Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080785.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_SRR3080785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,336,868
Mapped reads	2,066,064 / 88.41%
Unmapped reads	270,804 / 11.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,893 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	89,044 / 3.81%
Duplication rate	3.62%
Clipped reads	995,834 / 42.61%

2.2. ACGT Content

Number/percentage of A's	39,333,705 / 28.77%
Number/percentage of C's	26,386,609 / 19.3%
Number/percentage of T's	41,720,183 / 30.51%
Number/percentage of G's	29,289,874 / 21.42%
Number/percentage of N's	2,837 / 0%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.3222

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

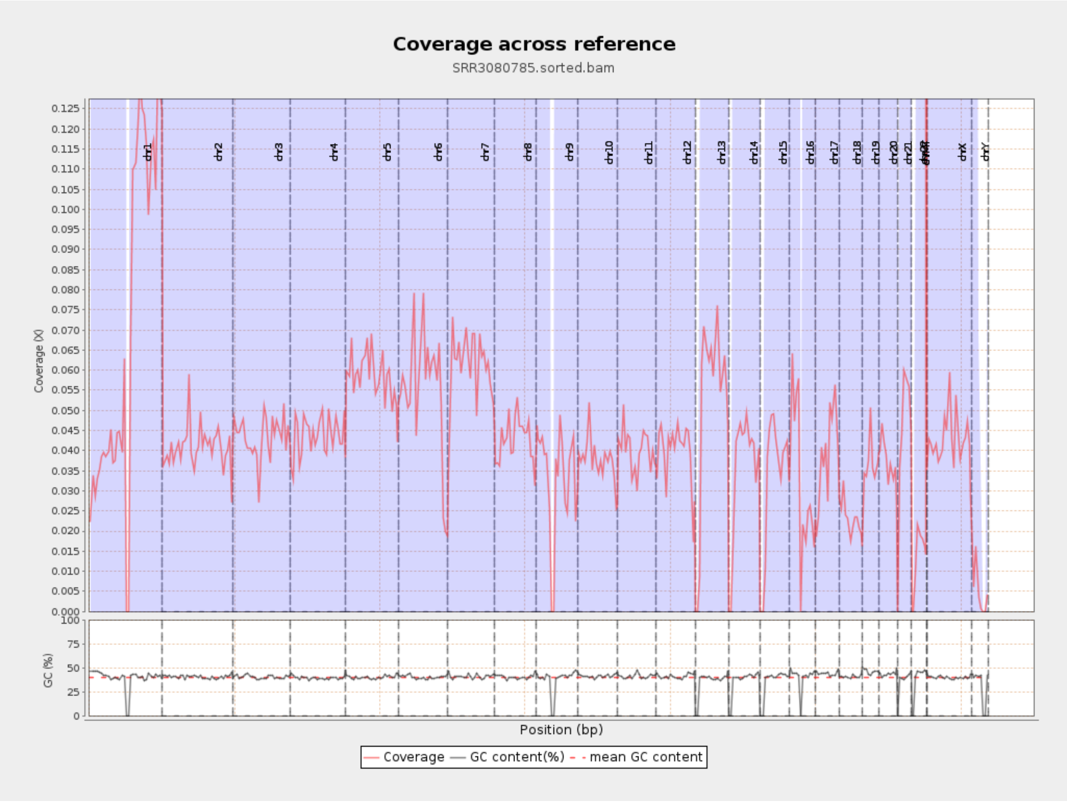
General error rate	0.75%
Mismatches	1,009,481
Insertions	10,249
Mapped reads with at least one insertion	0.49%
Deletions	28,813
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.73%

2.6. Chromosome stats

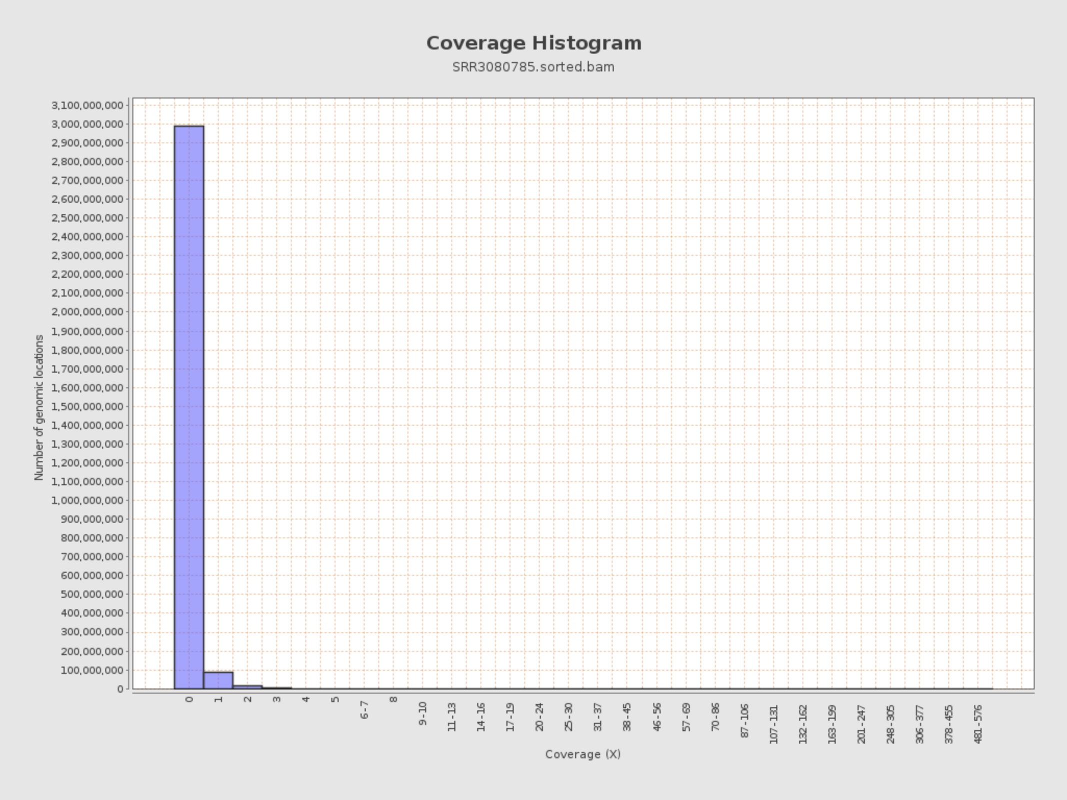
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17462350	0.0701	0.5071
chr2	243199373	9958459	0.0409	0.3479
chr3	198022430	8578220	0.0433	0.2495
chr4	191154276	8366078	0.0438	0.2601
chr5	180915260	10642472	0.0588	0.2927
chr6	171115067	9565693	0.0559	0.353
chr7	159138663	9836014	0.0618	0.4349

chr8	146364022	6241007	0.0426	0.4297
chr9	141213431	4645686	0.0329	0.2534
chr10	135534747	5151703	0.038	0.29
chr11	135006516	5392517	0.0399	0.2679
chr12	133851895	5321940	0.0398	0.2399
chr13	115169878	6028209	0.0523	0.2775
chr14	107349540	3785574	0.0353	0.234
chr15	102531392	3413831	0.0333	0.2244
chr16	90354753	2929215	0.0324	0.2262
chr17	81195210	3172247	0.0391	0.2481
chr18	78077248	1833922	0.0235	0.406
chr19	59128983	2159091	0.0365	0.3633
chr20	63025520	2363474	0.0375	0.2399
chr21	48129895	2180363	0.0453	0.2633
chr22	51304566	678348	0.0132	0.1352
chrMT	16571	108385	6.5406	4.1825
chrX	155270560	6649799	0.0428	0.2584
chrY	59373566	314443	0.0053	0.1187

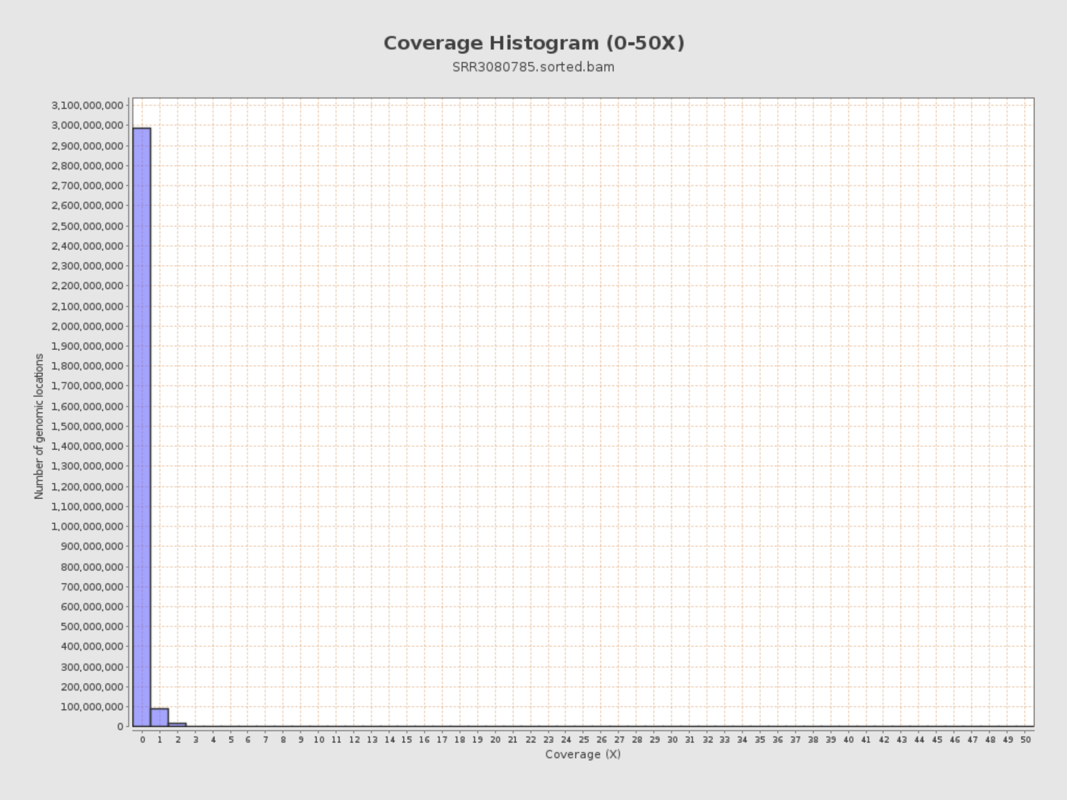
3. Results : Coverage across reference



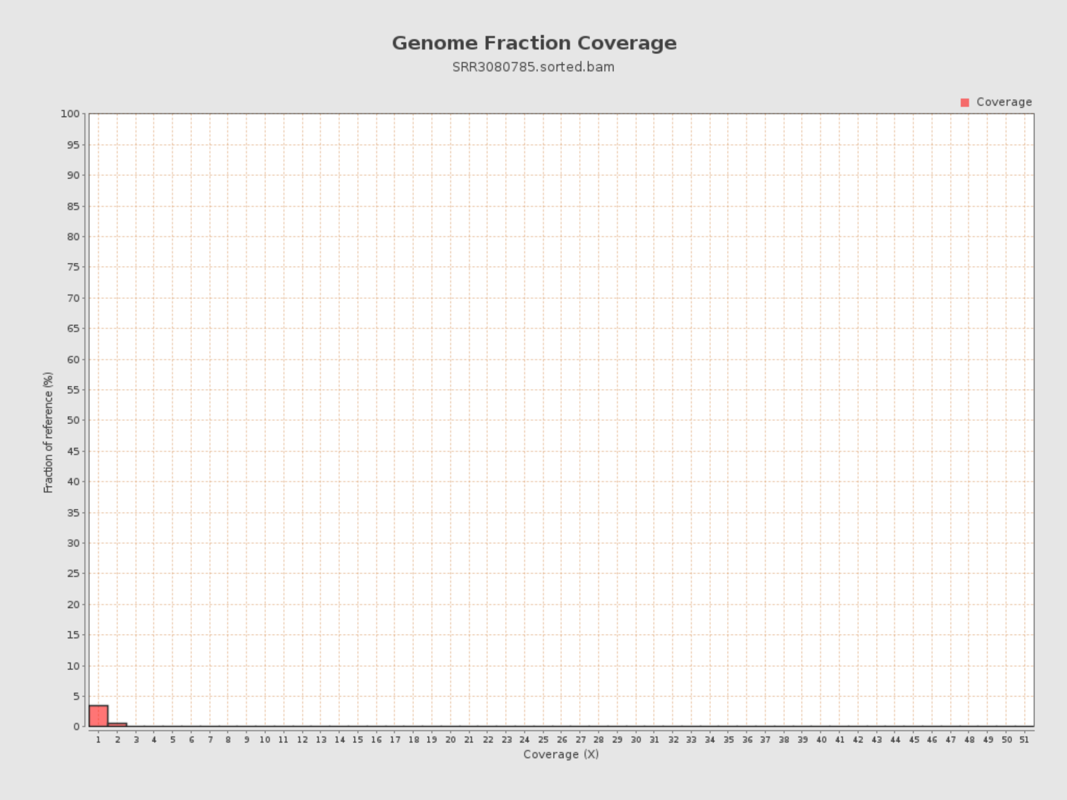
4. Results : Coverage Histogram



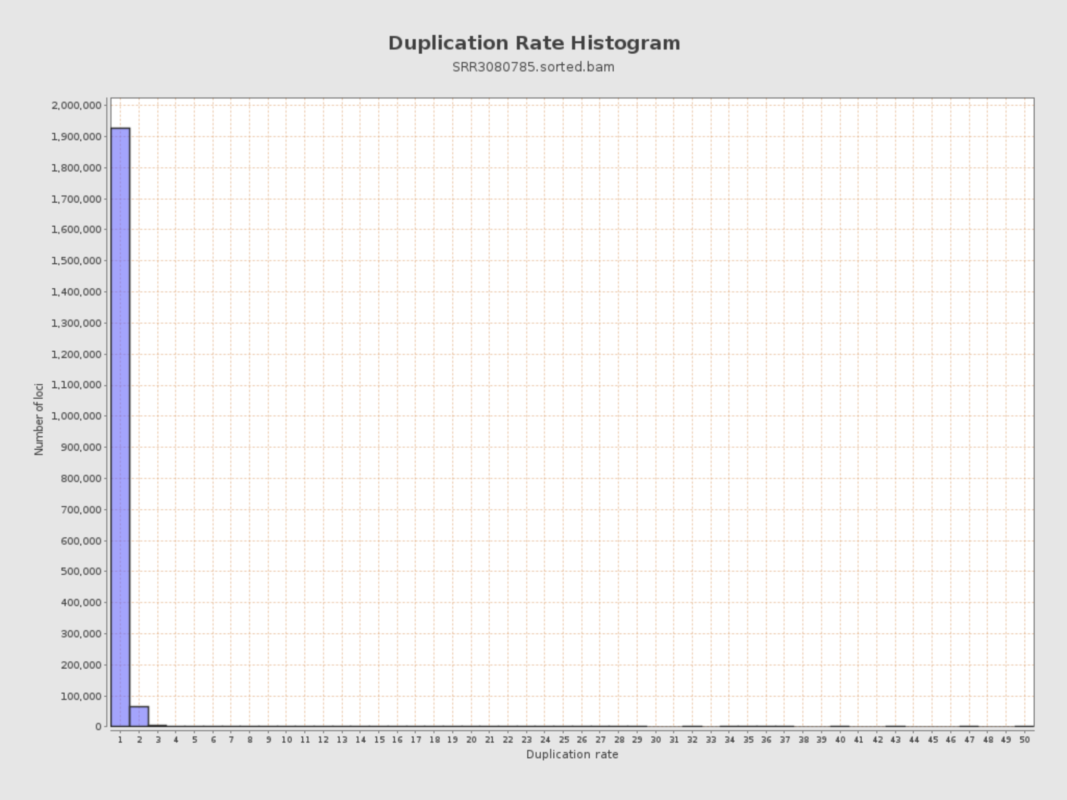
5. Results : Coverage Histogram (0-50X)



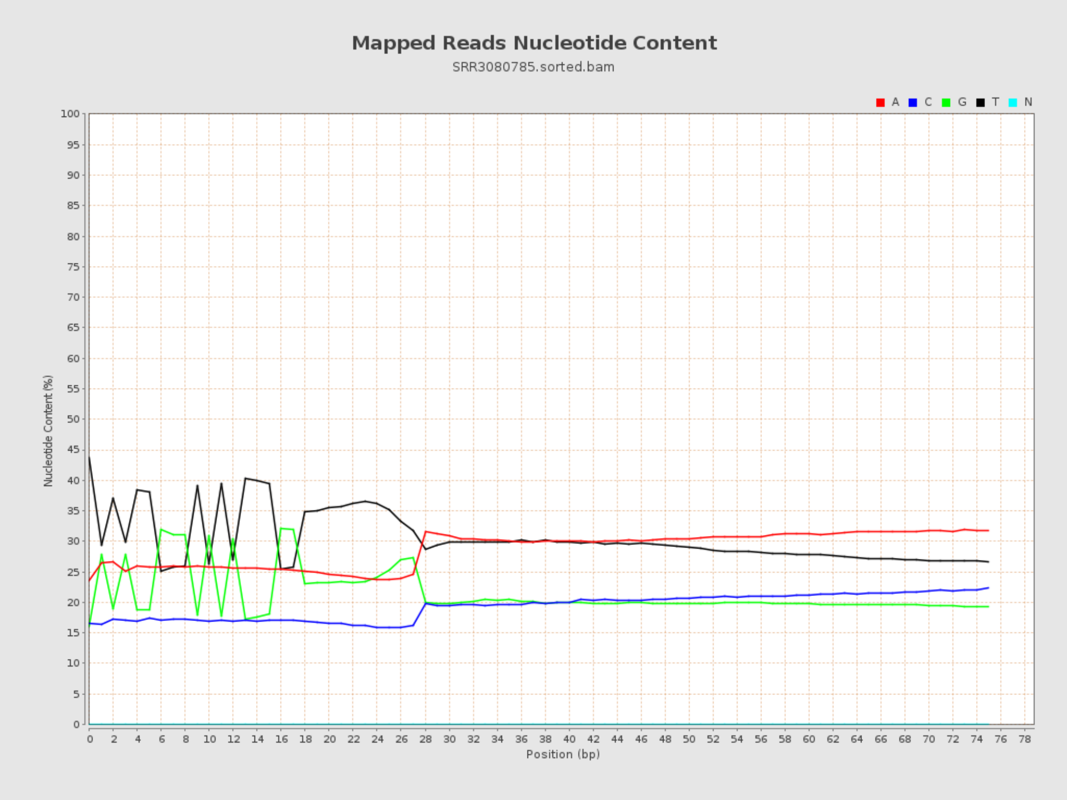
6. Results : Genome Fraction Coverage



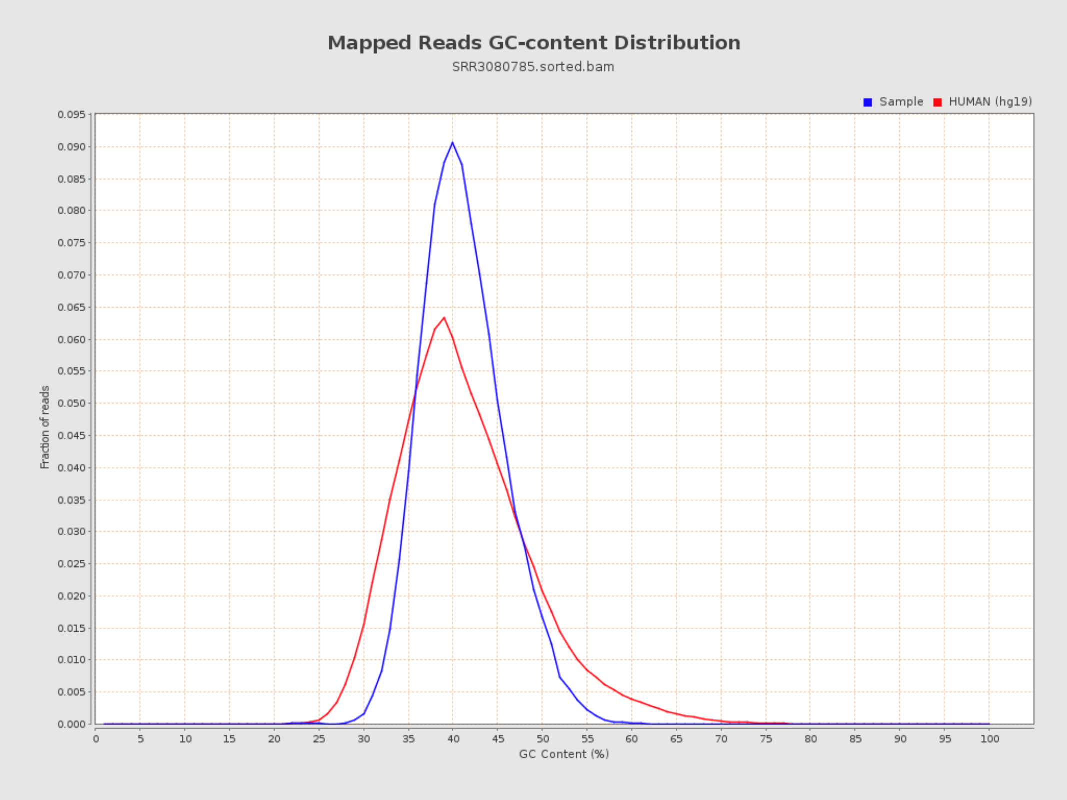
7. Results : Duplication Rate Histogram



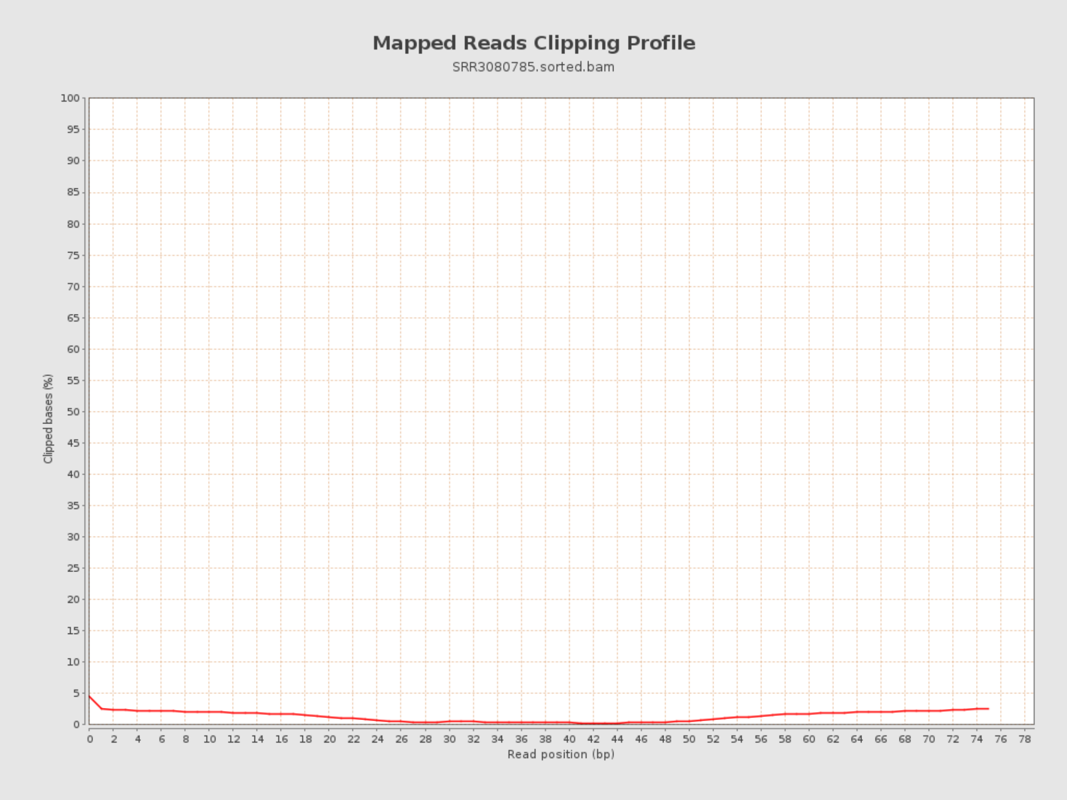
8. Results : Mapped Reads Nucleotide Content



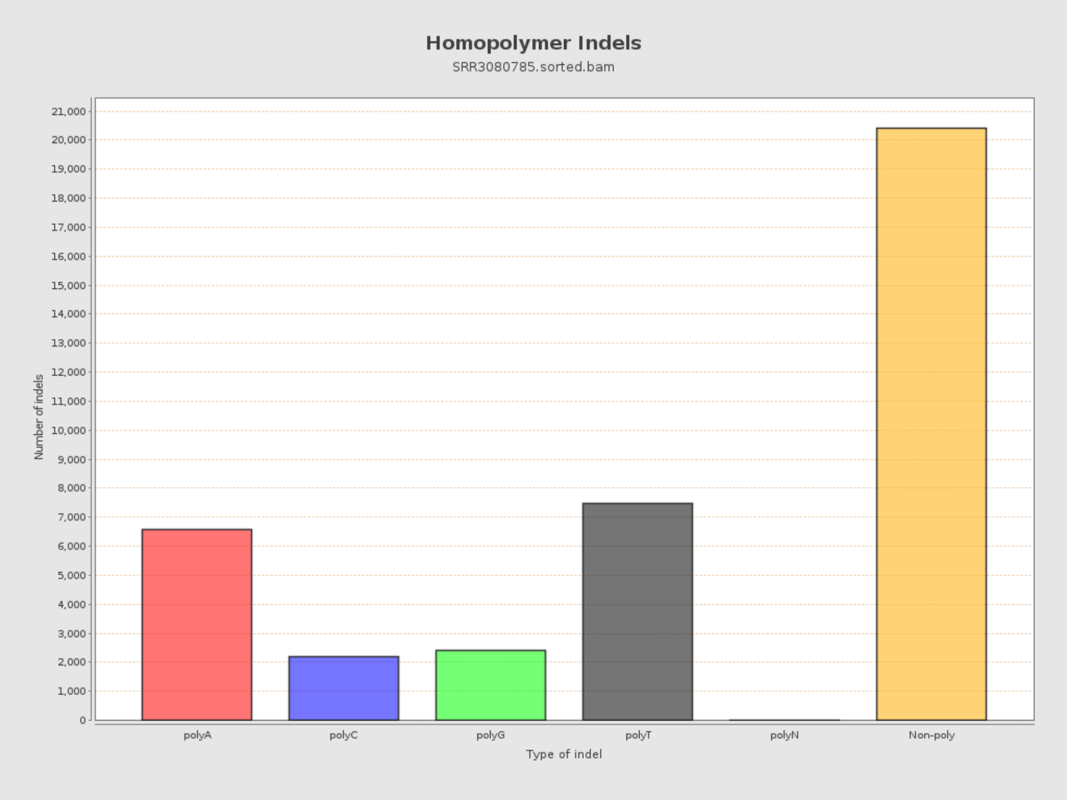
9. Results : Mapped Reads GC-content Distribution



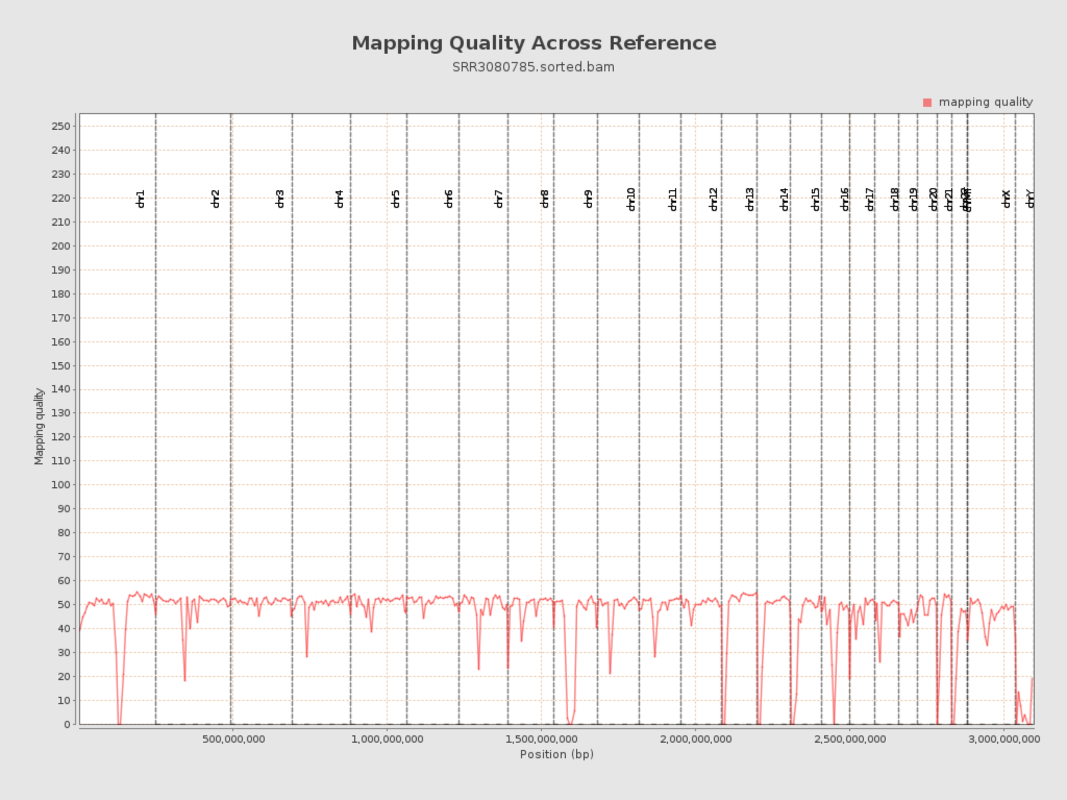
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram