Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:29:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505921.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_SRR1505921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:29:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,446,188
Mapped reads	4,606,889 / 71.47%
Unmapped reads	1,839,299 / 28.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	219,411 / 3.4%
Duplication rate	3.56%
Clipped reads	854,556 / 13.26%

2.2. ACGT Content

Number/percentage of A's	62,472,418 / 29.38%
Number/percentage of C's	43,979,095 / 20.69%
Number/percentage of T's	61,830,646 / 29.08%
Number/percentage of G's	44,329,621 / 20.85%
Number/percentage of N's	670 / 0%
GC Percentage	41.54%

2.3. Coverage

Mean	0.0687

Standard Deviation	0.5957

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Mismatches and indels

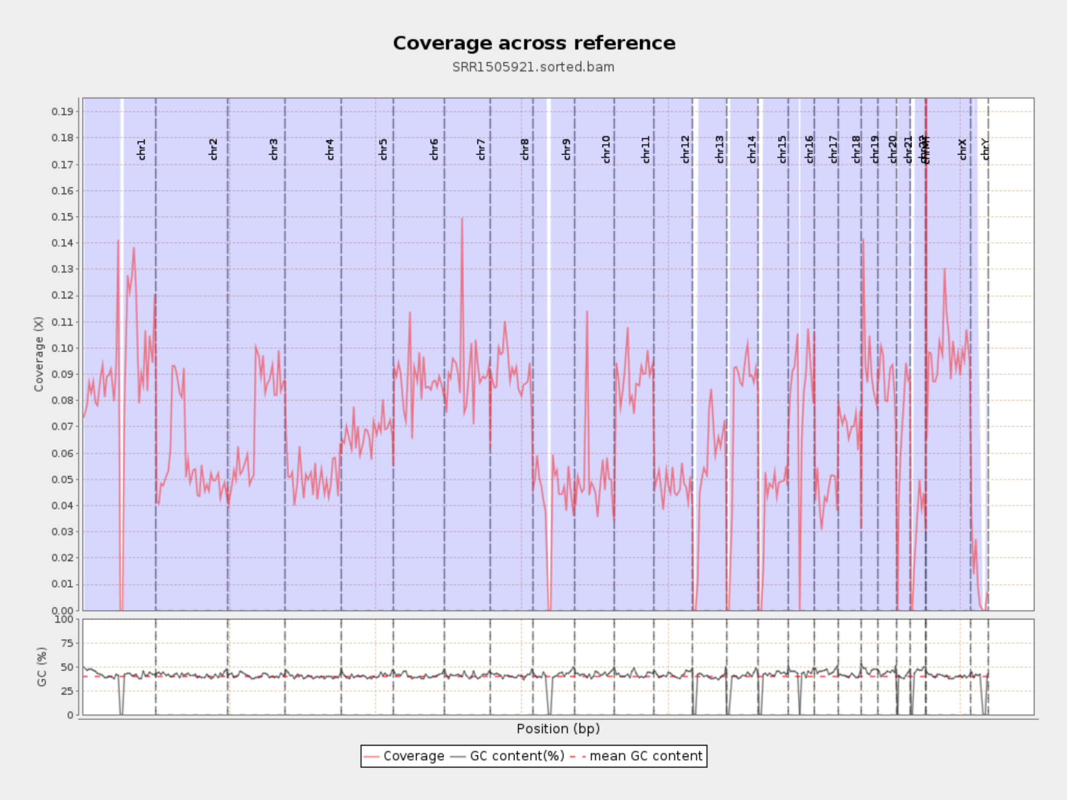
General error rate	0.51%
Mismatches	1,063,032
Insertions	9,286
Mapped reads with at least one insertion	0.2%
Deletions	30,567
Mapped reads with at least one deletion	0.66%
Homopolymer indels	45.87%

2.6. Chromosome stats

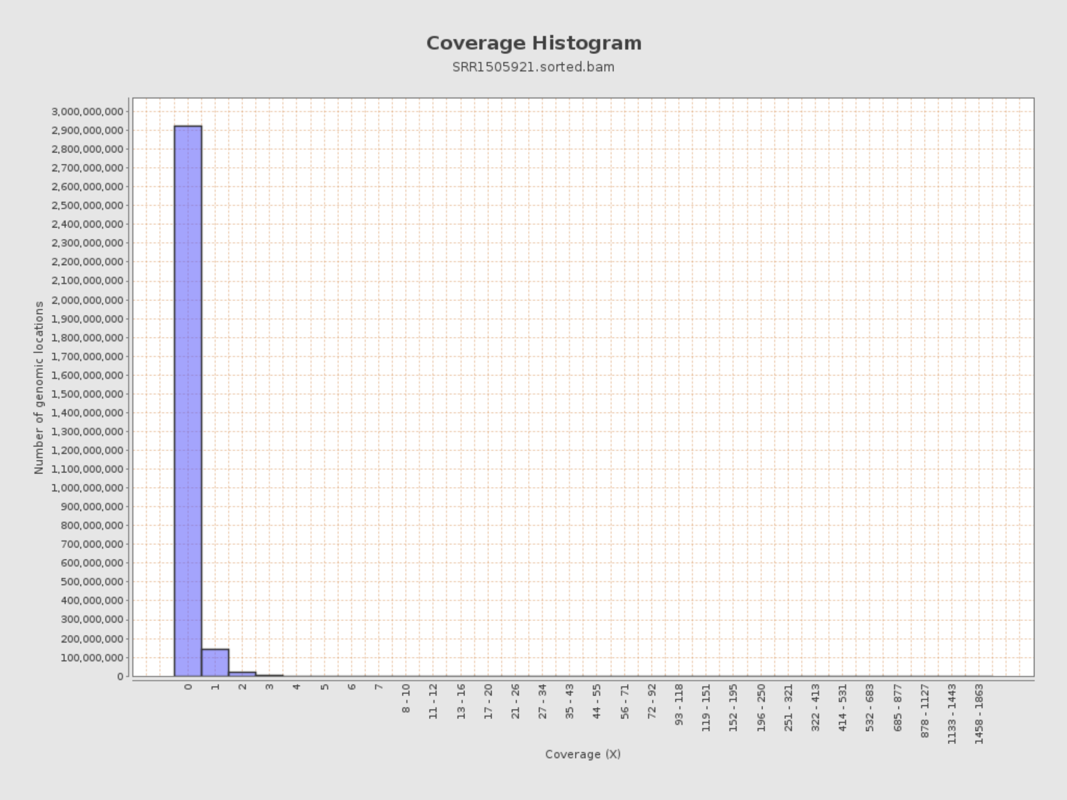
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22581621	0.0906	1.2918
chr2	243199373	13801183	0.0567	0.4404
chr3	198022430	14161124	0.0715	0.3205
chr4	191154276	9717206	0.0508	0.2723
chr5	180915260	12194503	0.0674	0.313
chr6	171115067	14979382	0.0875	0.4704
chr7	159138663	14541265	0.0914	0.8939

chr8	146364022	13260679	0.0906	0.8271
chr9	141213431	5999755	0.0425	0.3636
chr10	135534747	6923373	0.0511	0.6164
chr11	135006516	11804797	0.0874	0.4981
chr12	133851895	6392203	0.0478	0.2782
chr13	115169878	6072120	0.0527	0.2693
chr14	107349540	8133131	0.0758	0.5046
chr15	102531392	4048853	0.0395	0.2315
chr16	90354753	7250020	0.0802	0.4028
chr17	81195210	3647373	0.0449	0.2813
chr18	78077248	5560839	0.0712	0.7066
chr19	59128983	5518427	0.0933	0.9848
chr20	63025520	5576453	0.0885	0.3612
chr21	48129895	3264632	0.0678	0.328
chr22	51304566	1517170	0.0296	0.202
chrMT	16571	8585	0.5181	0.8733
chrX	155270560	15064741	0.097	0.4203
chrY	59373566	635358	0.0107	0.154

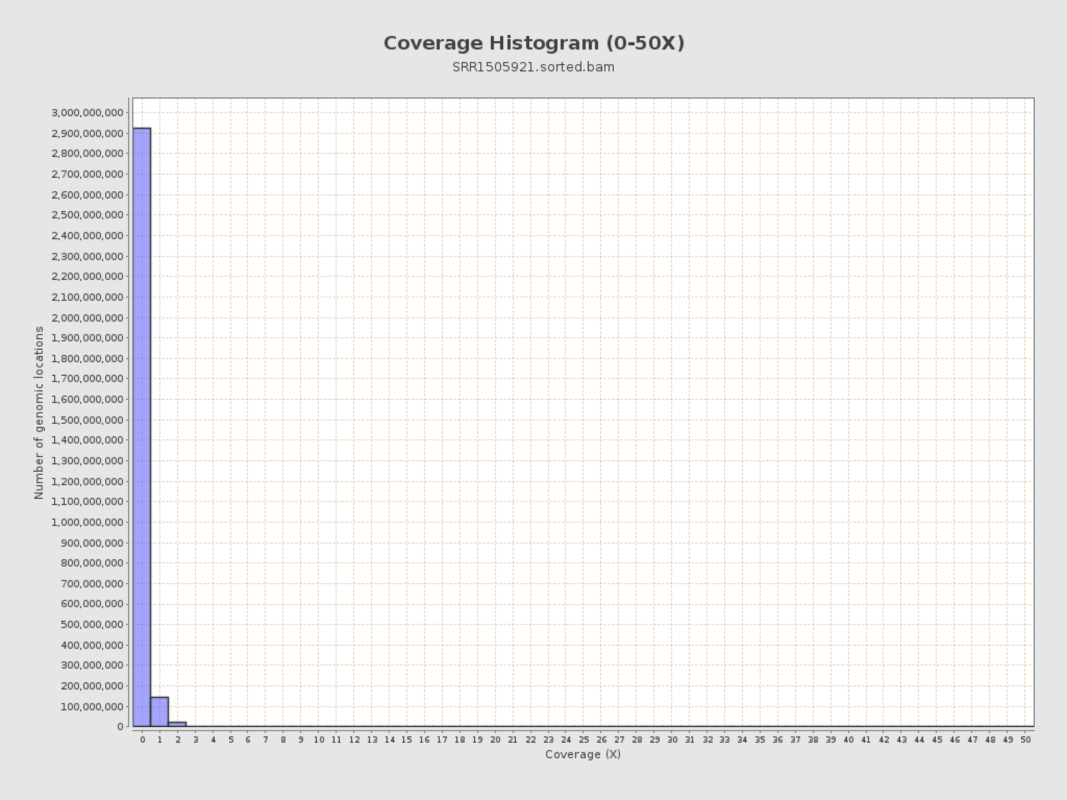
3. Results : Coverage across reference



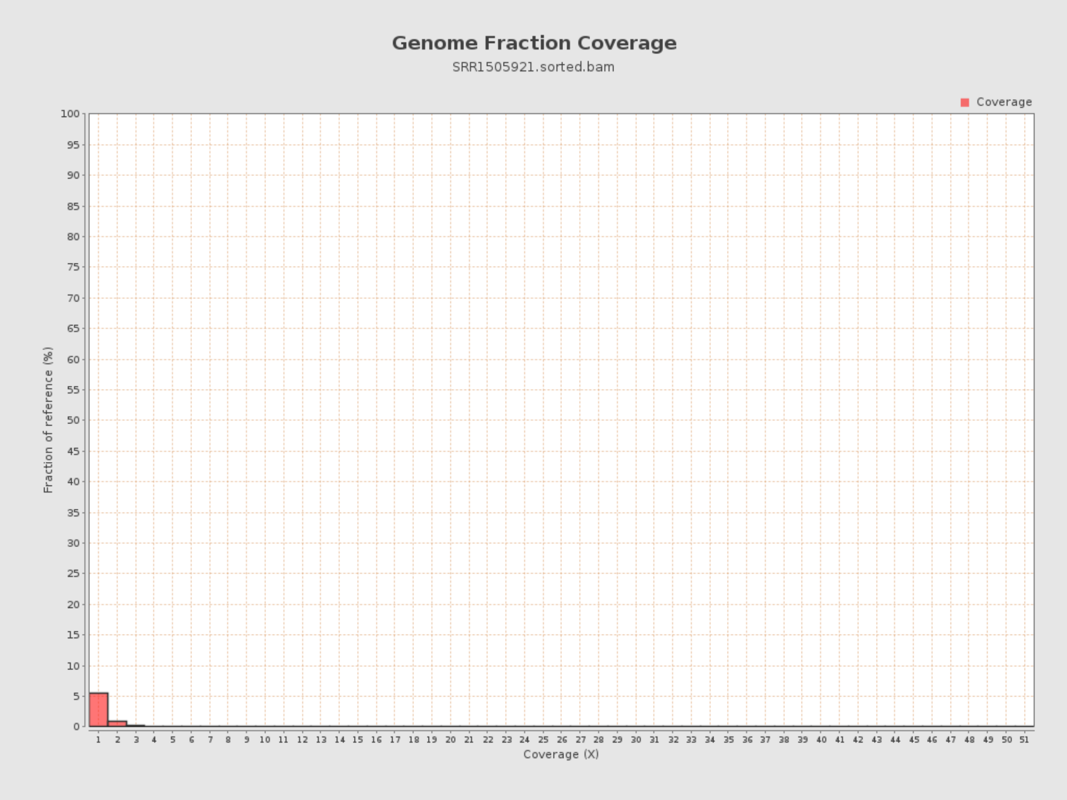
4. Results : Coverage Histogram



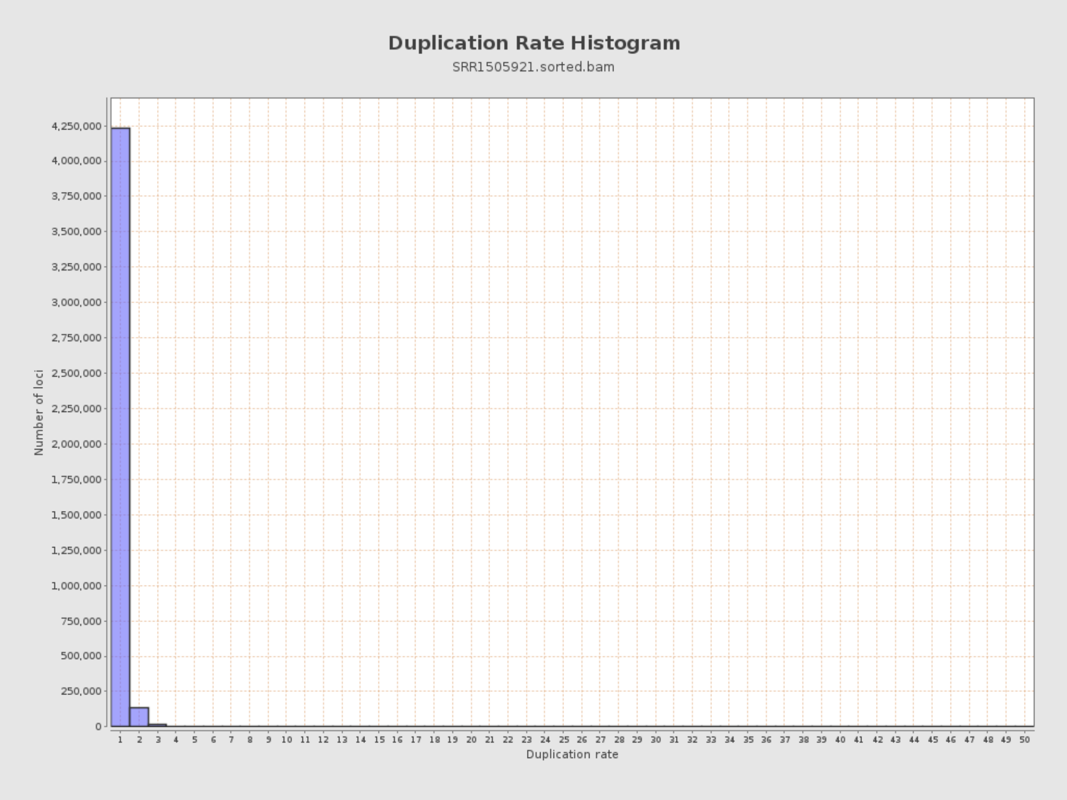
5. Results : Coverage Histogram (0-50X)



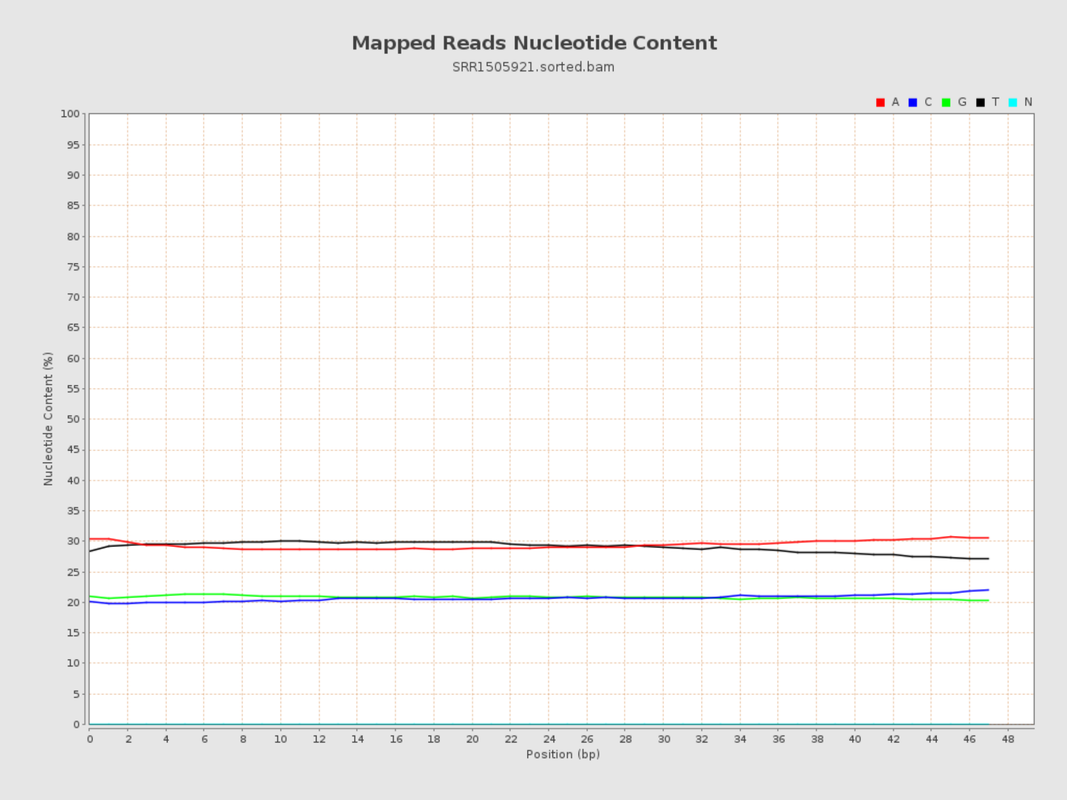
6. Results : Genome Fraction Coverage



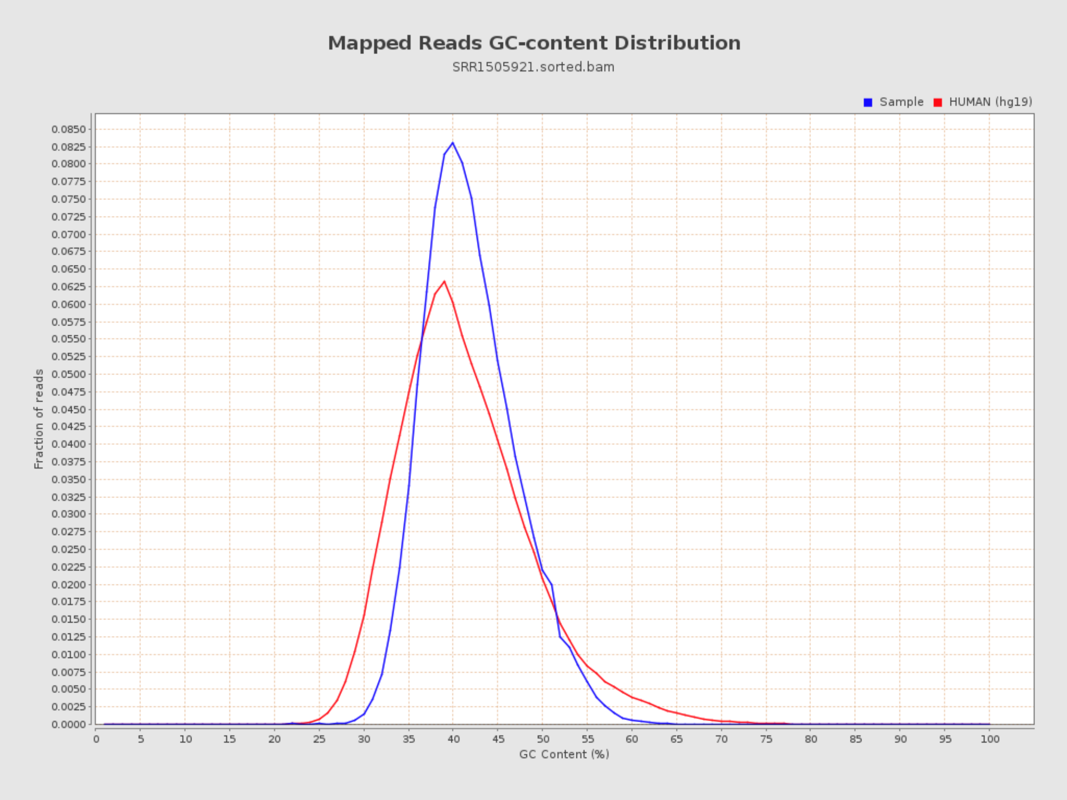
7. Results : Duplication Rate Histogram



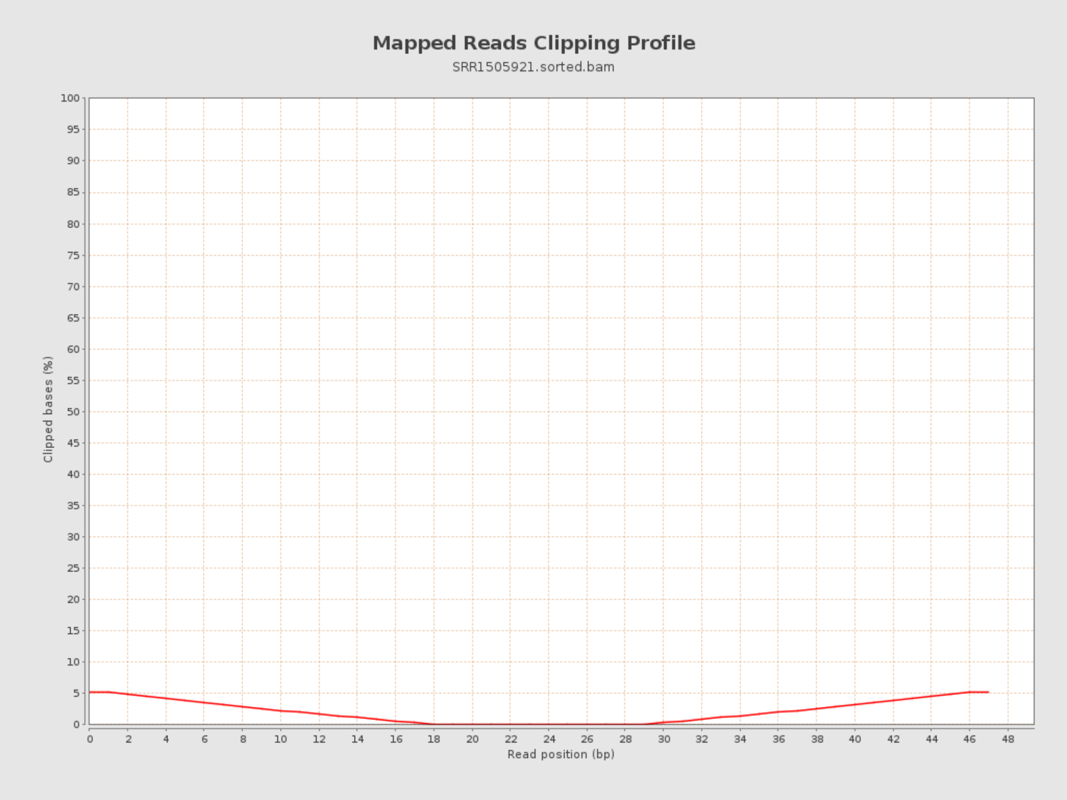
8. Results : Mapped Reads Nucleotide Content



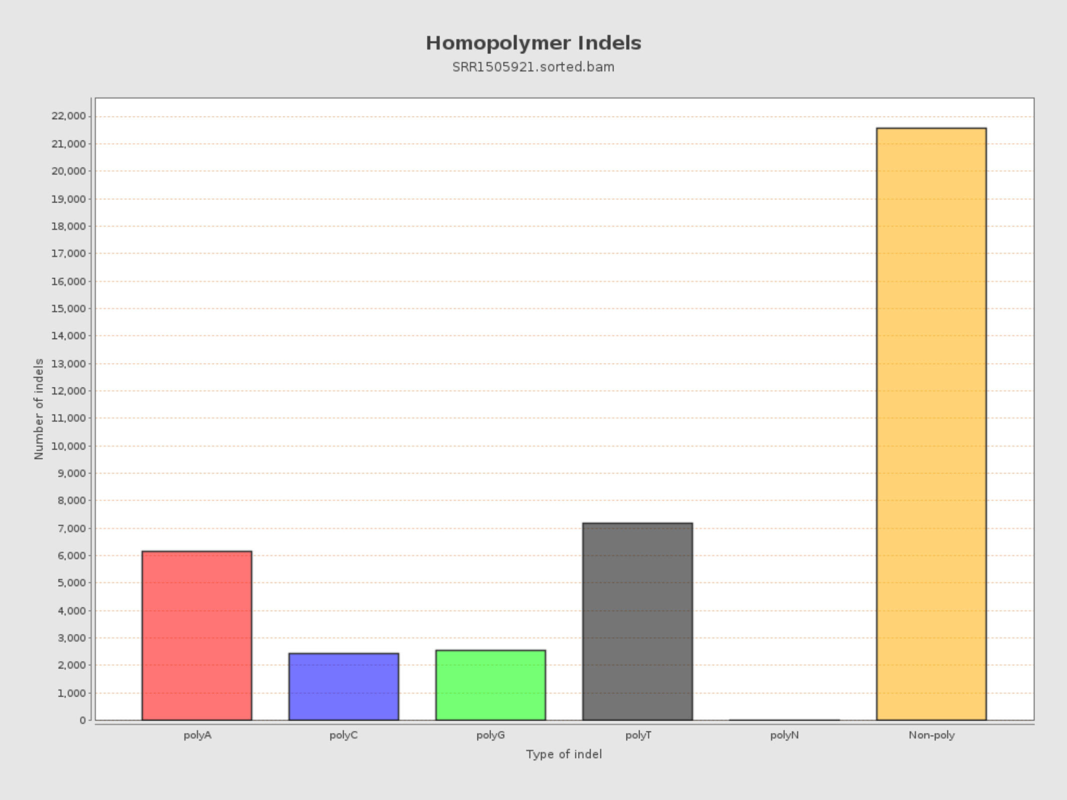
9. Results : Mapped Reads GC-content Distribution



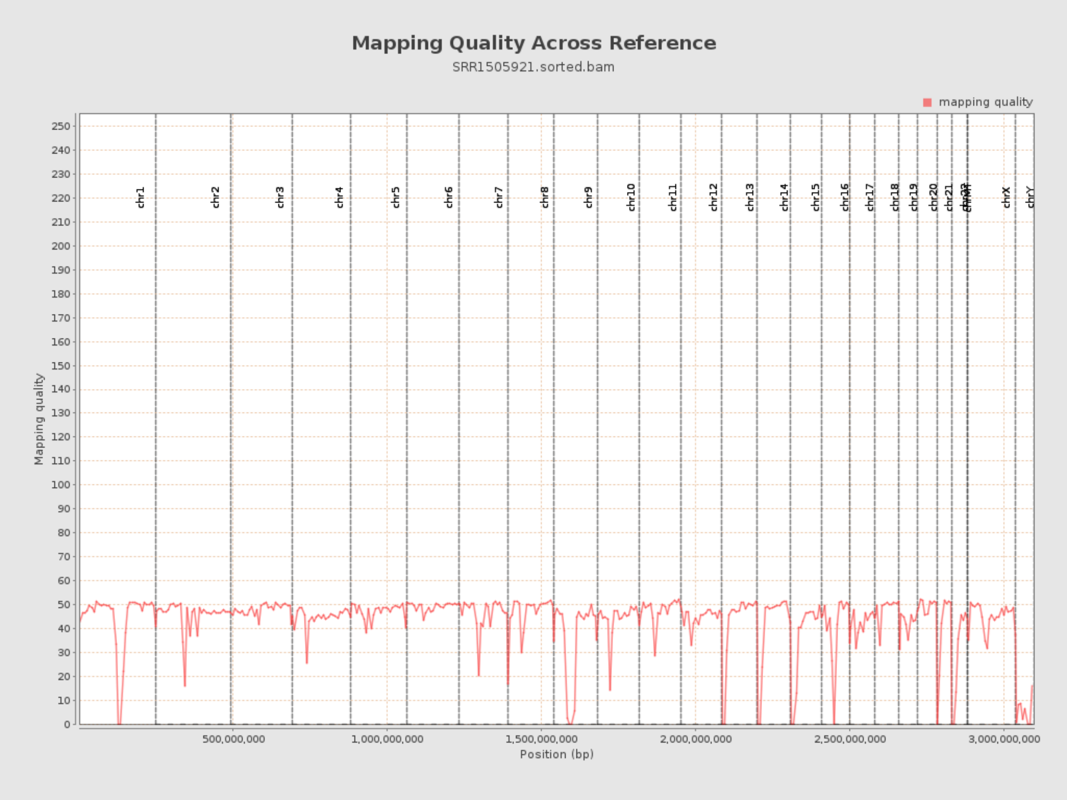
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram