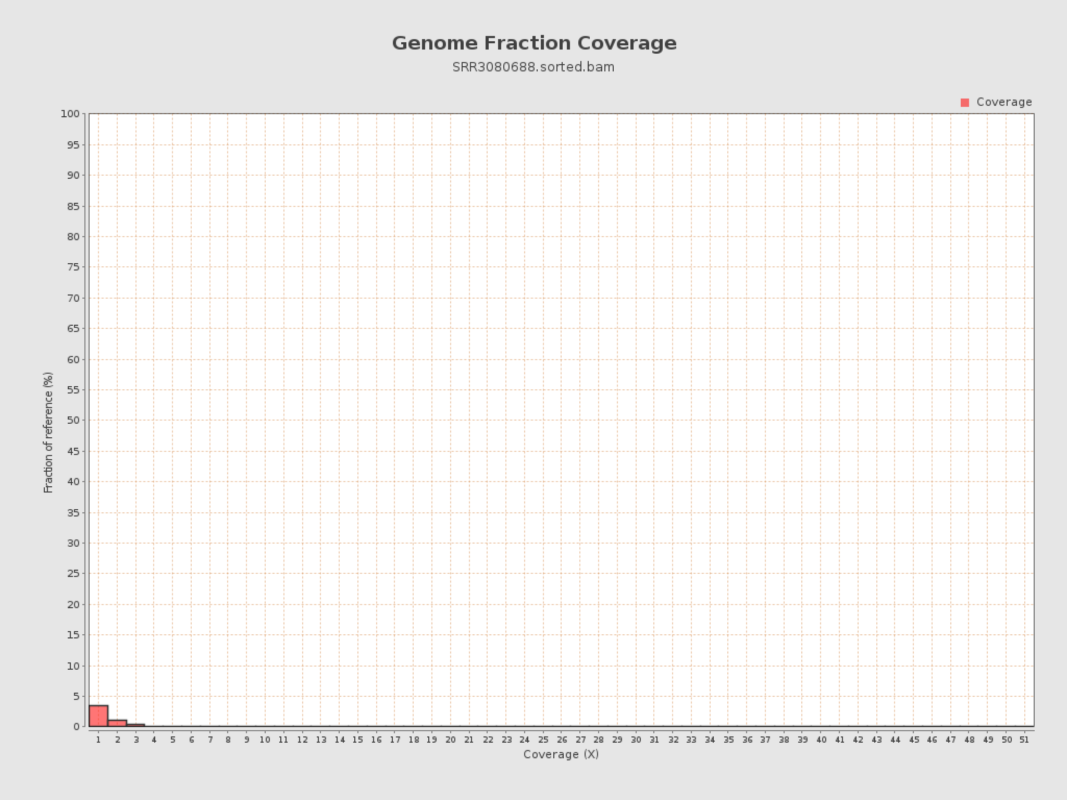
4. Results : Coverage Histogram



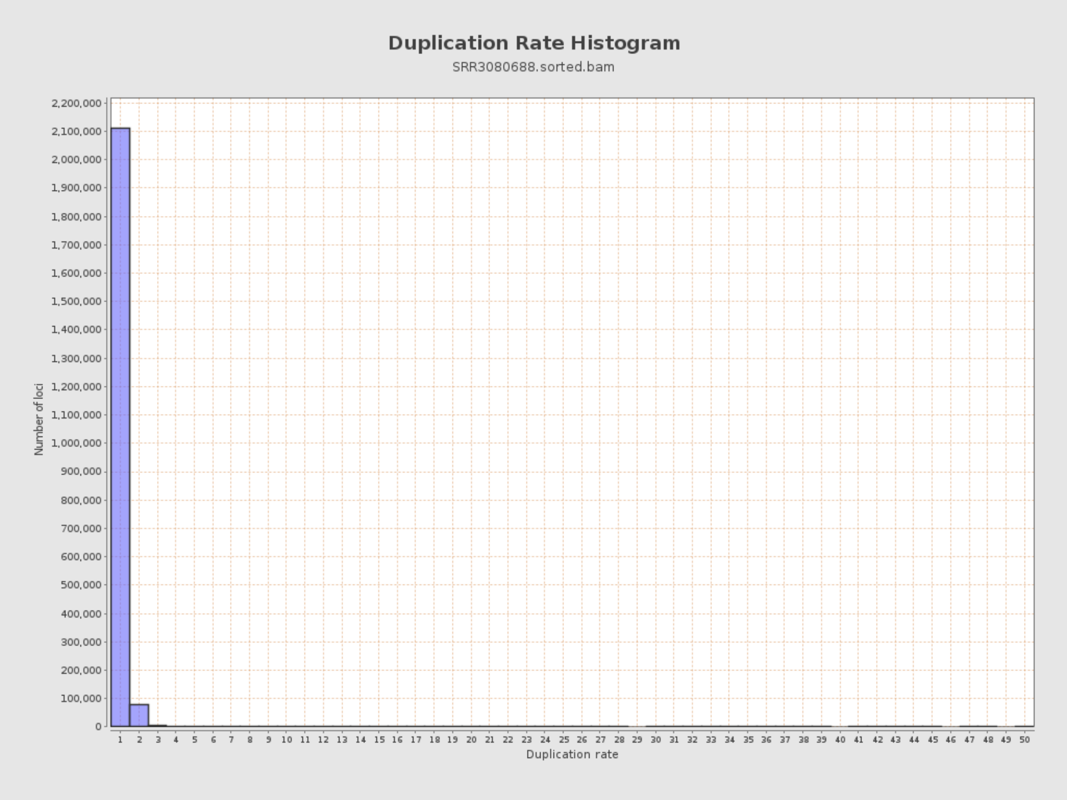
5. Results : Coverage Histogram (0-50X)



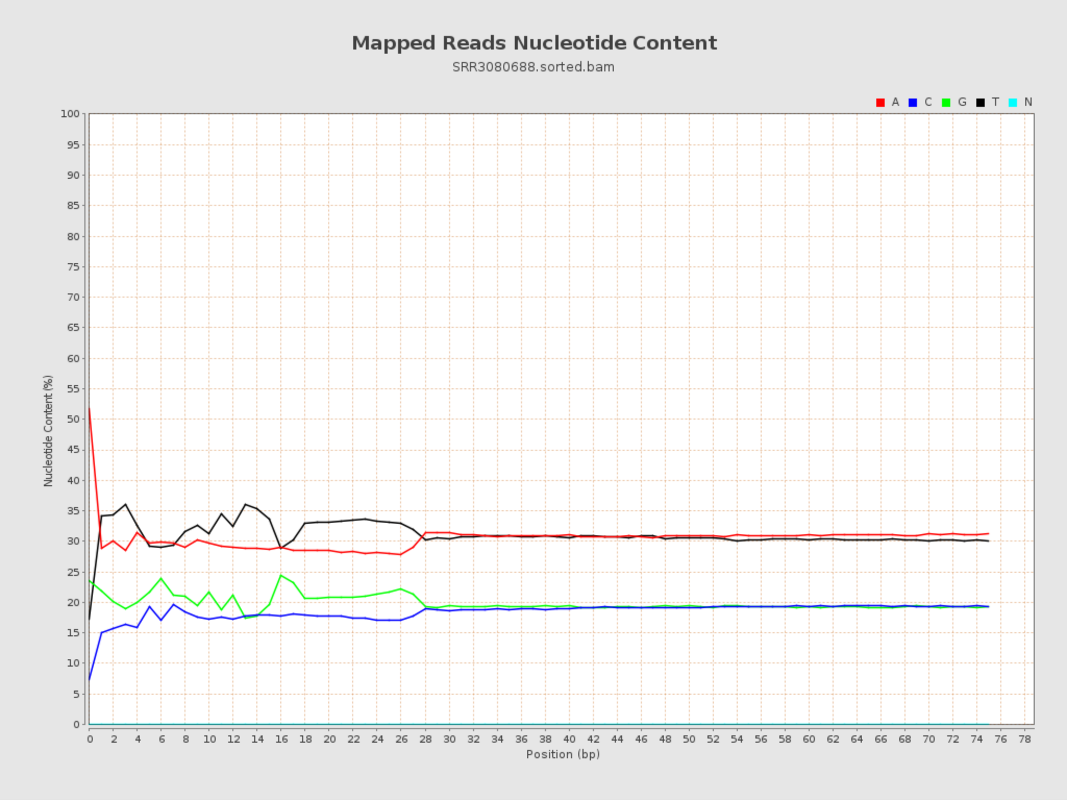
6. Results : Genome Fraction Coverage



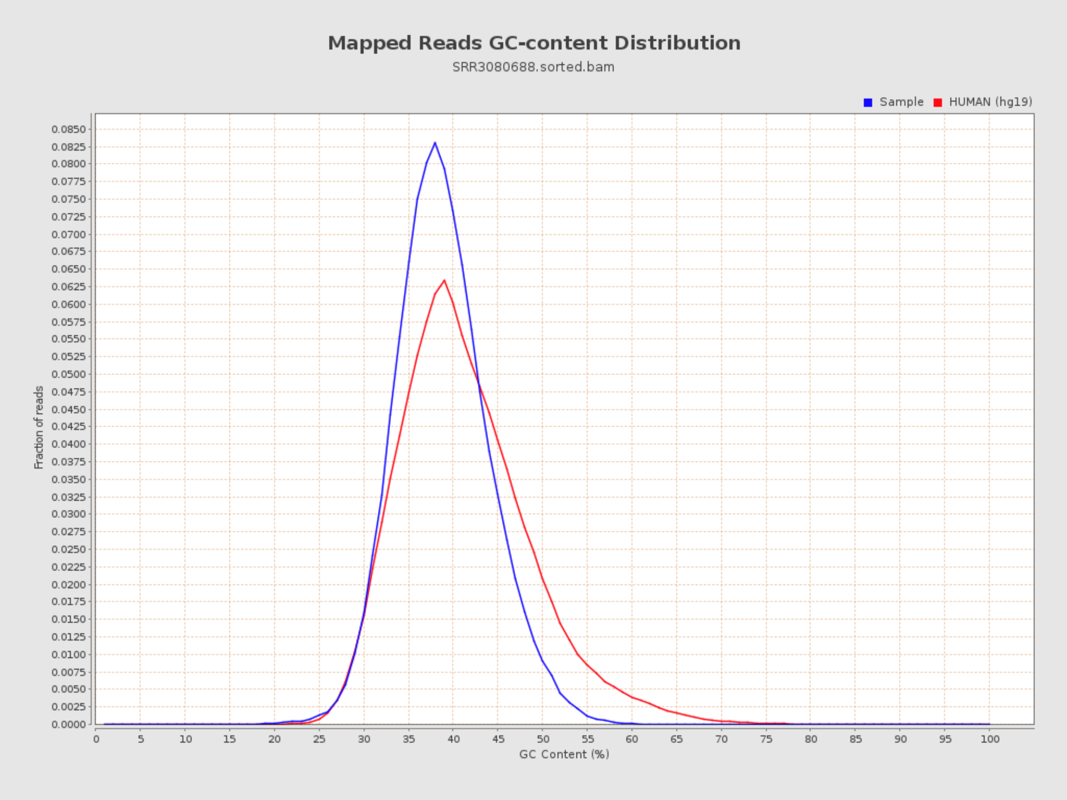
7. Results : Duplication Rate Histogram



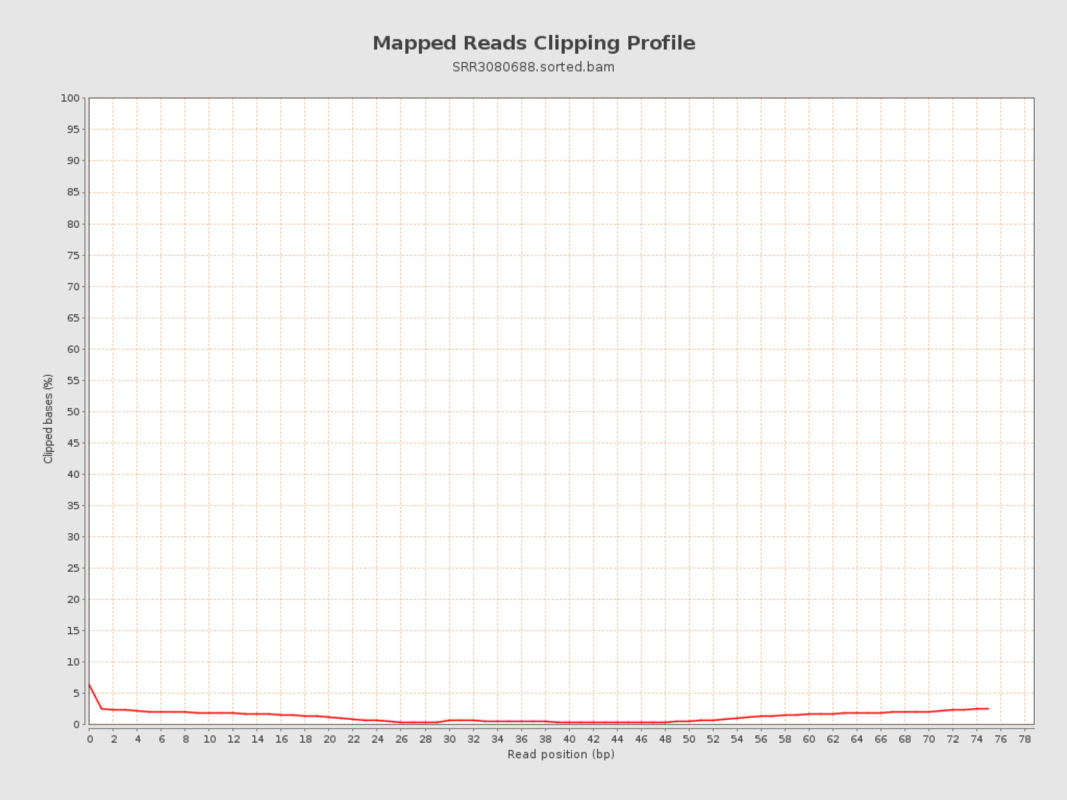
8. Results : Mapped Reads Nucleotide Content



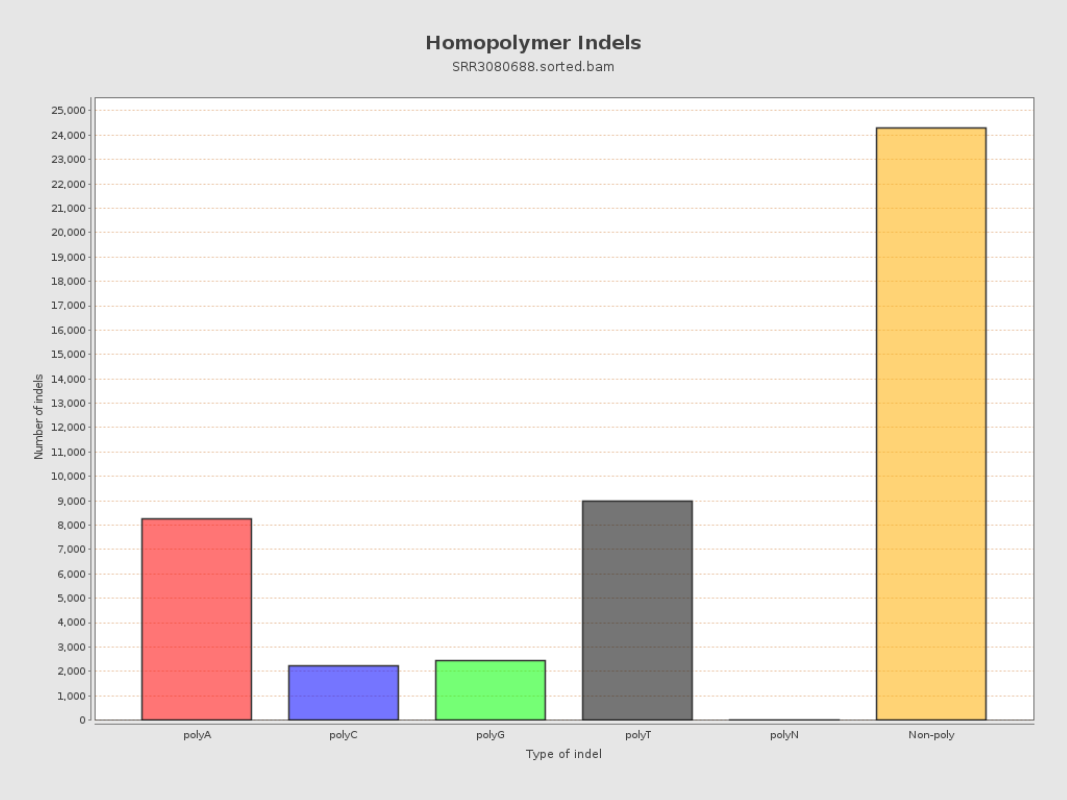
9. Results : Mapped Reads GC-content Distribution



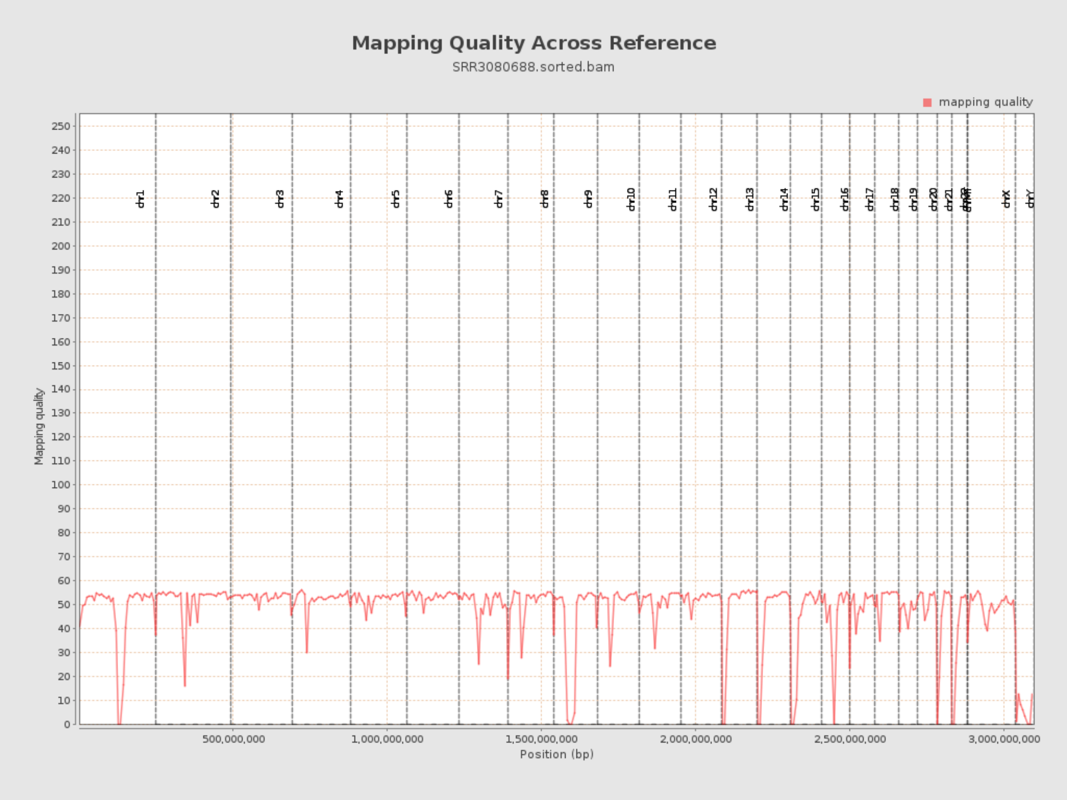
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram