Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:13:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080680.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_SRR3080680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080680.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:13:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,377,245
Mapped reads	1,273,328 / 92.45%
Unmapped reads	103,917 / 7.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,283 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	42,765 / 3.11%
Duplication rate	2.9%
Clipped reads	546,486 / 39.68%

2.2. ACGT Content

Number/percentage of A's	23,576,990 / 27.68%
Number/percentage of C's	15,512,501 / 18.21%
Number/percentage of T's	27,219,917 / 31.95%
Number/percentage of G's	18,878,798 / 22.16%
Number/percentage of N's	3,665 / 0%
GC Percentage	40.37%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.231

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

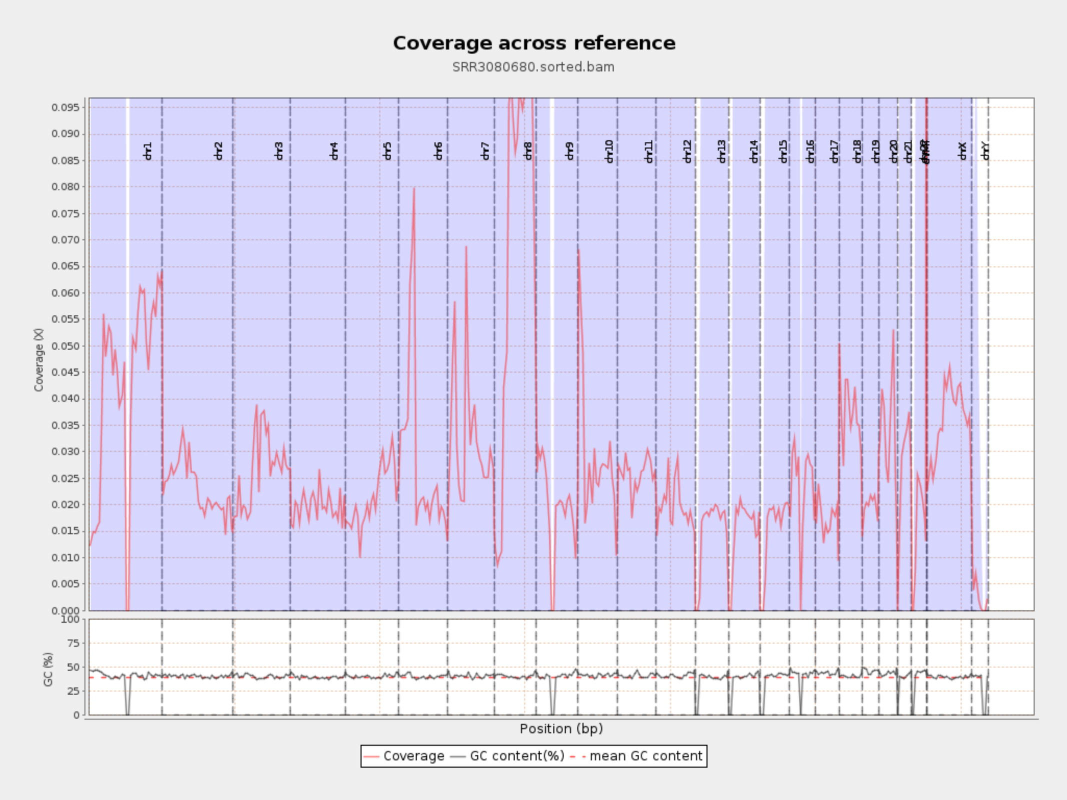
General error rate	0.69%
Mismatches	579,613
Insertions	6,255
Mapped reads with at least one insertion	0.49%
Deletions	20,149
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.83%

2.6. Chromosome stats

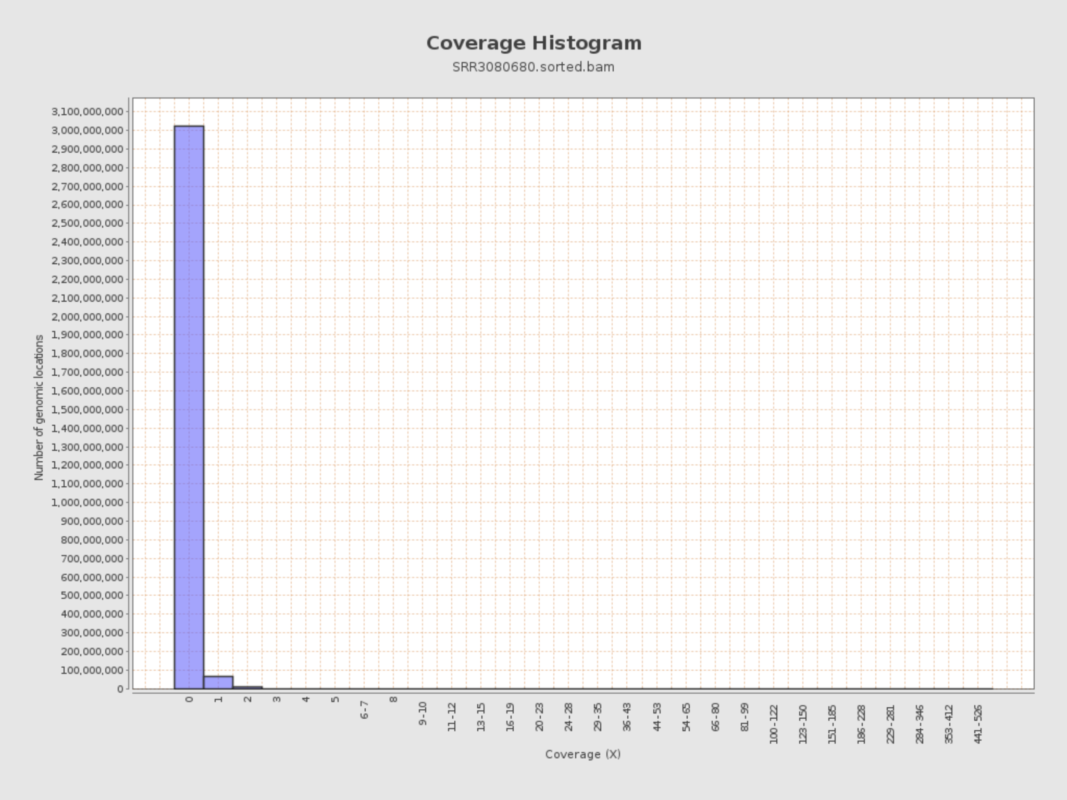
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10545963	0.0423	0.252
chr2	243199373	5683378	0.0234	0.2846
chr3	198022430	5282587	0.0267	0.1805
chr4	191154276	3759440	0.0197	0.1584
chr5	180915260	3881108	0.0215	0.1619
chr6	171115067	4981942	0.0291	0.2263
chr7	159138663	5303949	0.0333	0.5106

chr8	146364022	10455224	0.0714	0.3246
chr9	141213431	2720753	0.0193	0.1725
chr10	135534747	4054342	0.0299	0.2031
chr11	135006516	3471750	0.0257	0.1829
chr12	133851895	2650238	0.0198	0.1555
chr13	115169878	1724274	0.015	0.1361
chr14	107349540	1614830	0.015	0.1374
chr15	102531392	1548888	0.0151	0.1404
chr16	90354753	2124590	0.0235	0.1721
chr17	81195210	1384555	0.0171	0.1445
chr18	78077248	2924695	0.0375	0.2544
chr19	59128983	1188772	0.0201	0.175
chr20	63025520	2138334	0.0339	0.2049
chr21	48129895	1281034	0.0266	0.183
chr22	51304566	764095	0.0149	0.1342
chrMT	16571	8609	0.5195	0.8207
chrX	155270560	5568421	0.0359	0.2148
chrY	59373566	162932	0.0027	0.0614

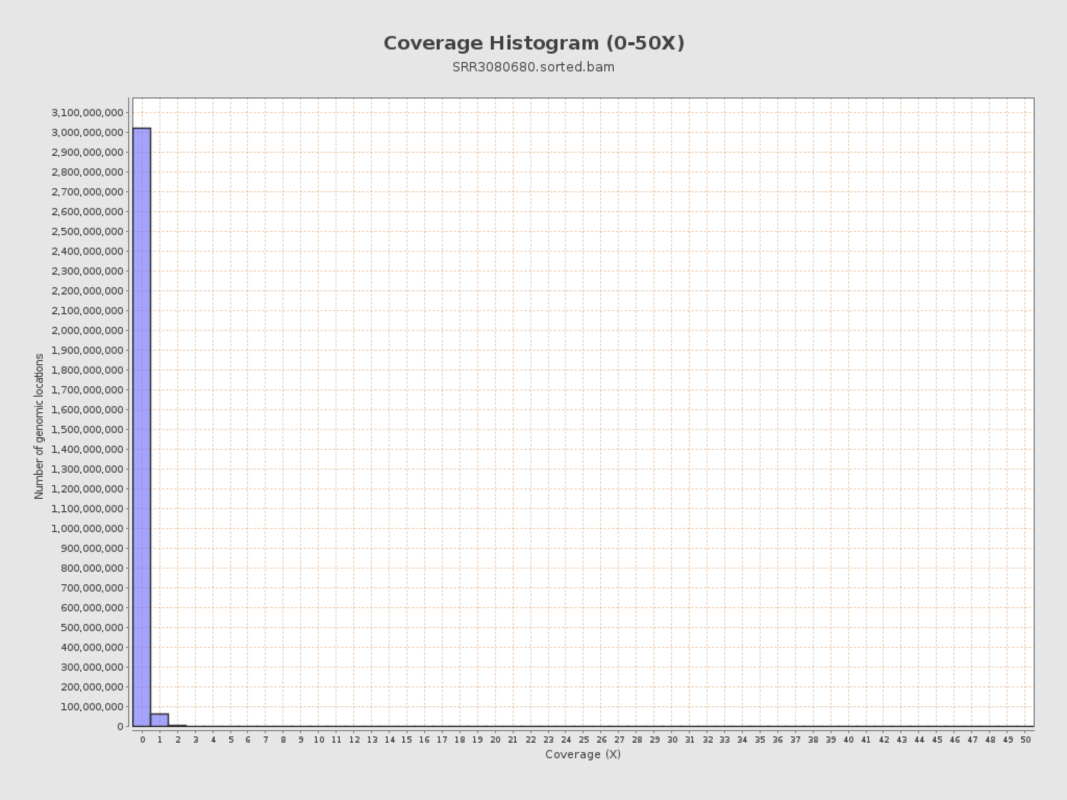
3. Results : Coverage across reference



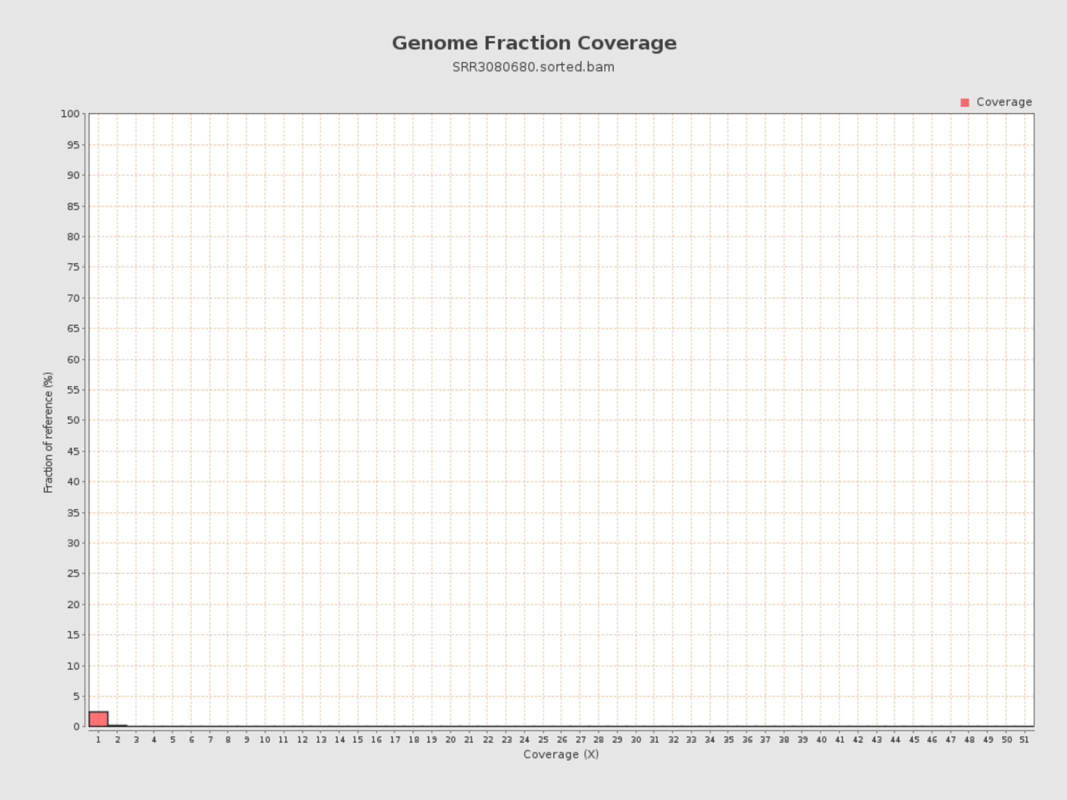
4. Results : Coverage Histogram



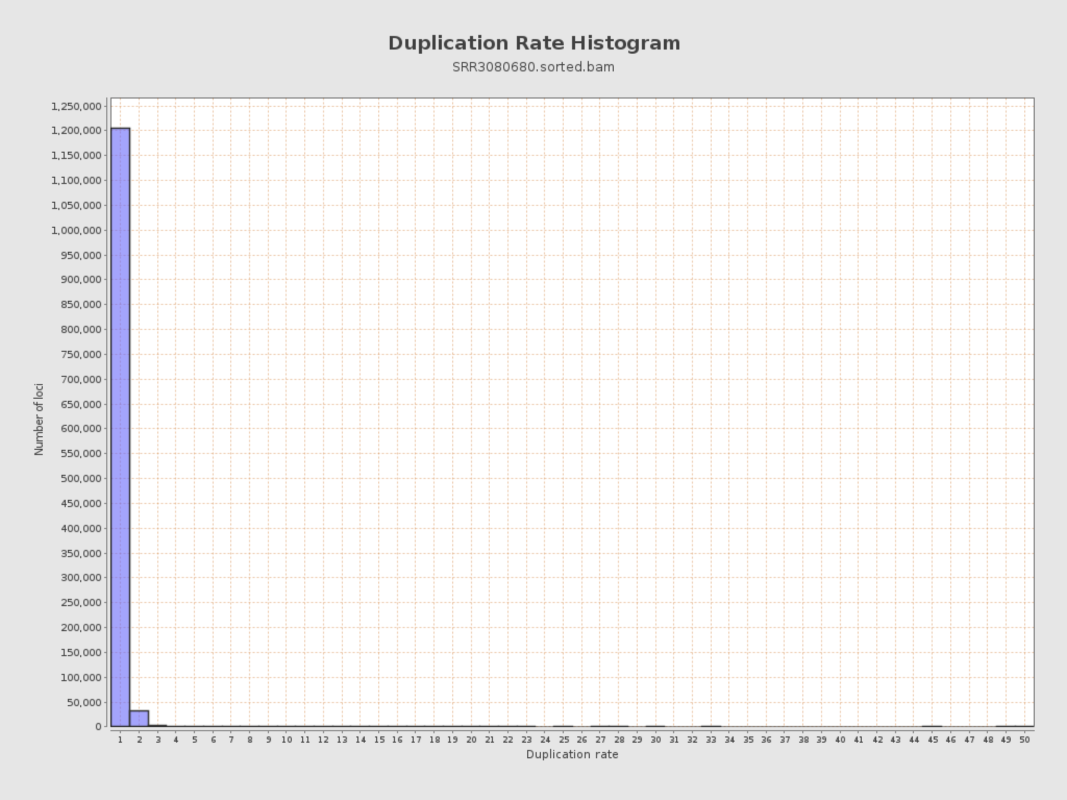
5. Results : Coverage Histogram (0-50X)



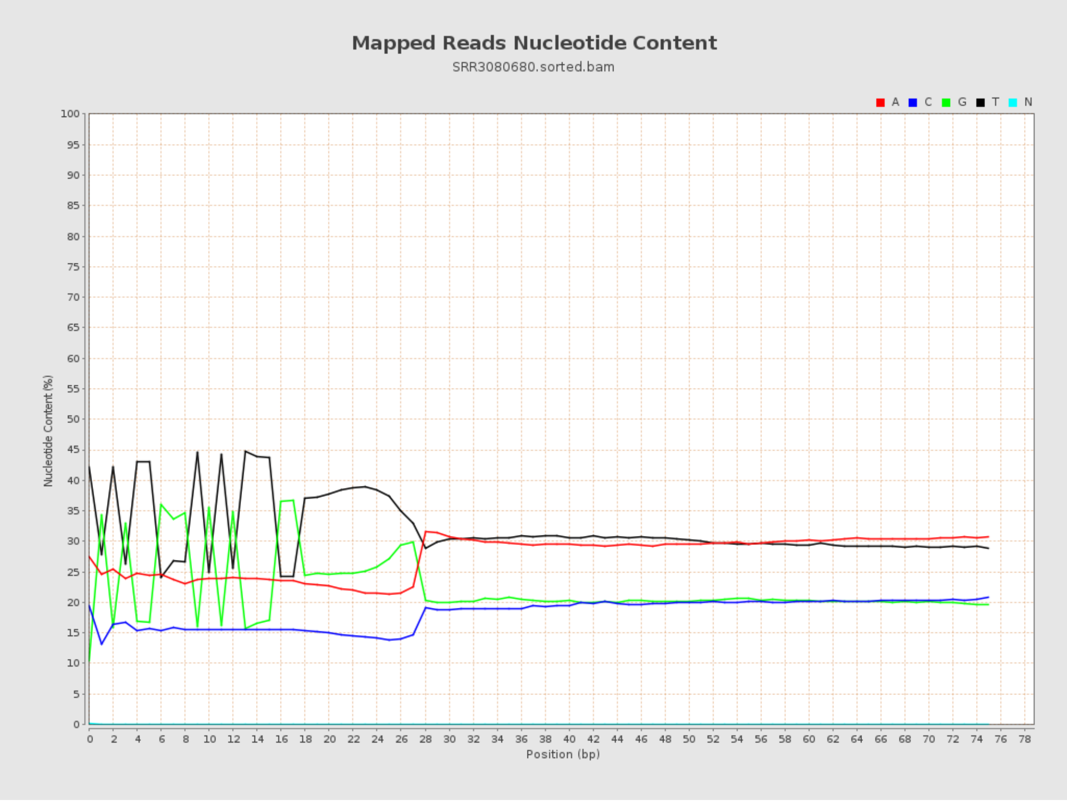
6. Results : Genome Fraction Coverage



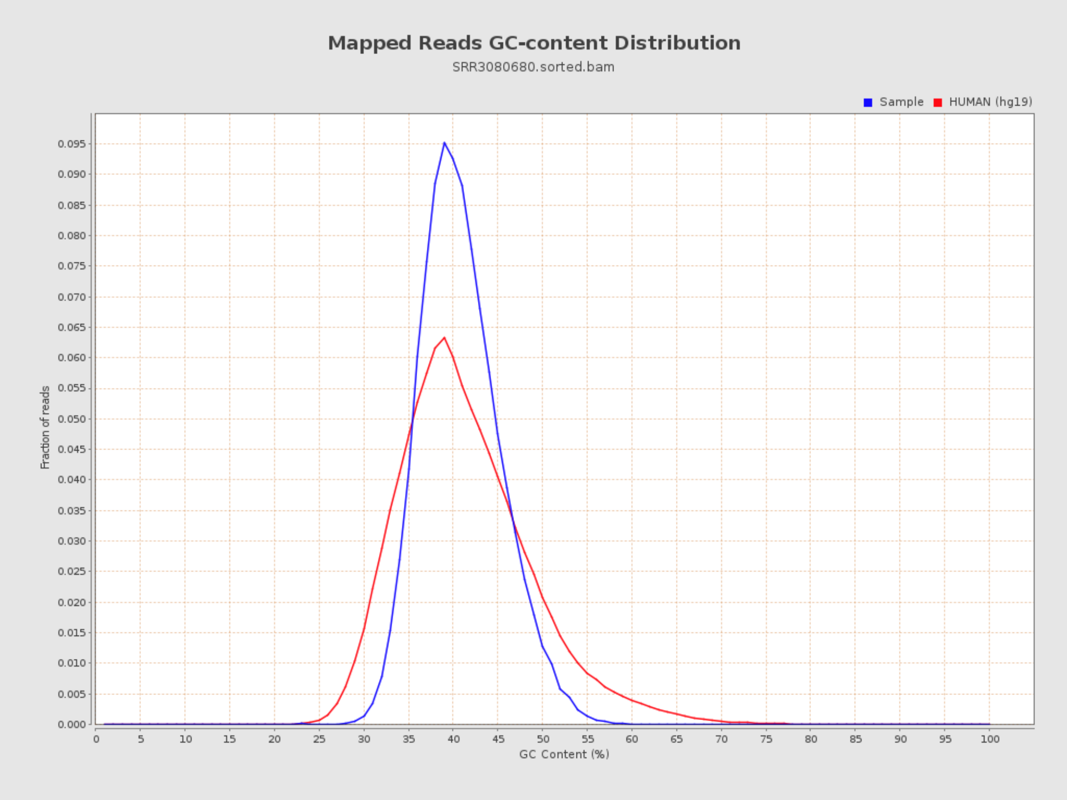
7. Results : Duplication Rate Histogram



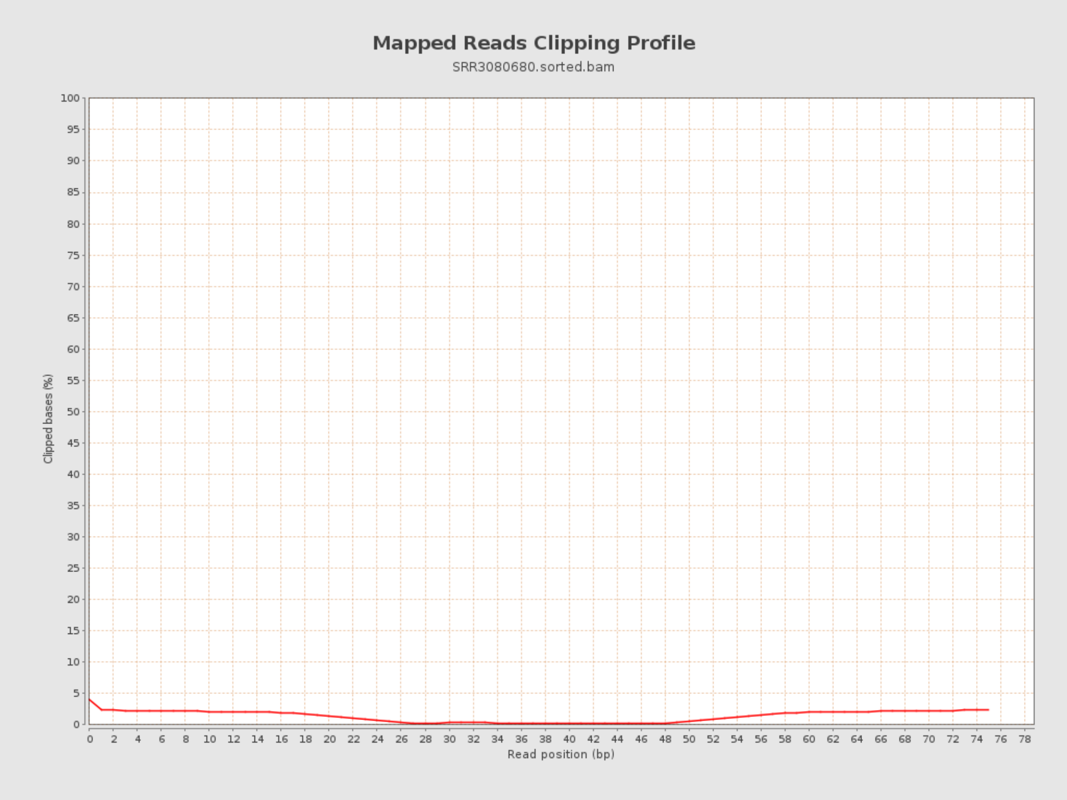
8. Results : Mapped Reads Nucleotide Content



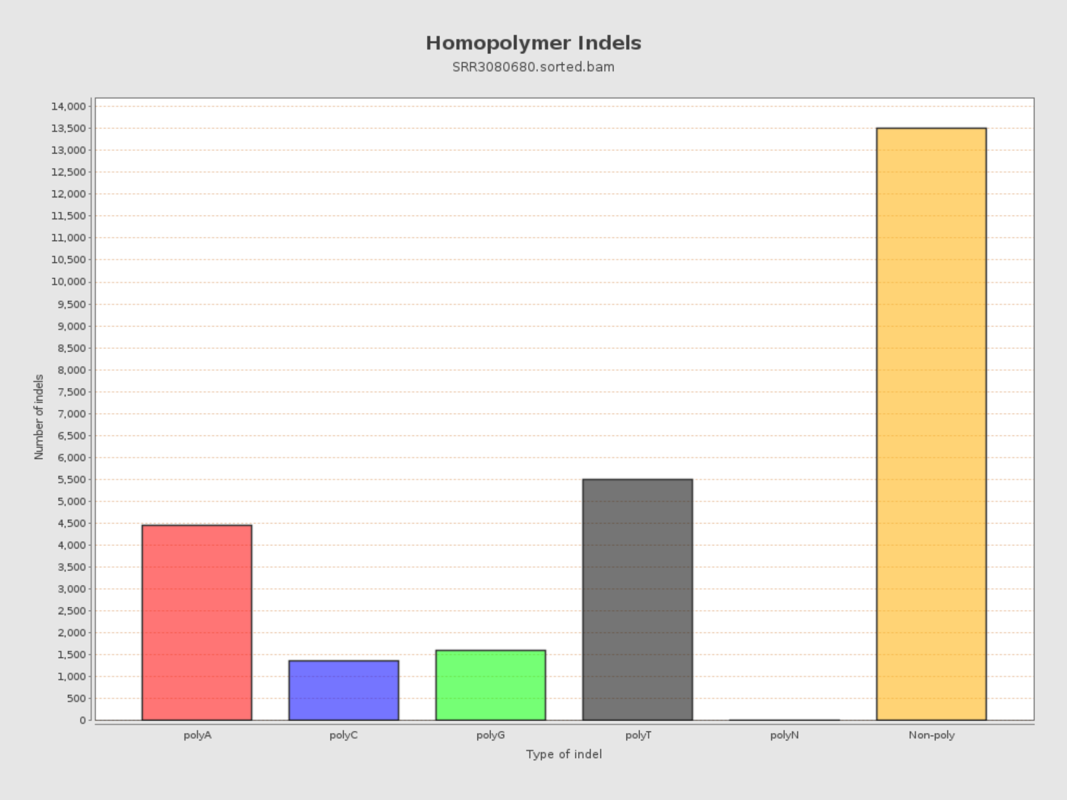
9. Results : Mapped Reads GC-content Distribution



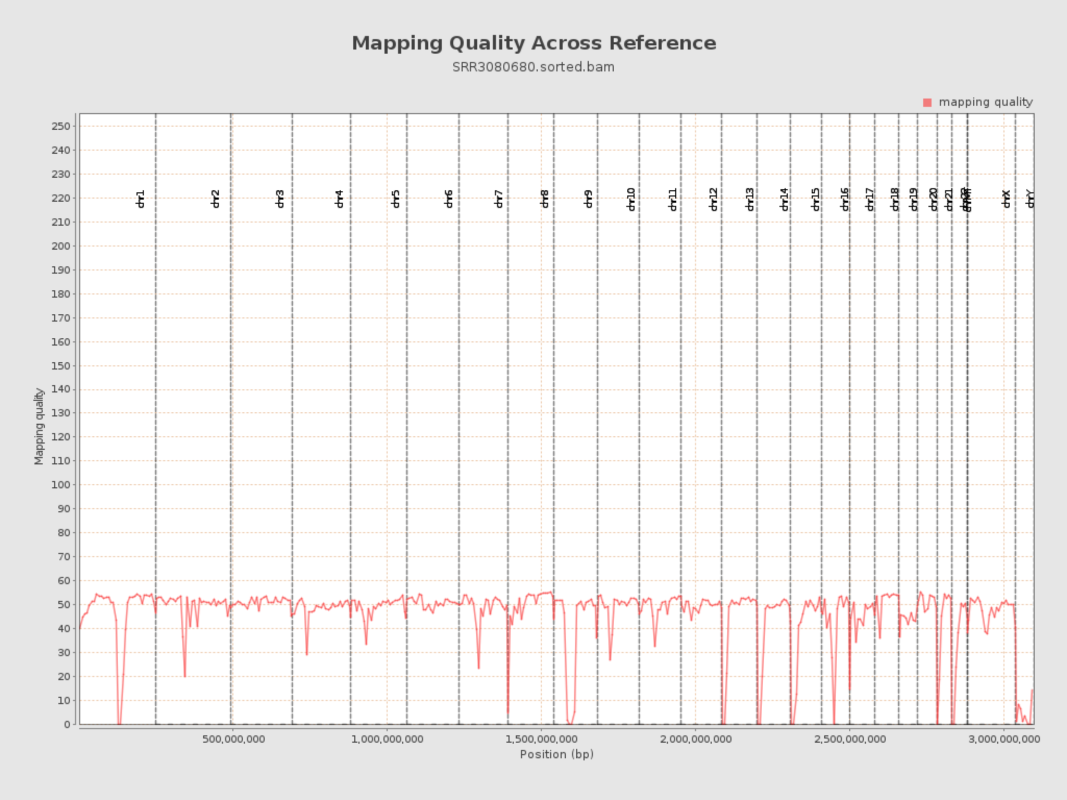
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram