Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:53:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212690.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_SRR3212690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212690.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:53:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212690.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,836,015
Mapped reads	1,864,418 / 65.74%
Unmapped reads	971,597 / 34.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,588 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	70,768 / 2.5%
Duplication rate	3.15%
Clipped reads	1,062,307 / 37.46%

2.2. ACGT Content

Number/percentage of A's	32,985,351 / 28.32%
Number/percentage of C's	22,047,676 / 18.93%
Number/percentage of T's	35,714,234 / 30.66%
Number/percentage of G's	25,745,490 / 22.1%
Number/percentage of N's	1,279 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.2864

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

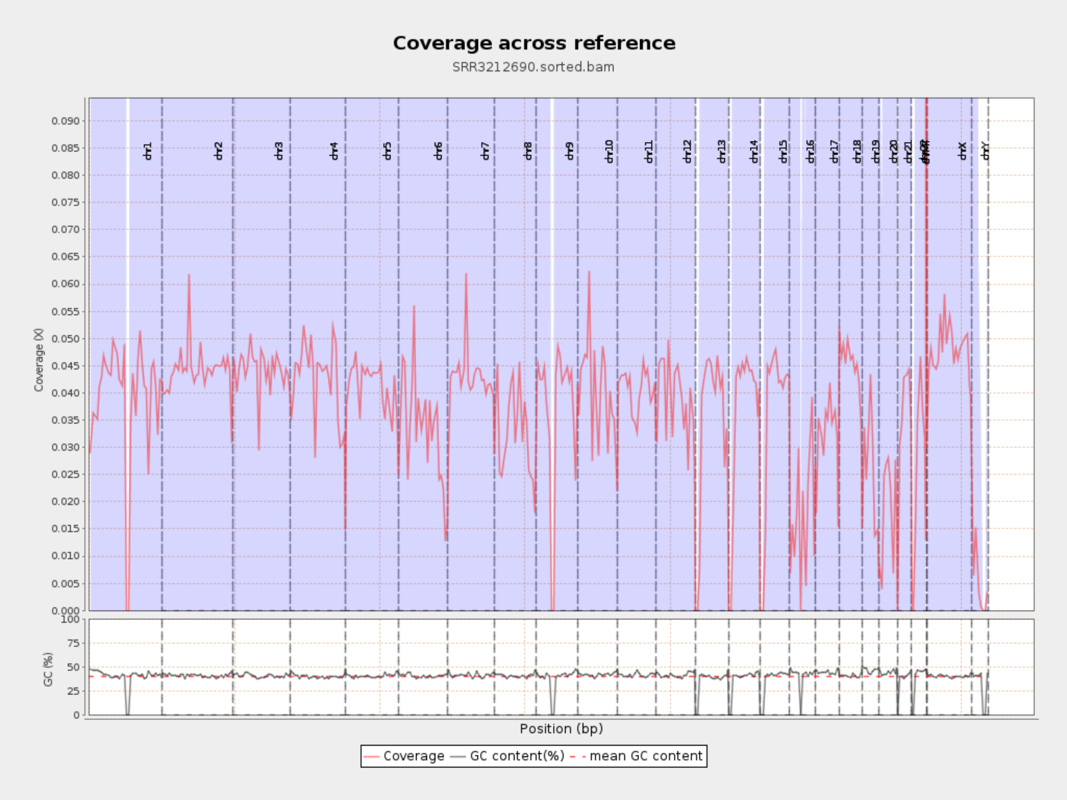
General error rate	0.83%
Mismatches	954,176
Insertions	8,479
Mapped reads with at least one insertion	0.45%
Deletions	23,319
Mapped reads with at least one deletion	1.24%
Homopolymer indels	46.75%

2.6. Chromosome stats

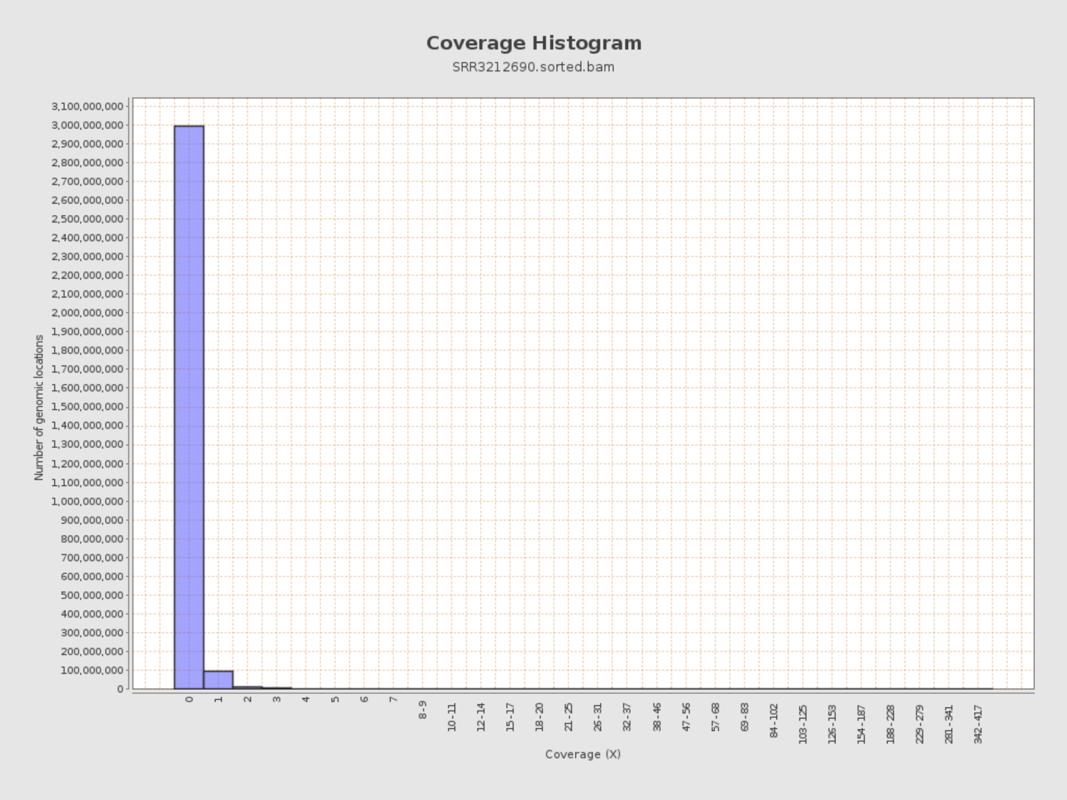
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9730326	0.039	0.3945
chr2	243199373	10780817	0.0443	0.351
chr3	198022430	8752710	0.0442	0.2331
chr4	191154276	8123117	0.0425	0.2379
chr5	180915260	7487926	0.0414	0.2264
chr6	171115067	5720102	0.0334	0.2535
chr7	159138663	6870707	0.0432	0.3849

chr8	146364022	4824488	0.033	0.3064
chr9	141213431	5182430	0.0367	0.271
chr10	135534747	5507044	0.0406	0.3009
chr11	135006516	5440680	0.0403	0.2548
chr12	133851895	5213486	0.0389	0.2214
chr13	115169878	3916303	0.034	0.2058
chr14	107349540	3845467	0.0358	0.2222
chr15	102531392	3630811	0.0354	0.2129
chr16	90354753	1614862	0.0179	0.1705
chr17	81195210	2618248	0.0322	0.2205
chr18	78077248	3557682	0.0456	0.4997
chr19	59128983	1559213	0.0264	0.2822
chr20	63025520	1199913	0.019	0.1714
chr21	48129895	1680738	0.0349	0.216
chr22	51304566	1296770	0.0253	0.1767
chrMT	16571	261188	15.7618	8.8877
chrX	155270560	7411902	0.0477	0.2589
chrY	59373566	304183	0.0051	0.1092

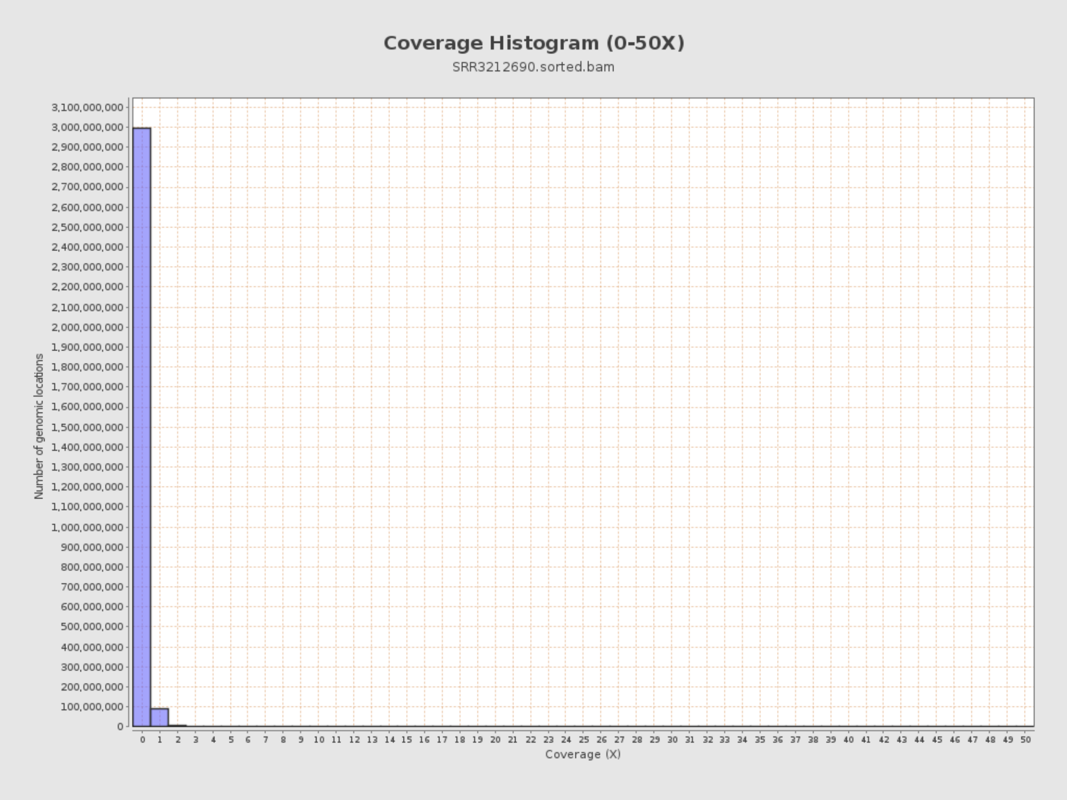
3. Results : Coverage across reference



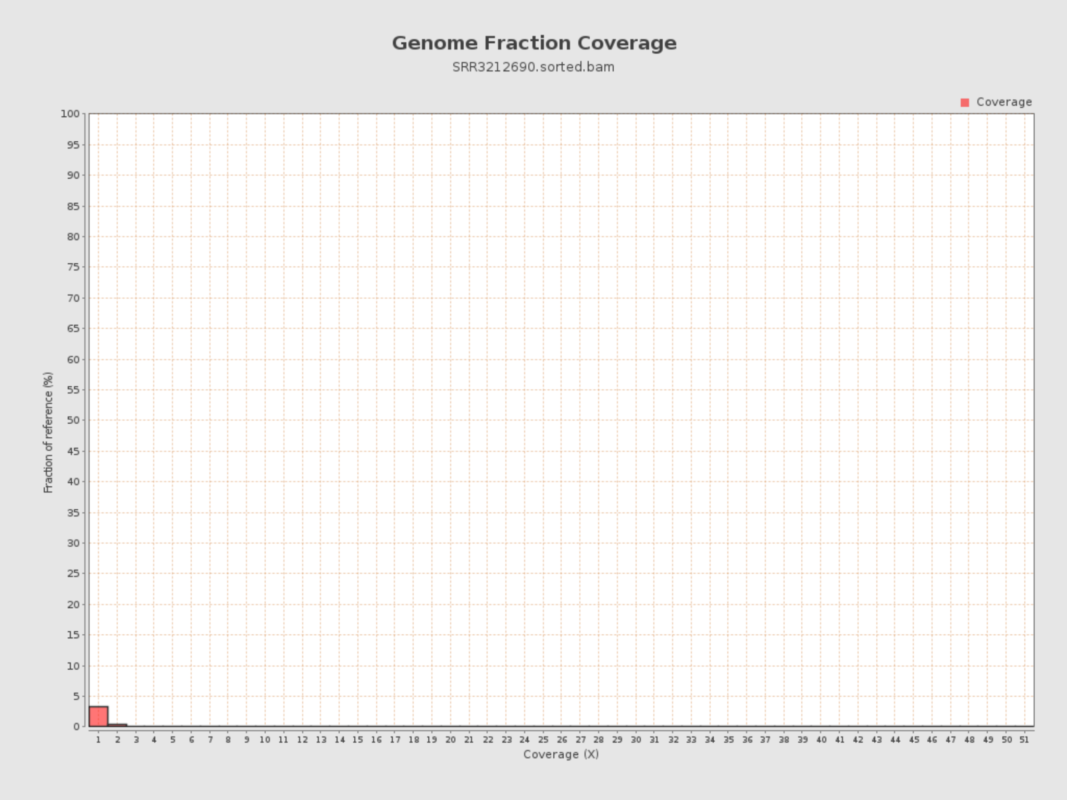
4. Results : Coverage Histogram



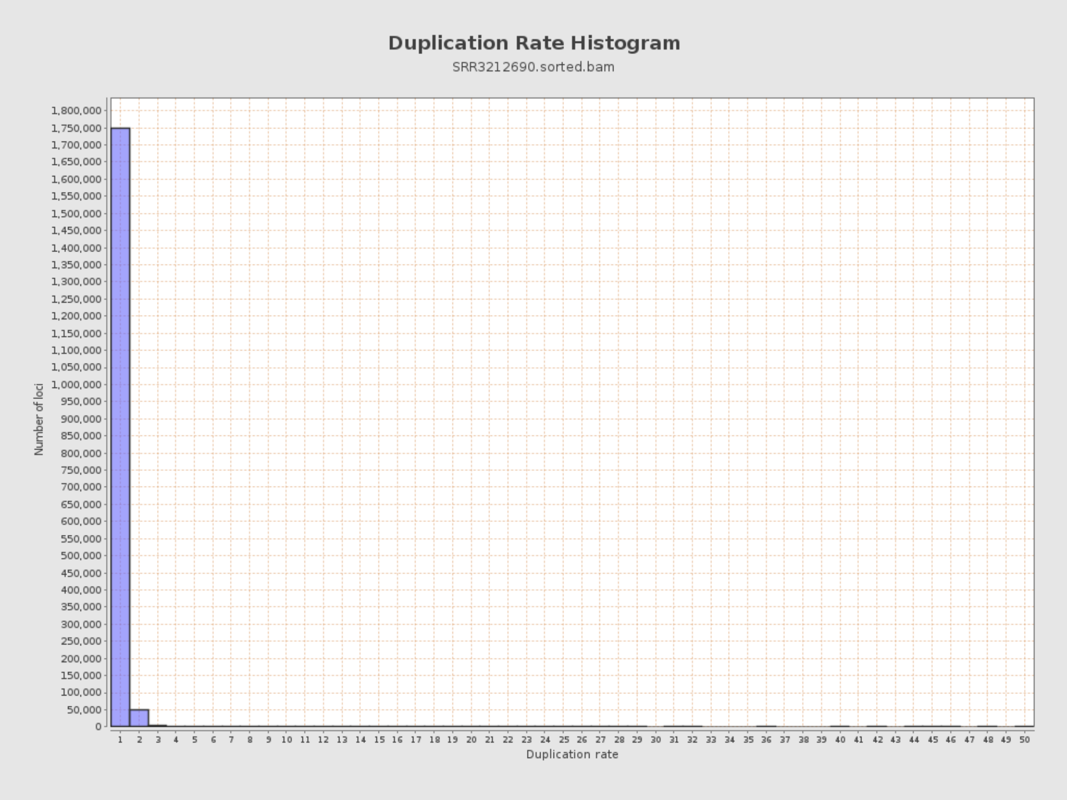
5. Results : Coverage Histogram (0-50X)



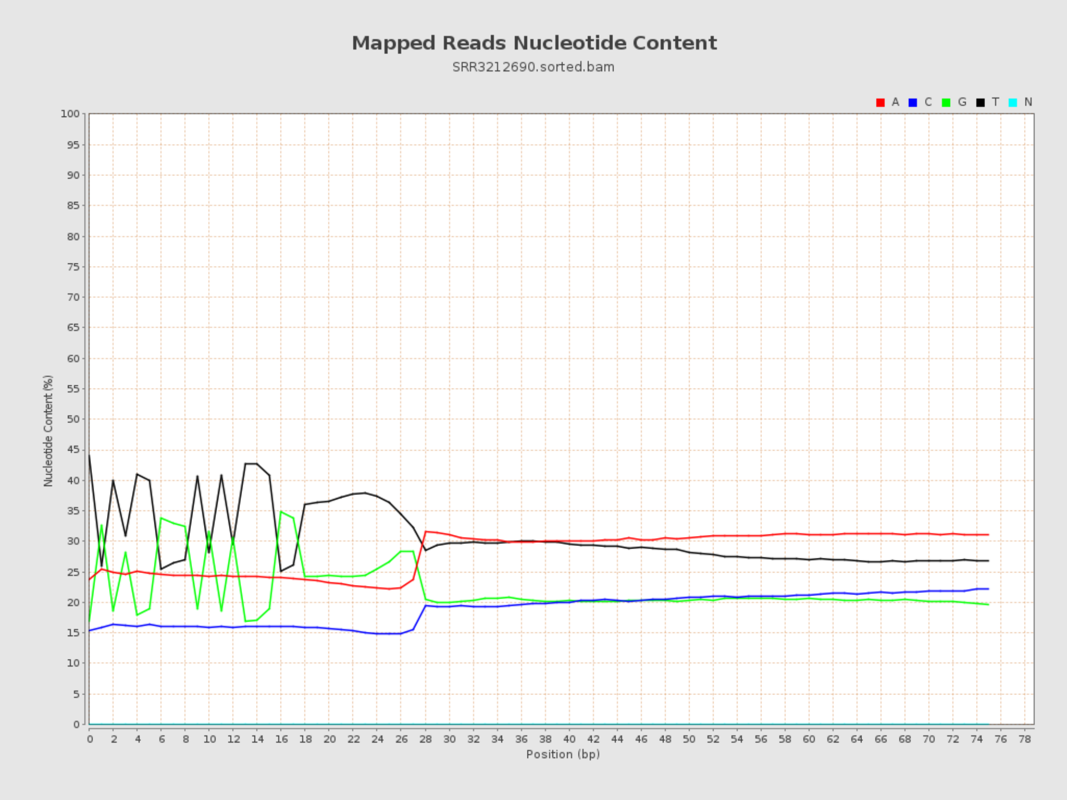
6. Results : Genome Fraction Coverage



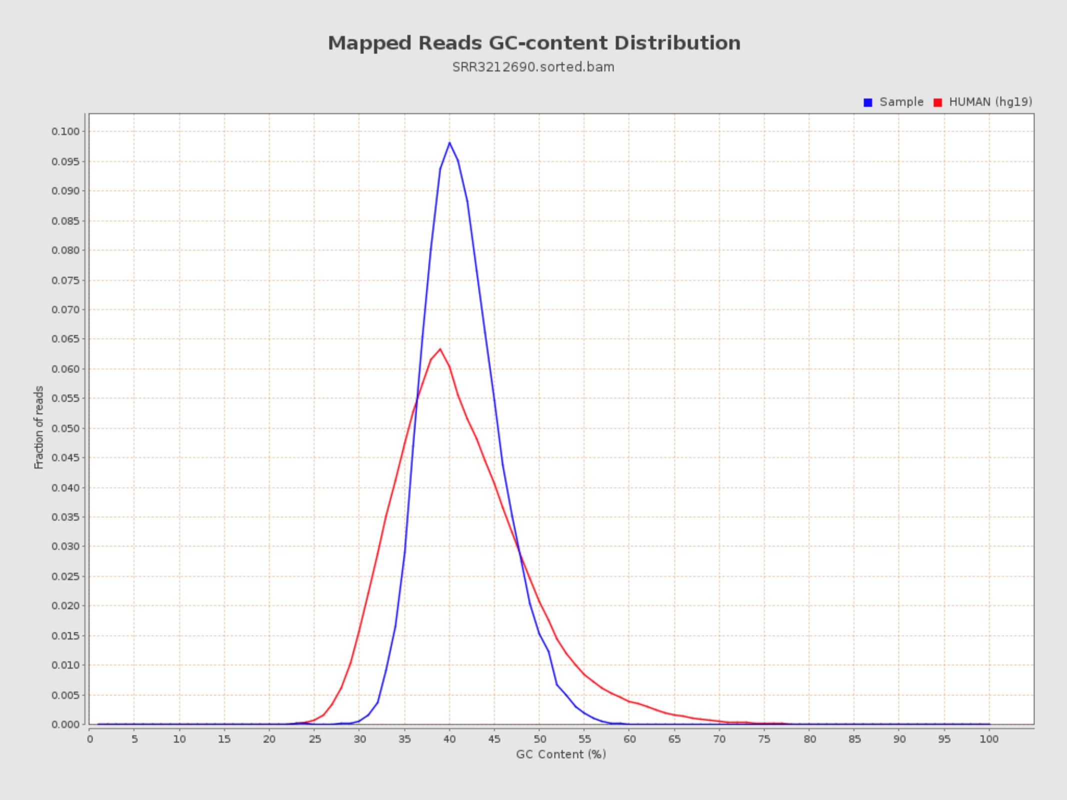
7. Results : Duplication Rate Histogram



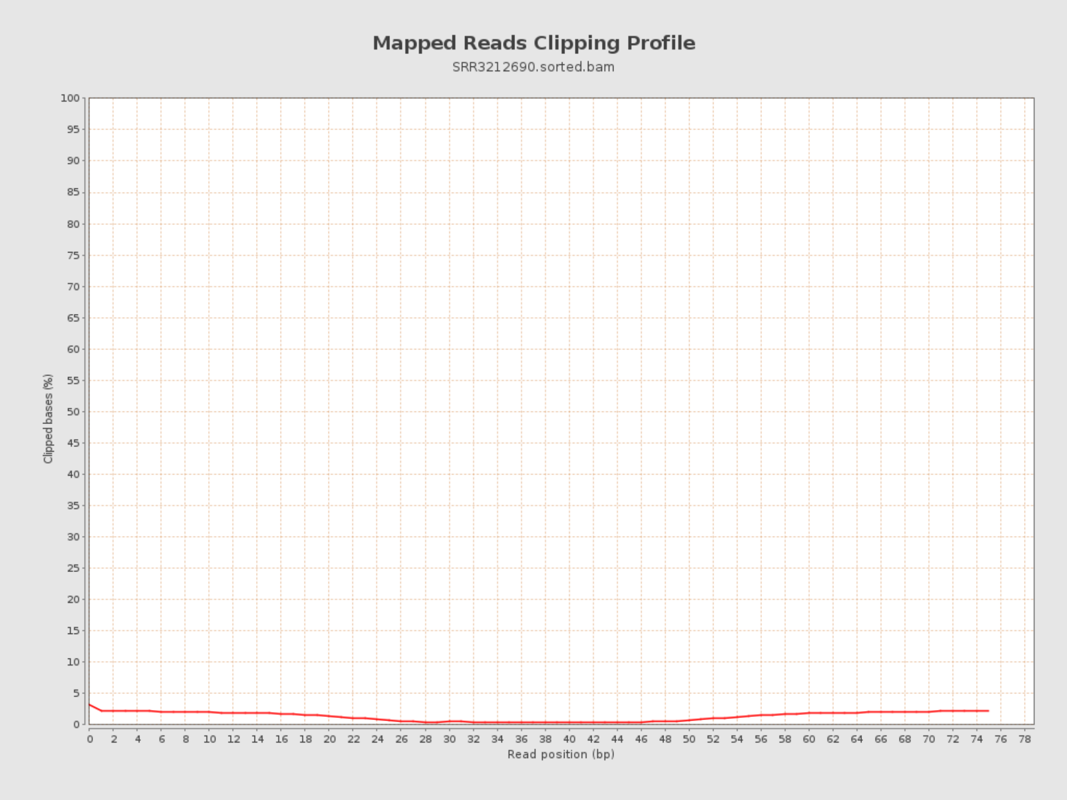
8. Results : Mapped Reads Nucleotide Content



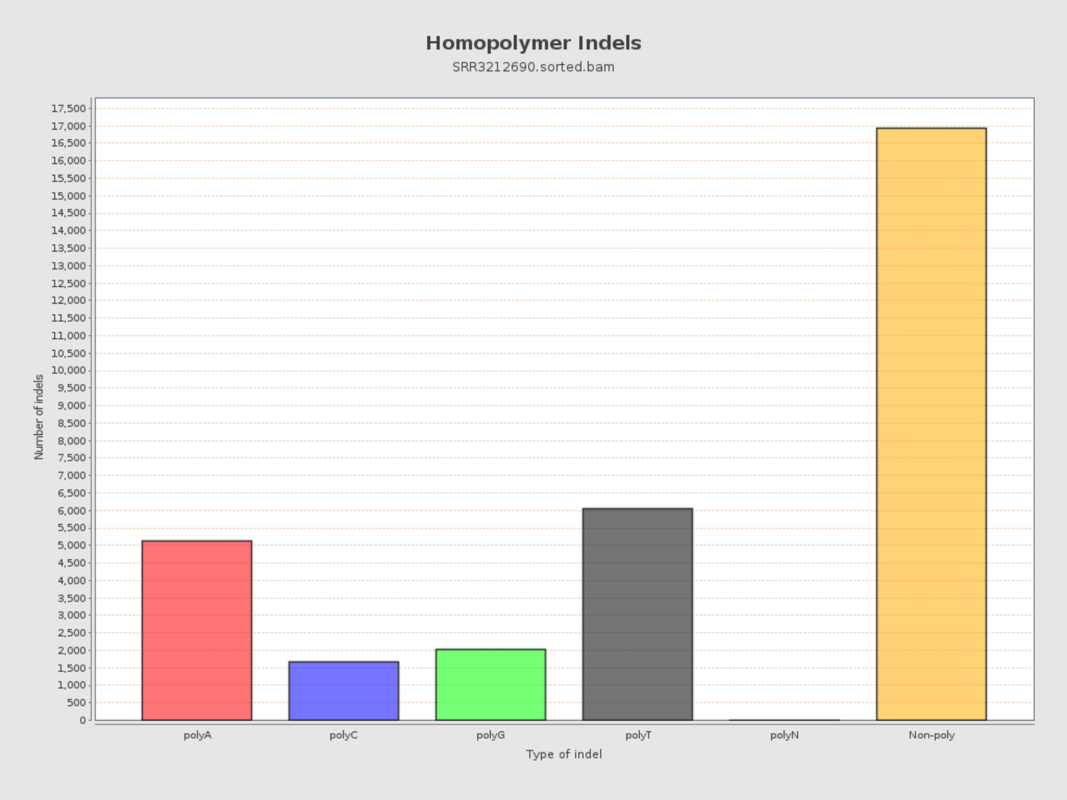
9. Results : Mapped Reads GC-content Distribution



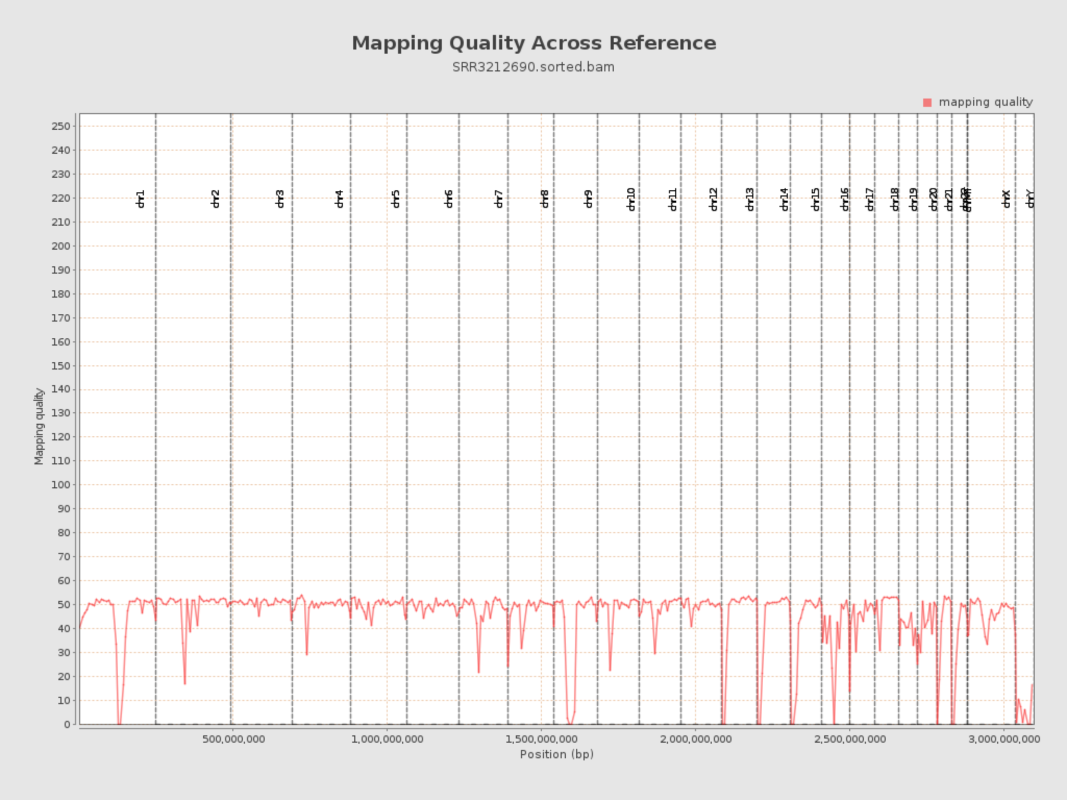
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram