Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:22:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080554.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_SRR3080554 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080554.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:22:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080554.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,702,161
Mapped reads	3,135,616 / 84.7%
Unmapped reads	566,545 / 15.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,499 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	152,035 / 4.11%
Duplication rate	3.87%
Clipped reads	1,521,383 / 41.09%

2.2. ACGT Content

Number/percentage of A's	56,920,067 / 27.27%
Number/percentage of C's	37,339,211 / 17.89%
Number/percentage of T's	67,495,175 / 32.34%
Number/percentage of G's	46,811,808 / 22.43%
Number/percentage of N's	170,324 / 0.08%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0675

Standard Deviation	0.4748

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

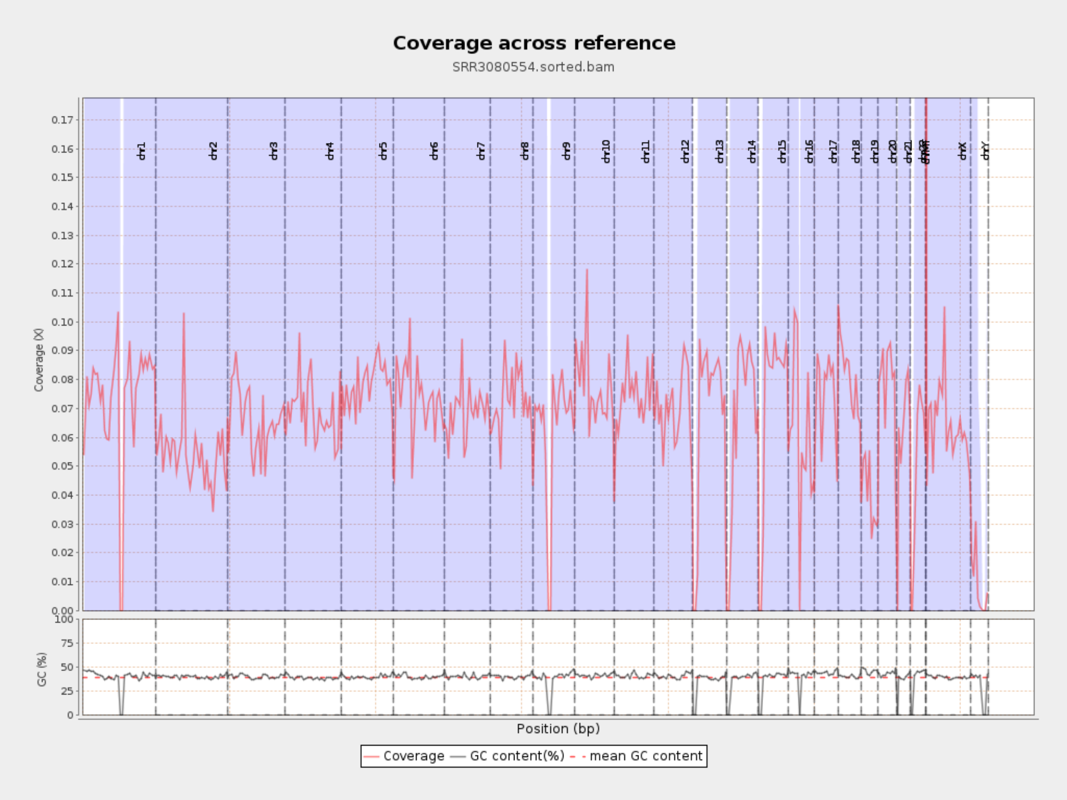
General error rate	0.94%
Mismatches	1,936,558
Insertions	18,277
Mapped reads with at least one insertion	0.58%
Deletions	53,227
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.31%

2.6. Chromosome stats

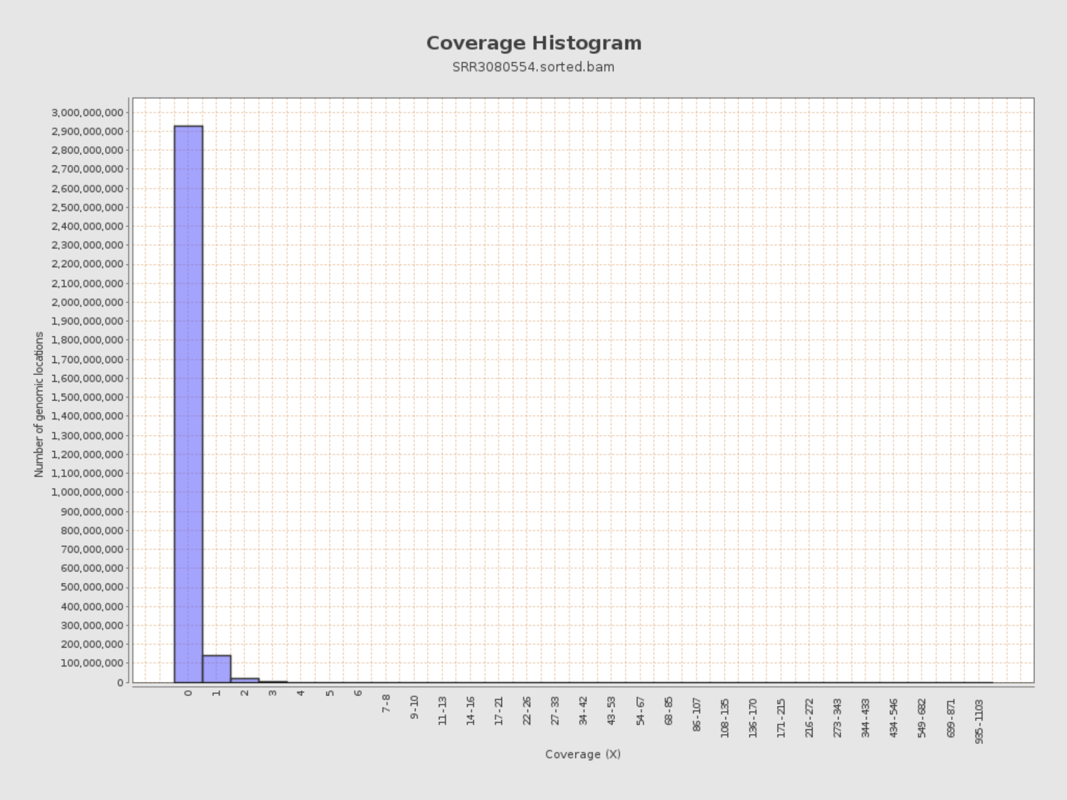
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18314631	0.0735	0.6646
chr2	243199373	13199075	0.0543	0.5345
chr3	198022430	13117070	0.0662	0.312
chr4	191154276	13183123	0.069	0.3429
chr5	180915260	14139977	0.0782	0.333
chr6	171115067	12636901	0.0739	0.4063
chr7	159138663	10985046	0.069	0.6922

chr8	146364022	10638195	0.0727	0.7423
chr9	141213431	8864239	0.0628	0.4699
chr10	135534747	10557135	0.0779	0.5319
chr11	135006516	10028746	0.0743	0.4618
chr12	133851895	9496243	0.0709	0.3305
chr13	115169878	7763746	0.0674	0.308
chr14	107349540	7259248	0.0676	0.345
chr15	102531392	7359596	0.0718	0.3186
chr16	90354753	5320521	0.0589	0.3455
chr17	81195210	6128665	0.0755	0.3646
chr18	78077248	6348838	0.0813	0.7791
chr19	59128983	2385894	0.0404	0.5353
chr20	63025520	5096815	0.0809	0.3511
chr21	48129895	2990273	0.0621	0.3335
chr22	51304566	2508530	0.0489	0.262
chrMT	16571	47430	2.8622	2.6722
chrX	155270560	9943766	0.064	0.3435
chrY	59373566	510965	0.0086	0.2196

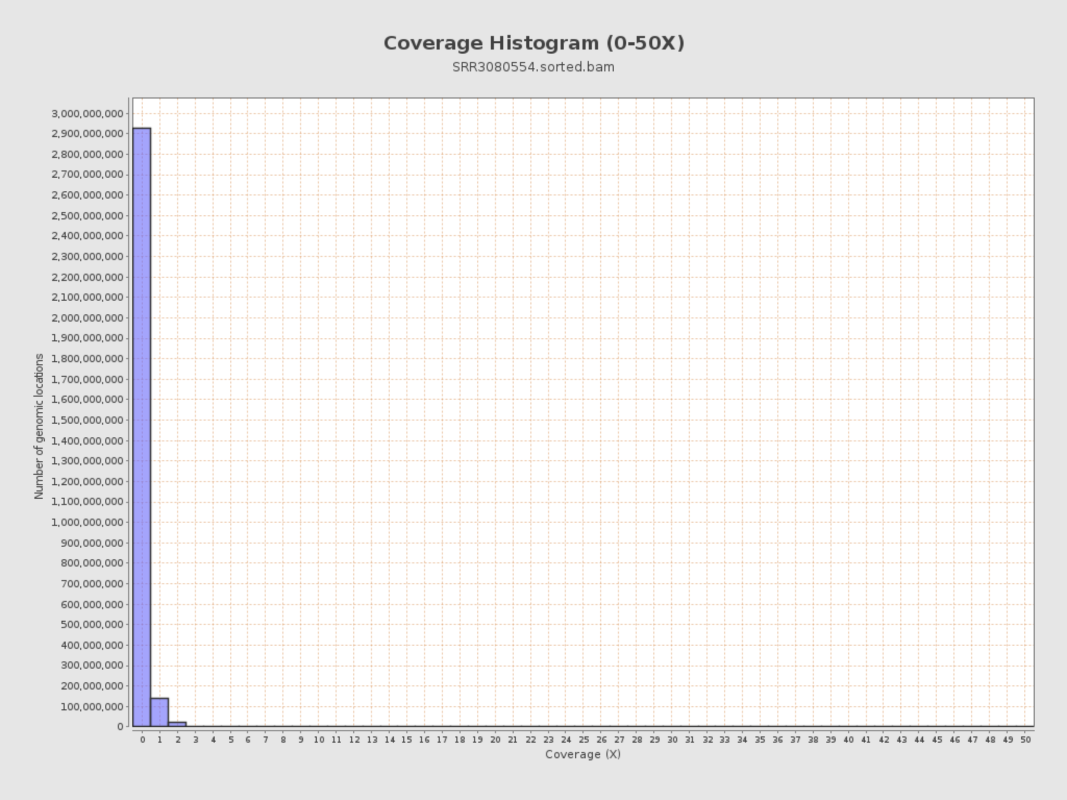
3. Results : Coverage across reference



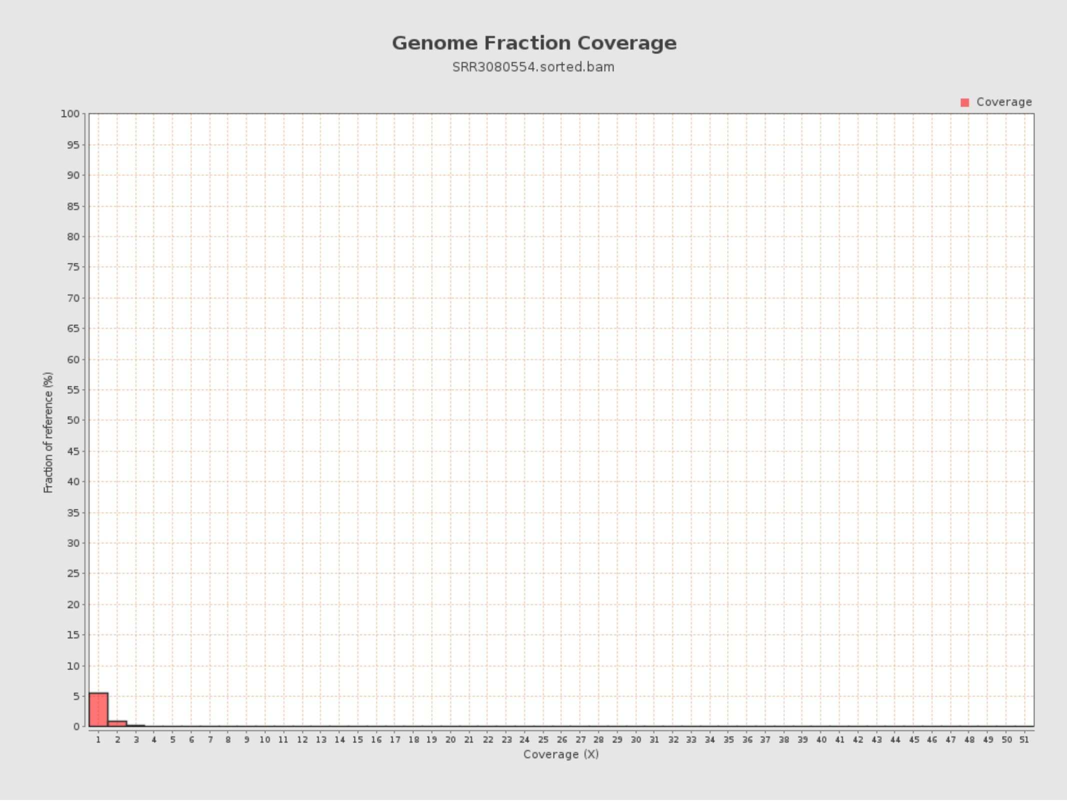
4. Results : Coverage Histogram



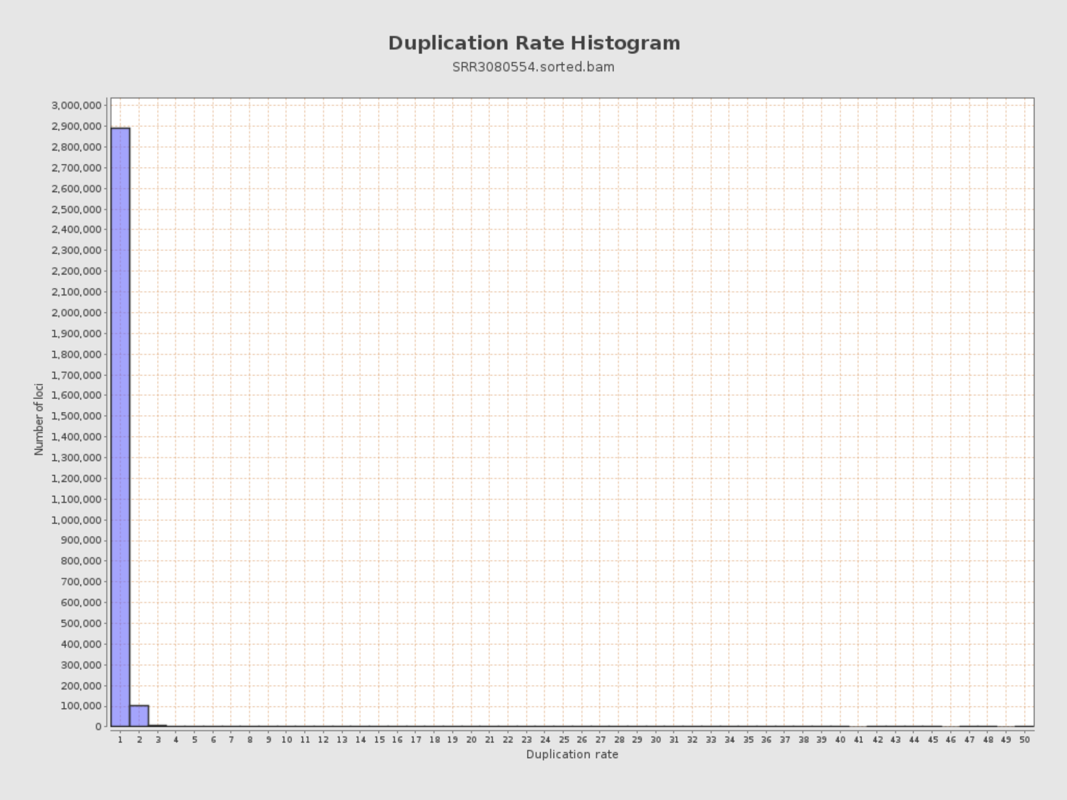
5. Results : Coverage Histogram (0-50X)



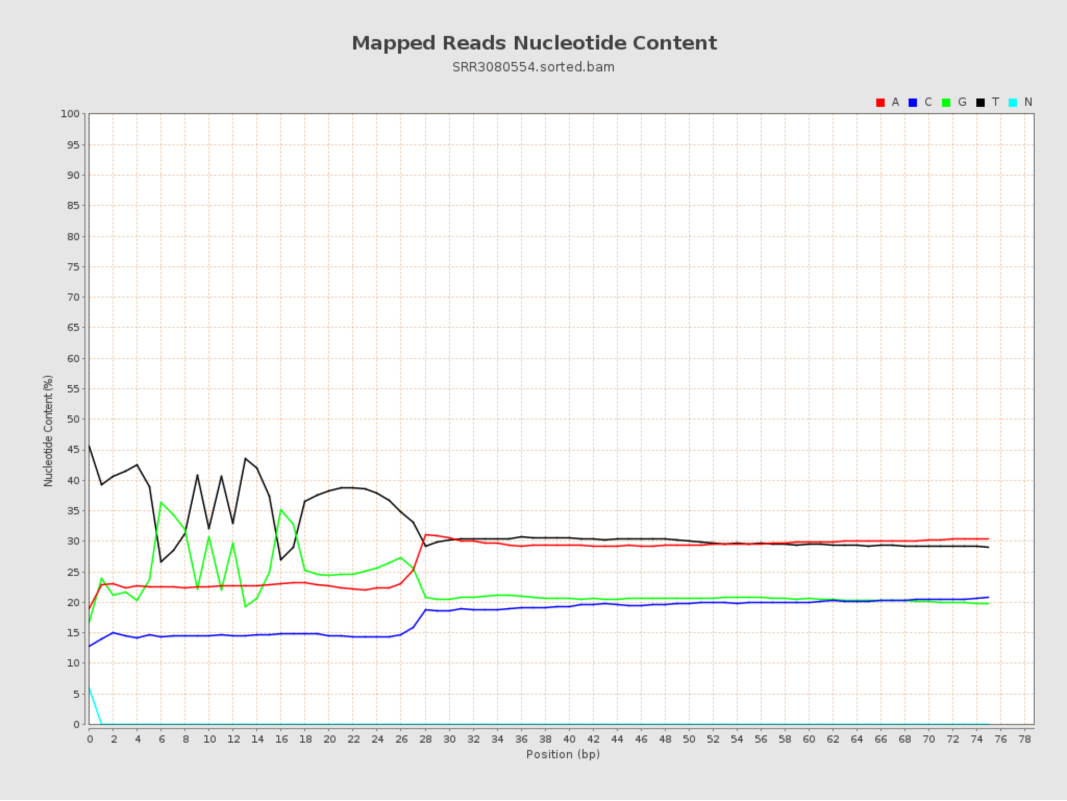
6. Results : Genome Fraction Coverage



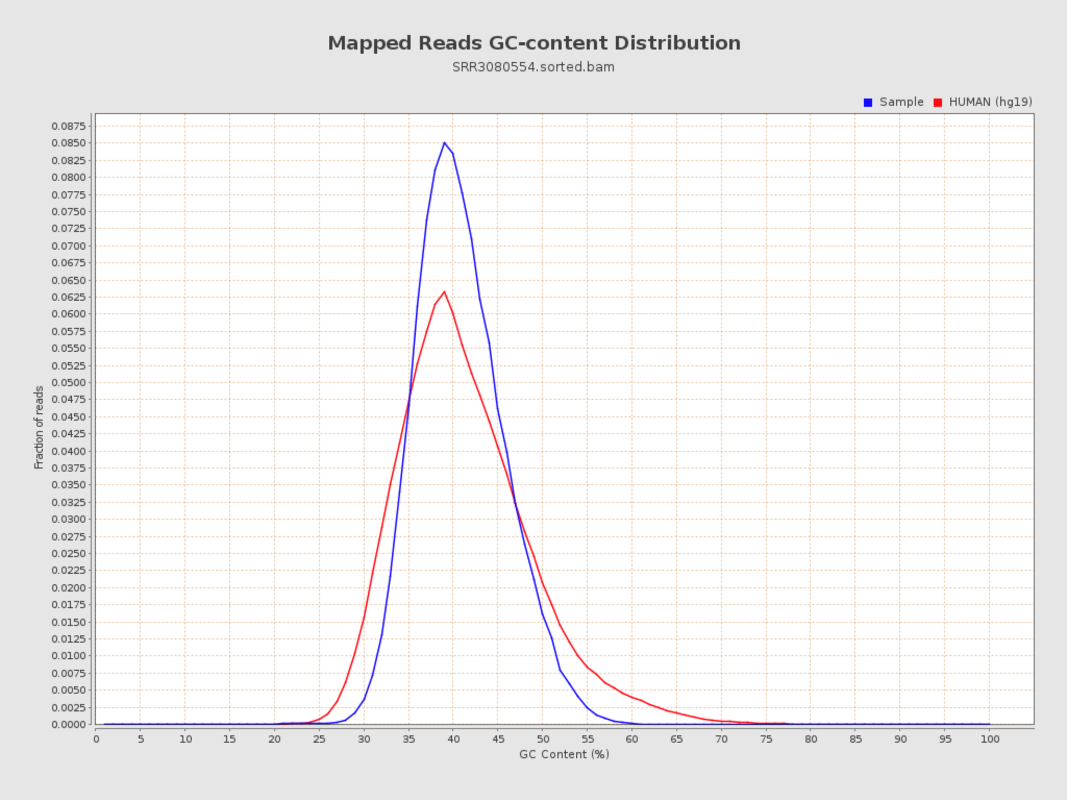
7. Results : Duplication Rate Histogram



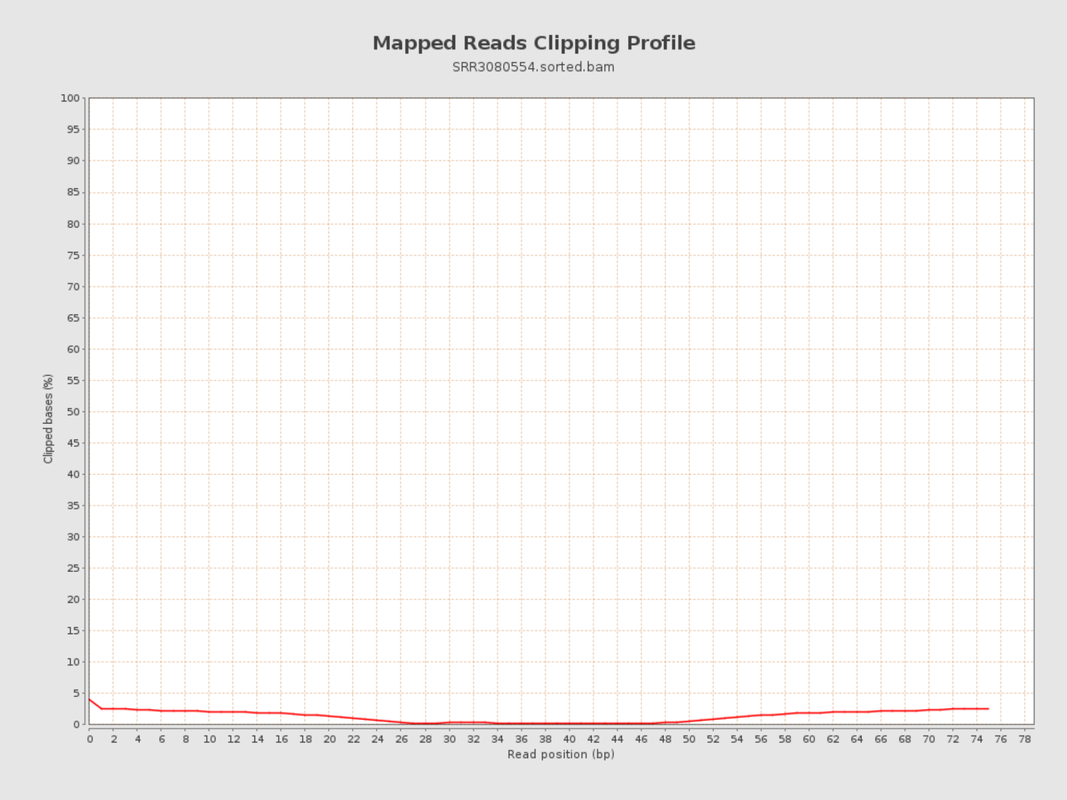
8. Results : Mapped Reads Nucleotide Content



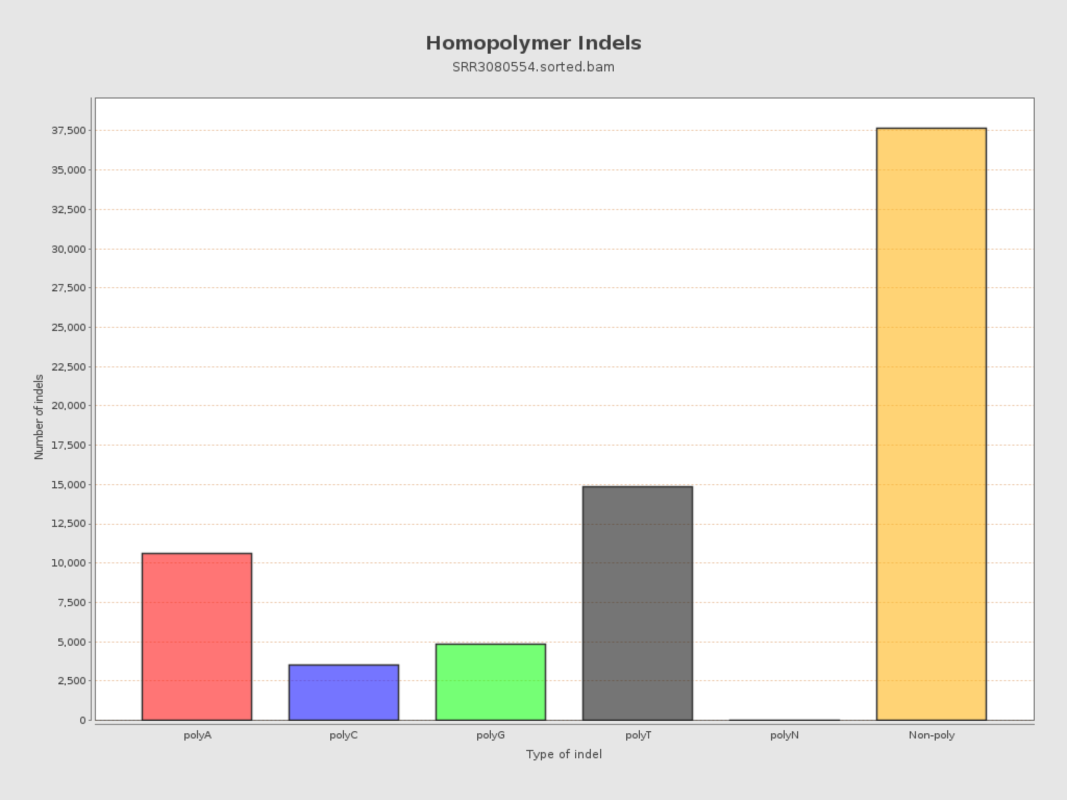
9. Results : Mapped Reads GC-content Distribution



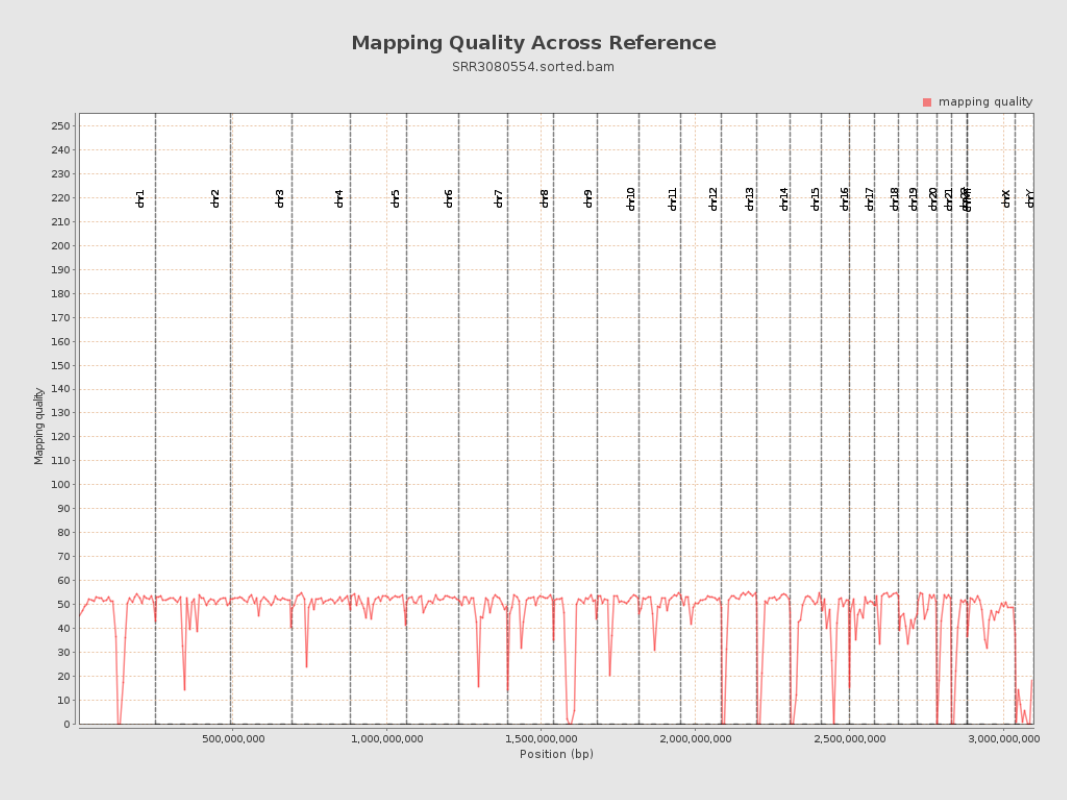
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram