Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525202.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_SRR10525202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:51:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,117,801
Mapped reads	1,946,749 / 91.92%
Unmapped reads	171,052 / 8.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,979 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	78,695 / 3.72%
Duplication rate	2.94%
Clipped reads	1,950,227 / 92.09%

2.2. ACGT Content

Number/percentage of A's	28,815,943 / 25.21%
Number/percentage of C's	21,349,735 / 18.68%
Number/percentage of T's	36,623,473 / 32.04%
Number/percentage of G's	27,521,227 / 24.08%
Number/percentage of N's	2,936 / 0%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0369

Standard Deviation	0.3476

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

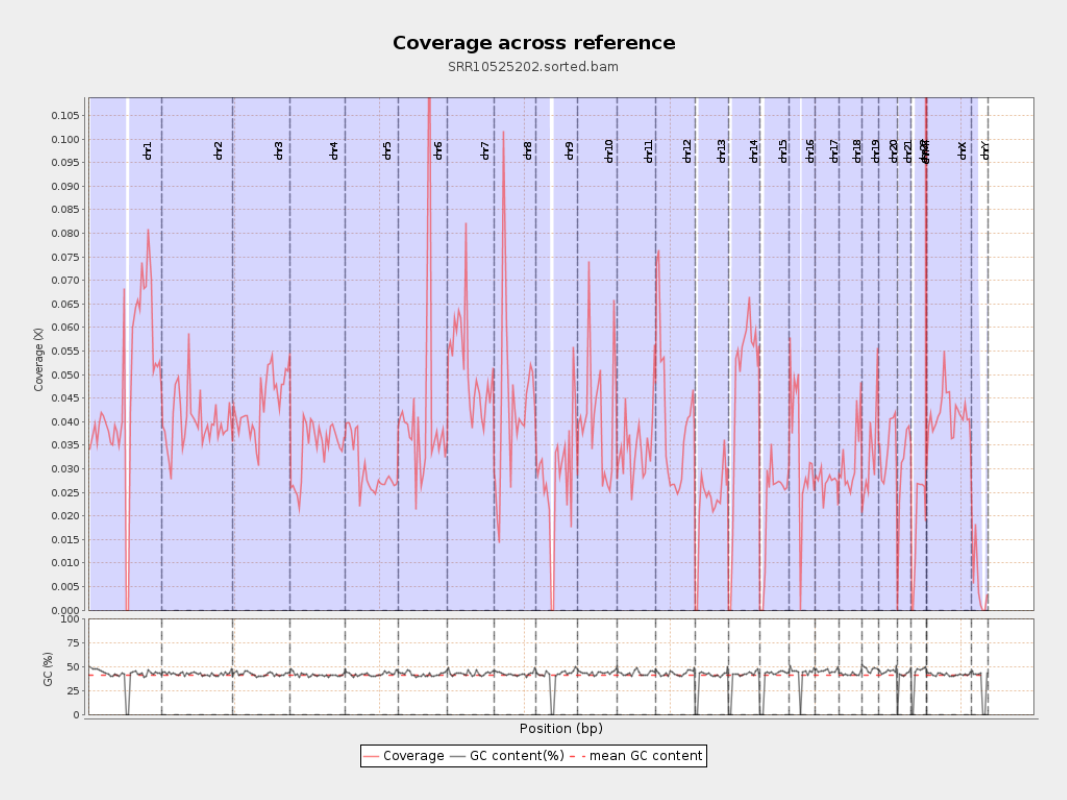
General error rate	0.5%
Mismatches	563,623
Insertions	7,264
Mapped reads with at least one insertion	0.37%
Deletions	22,805
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.65%

2.6. Chromosome stats

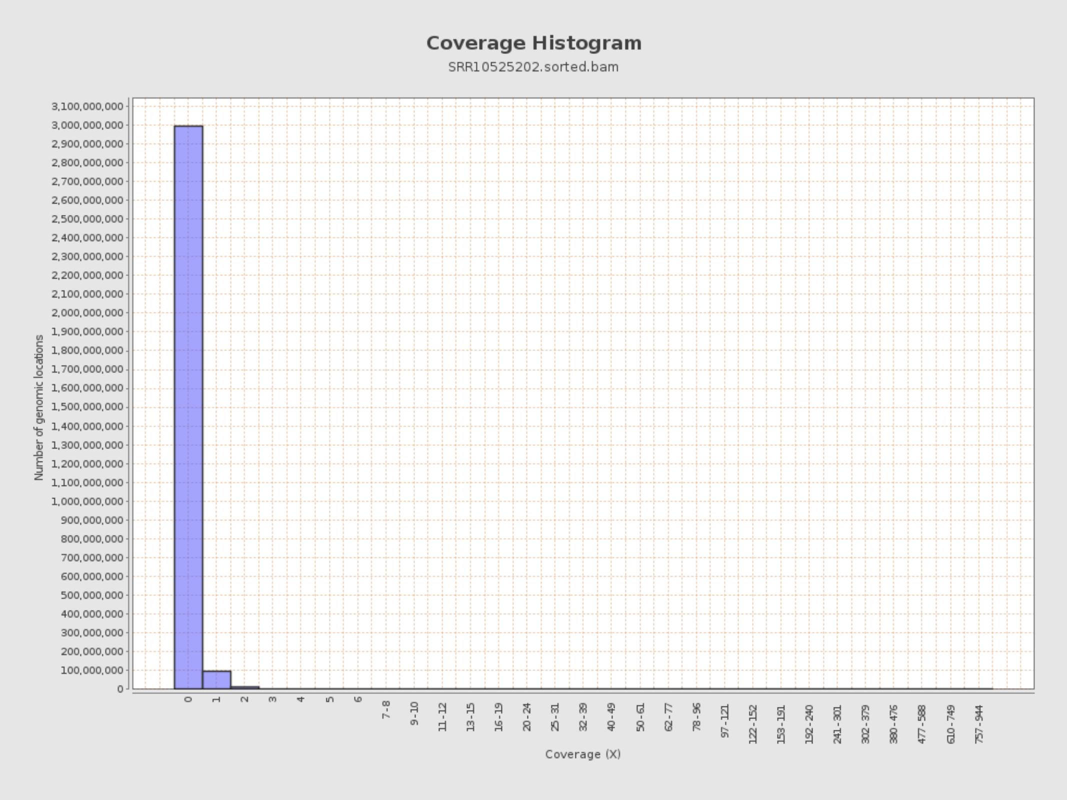
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11706898	0.047	0.6555
chr2	243199373	9698488	0.0399	0.4514
chr3	198022430	8689348	0.0439	0.2338
chr4	191154276	6543598	0.0342	0.2231
chr5	180915260	5380771	0.0297	0.1898
chr6	171115067	7210146	0.0421	0.2566
chr7	159138663	8196050	0.0515	0.6109

chr8	146364022	6362330	0.0435	0.3115
chr9	141213431	3979397	0.0282	0.2461
chr10	135534747	5580145	0.0412	0.3595
chr11	135006516	4751722	0.0352	0.2617
chr12	133851895	5330310	0.0398	0.2243
chr13	115169878	2612099	0.0227	0.1715
chr14	107349540	4993254	0.0465	0.2431
chr15	102531392	2297282	0.0224	0.1683
chr16	90354753	2998089	0.0332	0.2257
chr17	81195210	2204956	0.0272	0.1912
chr18	78077248	2495559	0.032	0.437
chr19	59128983	1954241	0.0331	0.4418
chr20	63025520	2173331	0.0345	0.2075
chr21	48129895	1444356	0.03	0.2045
chr22	51304566	939903	0.0183	0.1483
chrMT	16571	24554	1.4817	1.5108
chrX	155270560	6455755	0.0416	0.2447
chrY	59373566	327389	0.0055	0.1628

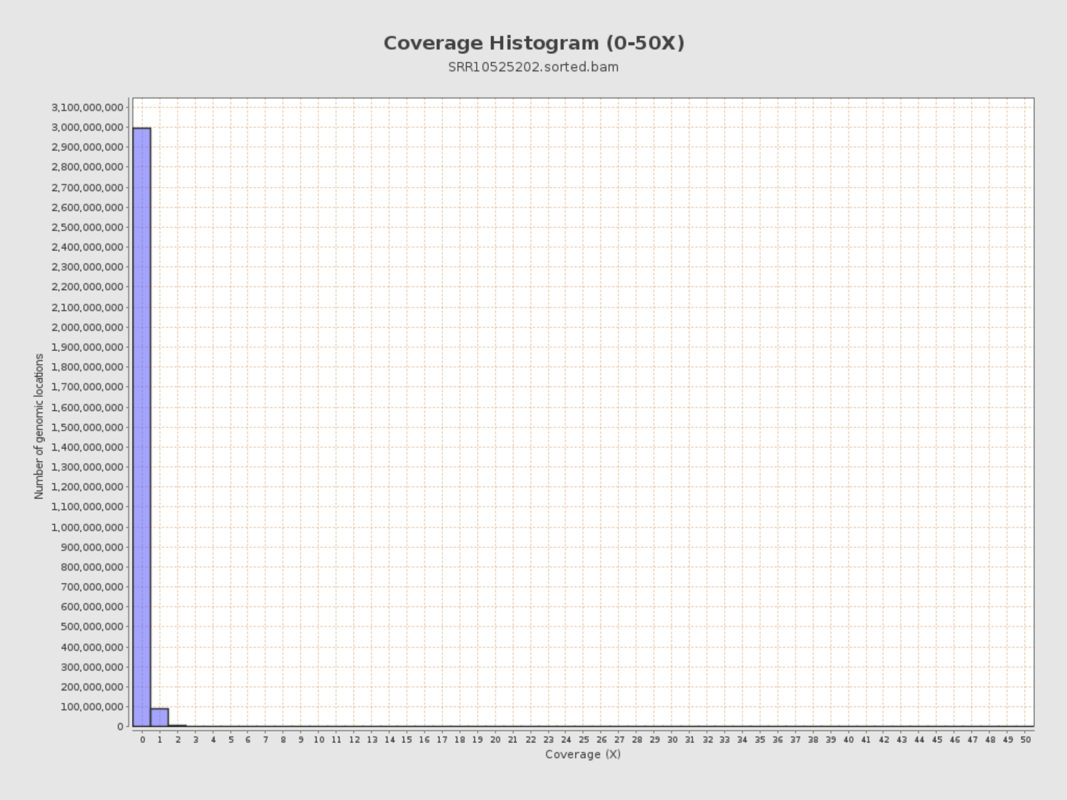
3. Results : Coverage across reference



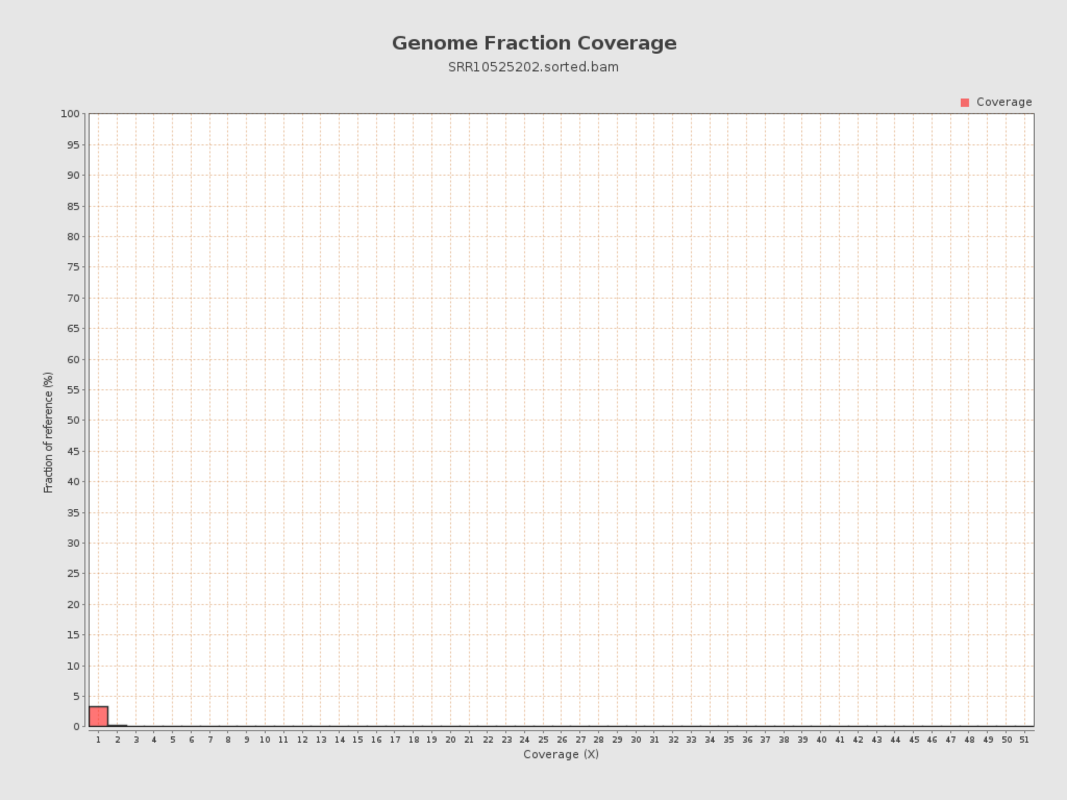
4. Results : Coverage Histogram



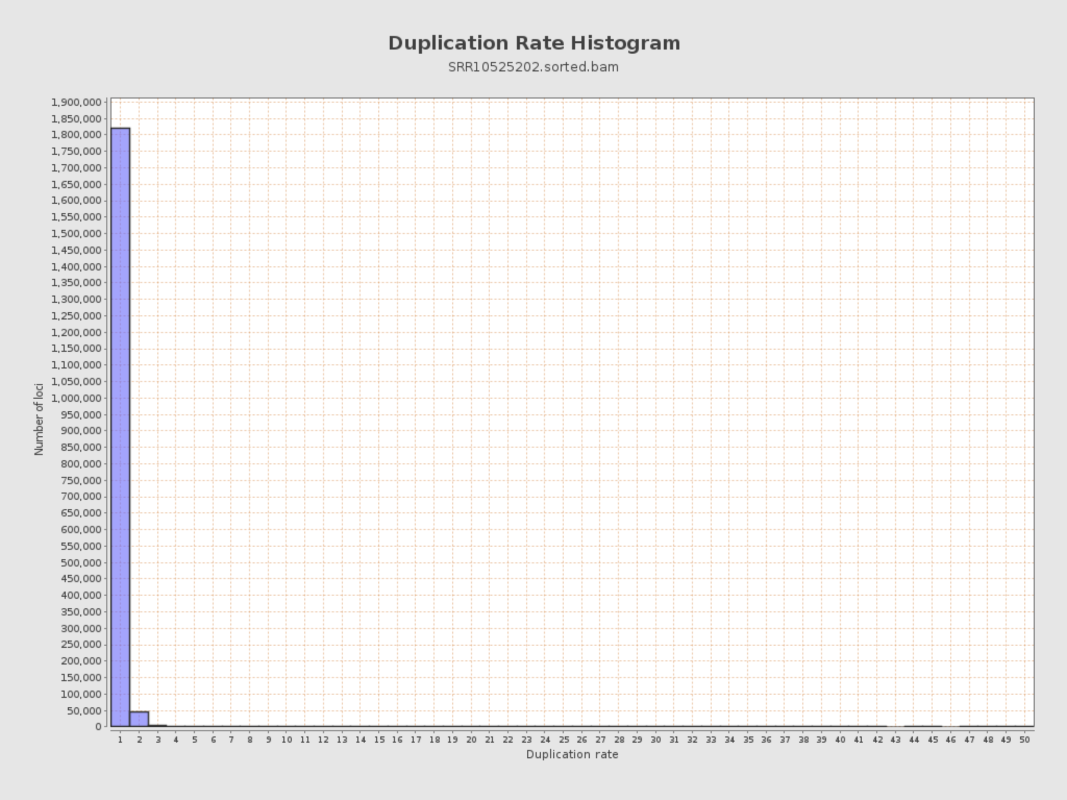
5. Results : Coverage Histogram (0-50X)



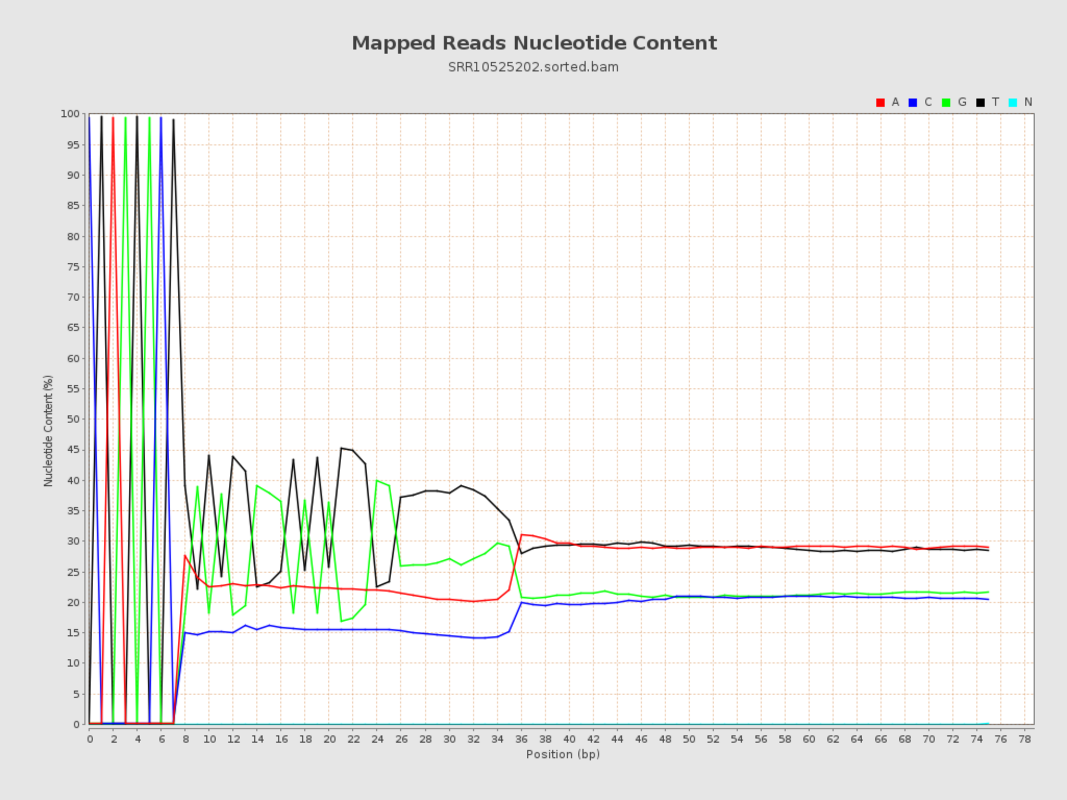
6. Results : Genome Fraction Coverage



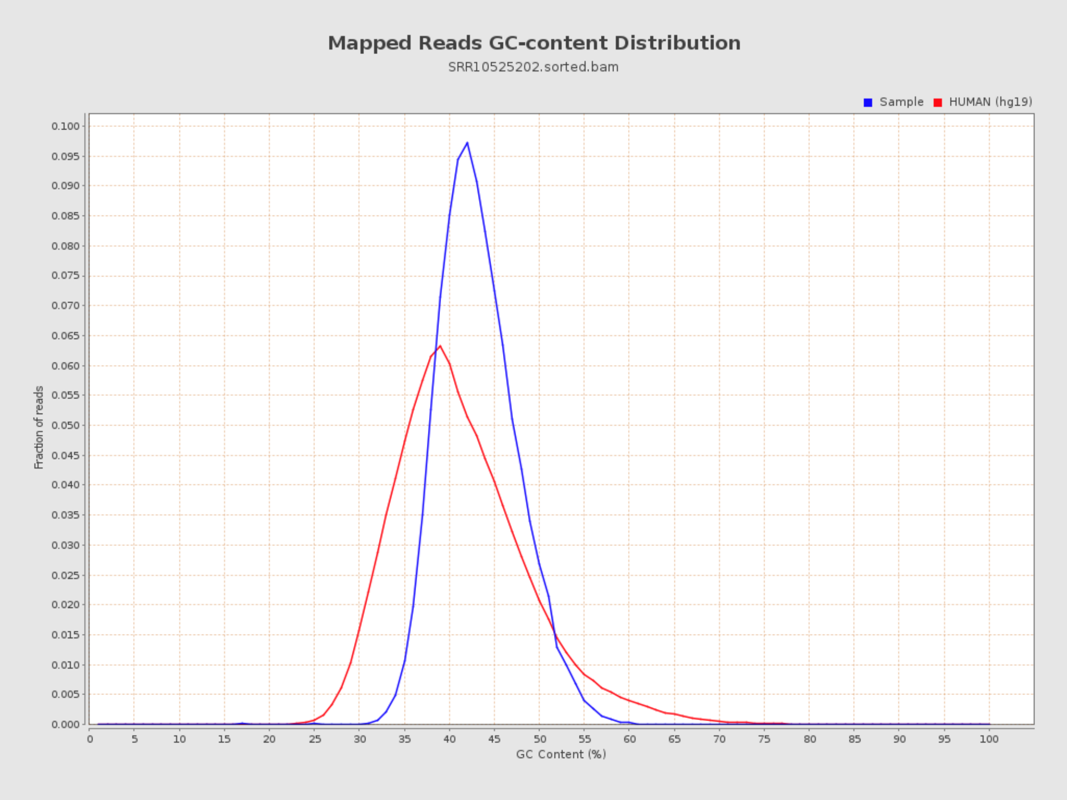
7. Results : Duplication Rate Histogram



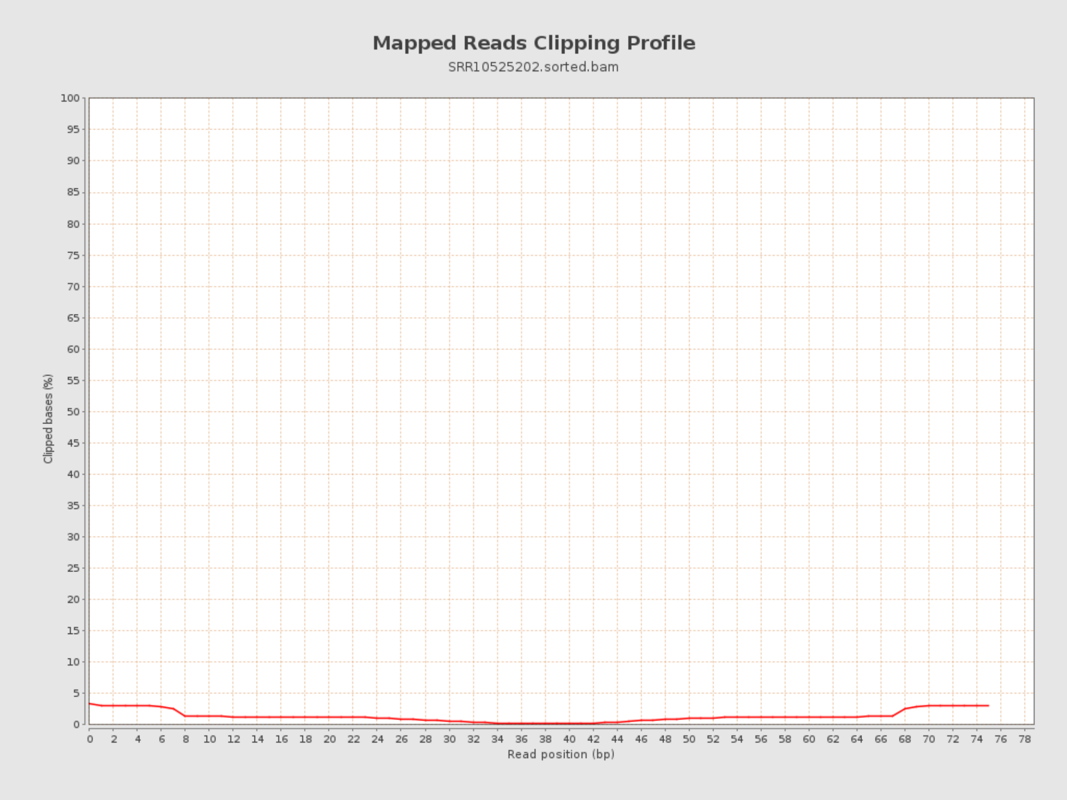
8. Results : Mapped Reads Nucleotide Content



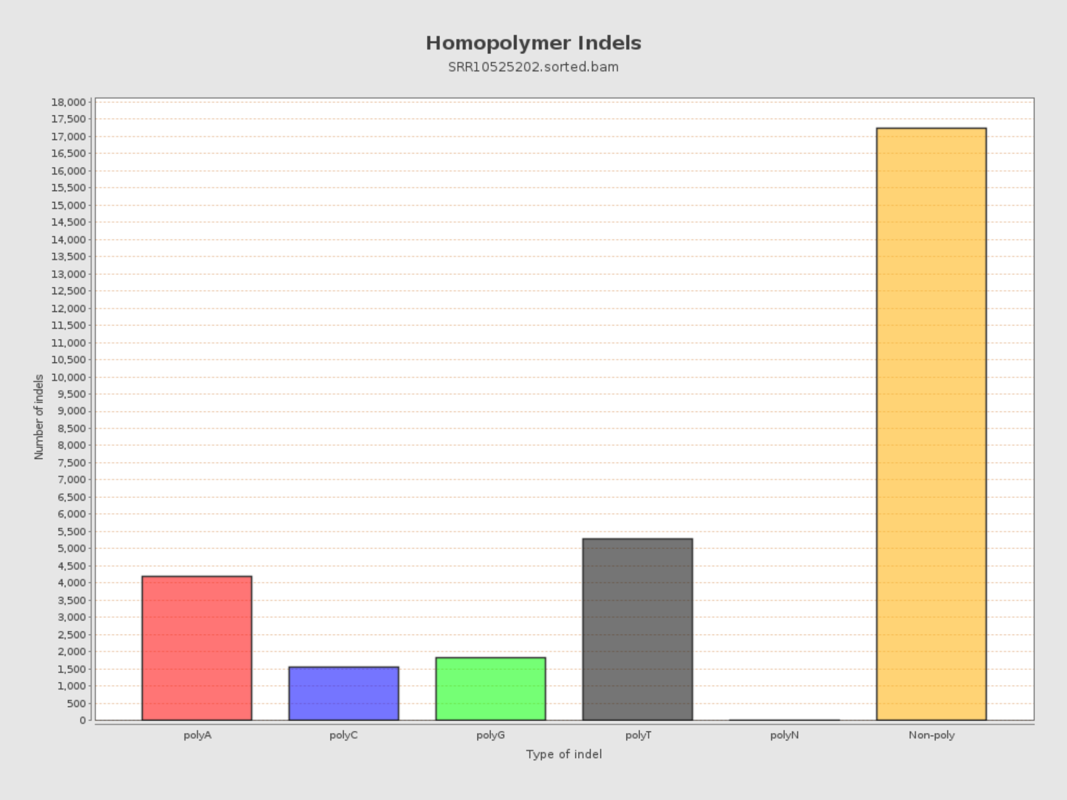
9. Results : Mapped Reads GC-content Distribution



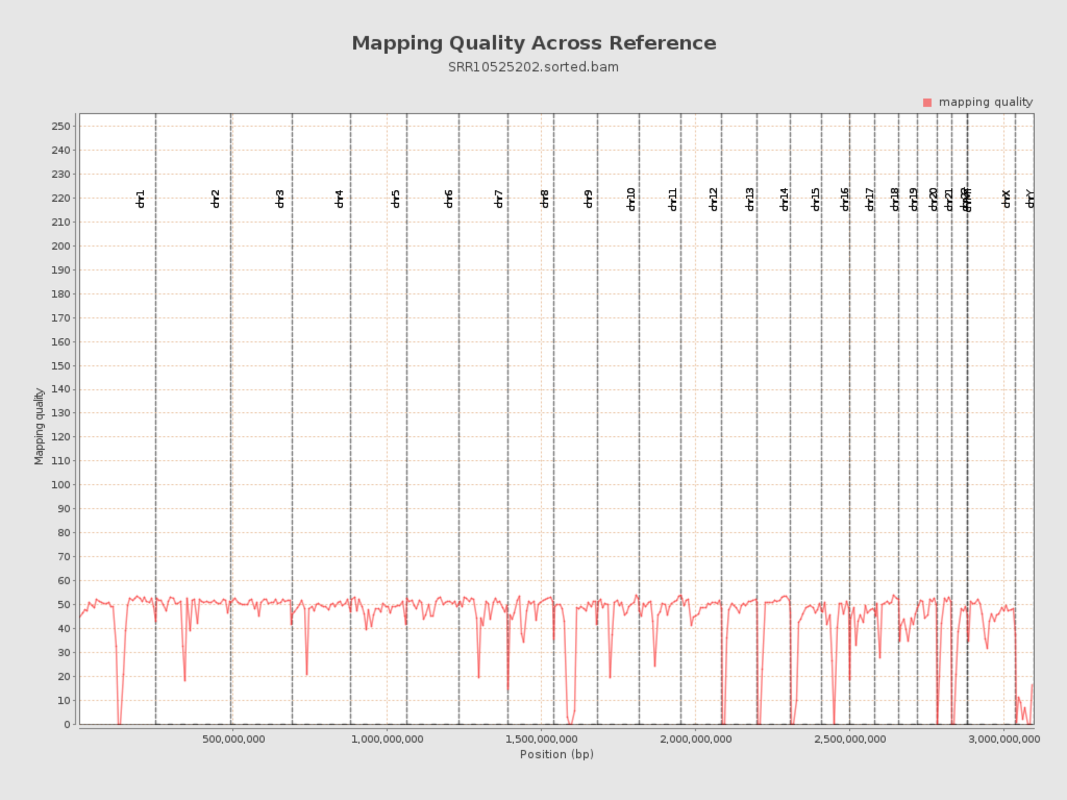
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram