Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:50:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505991.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_SRR1505991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505991.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:50:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,961,598
Mapped reads	5,305,907 / 48.4%
Unmapped reads	5,655,691 / 51.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	196 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	348,302 / 3.18%
Duplication rate	4.99%
Clipped reads	917,747 / 8.37%

2.2. ACGT Content

Number/percentage of A's	70,740,075 / 28.76%
Number/percentage of C's	51,614,012 / 20.98%
Number/percentage of T's	70,322,588 / 28.59%
Number/percentage of G's	52,508,531 / 21.35%
Number/percentage of N's	774,404 / 0.31%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0795

Standard Deviation	0.6589

2.4. Mapping Quality

Mean Mapping Quality	43.32

2.5. Mismatches and indels

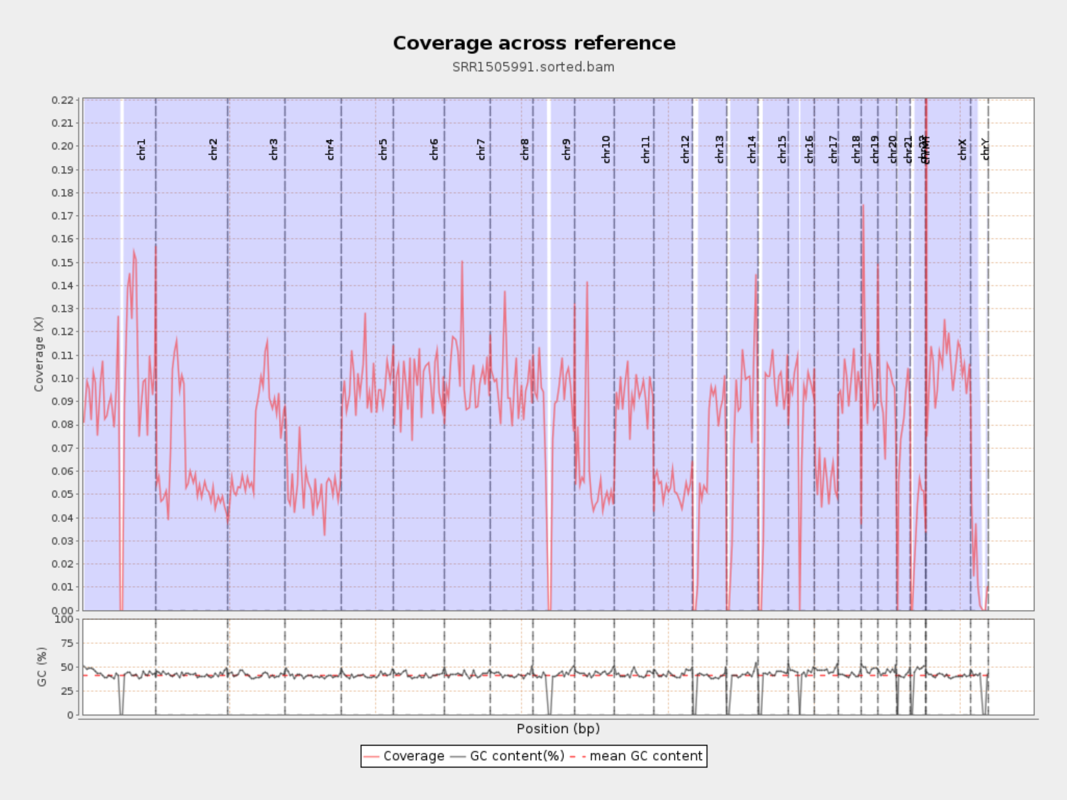
General error rate	0.79%
Mismatches	1,938,026
Insertions	10,870
Mapped reads with at least one insertion	0.2%
Deletions	35,416
Mapped reads with at least one deletion	0.67%
Homopolymer indels	43.77%

2.6. Chromosome stats

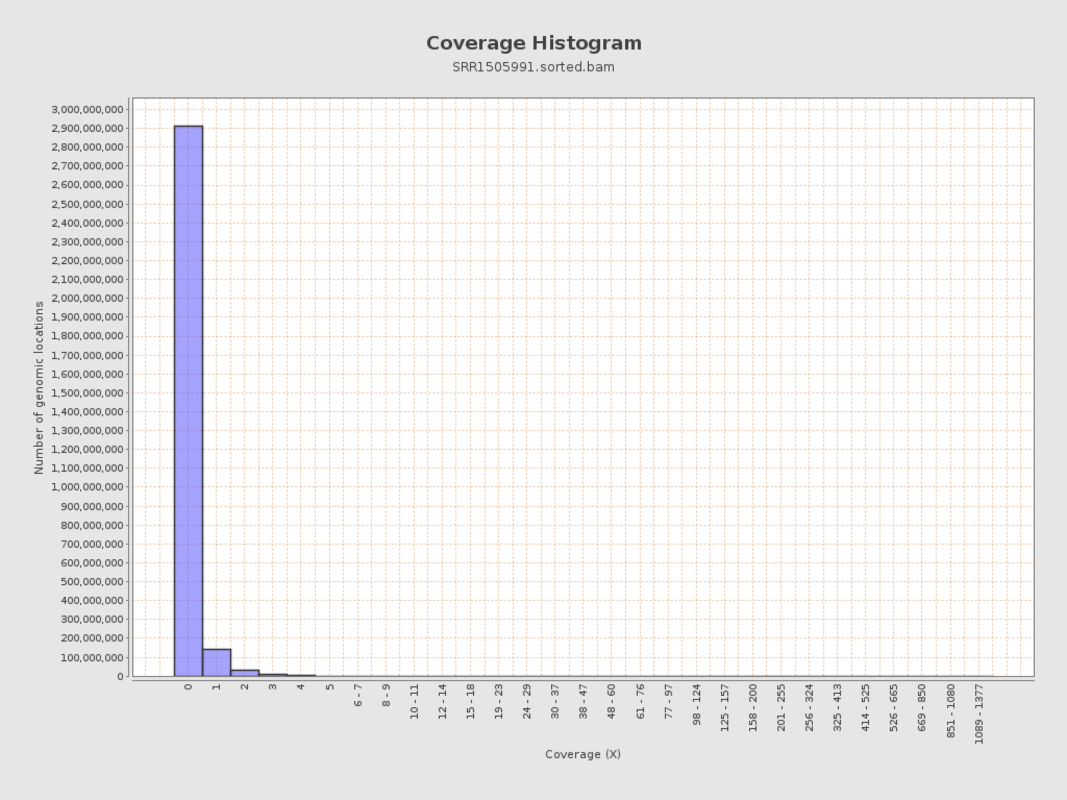
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23765119	0.0953	1.0046
chr2	243199373	14959303	0.0615	0.4869
chr3	198022430	14532029	0.0734	0.3497
chr4	191154276	10145773	0.0531	0.3226
chr5	180915260	17645335	0.0975	0.4042
chr6	171115067	16654497	0.0973	0.4884
chr7	159138663	16122497	0.1013	0.884

chr8	146364022	14170744	0.0968	0.7487
chr9	141213431	11706703	0.0829	0.47
chr10	135534747	7783983	0.0574	0.7097
chr11	135006516	12388703	0.0918	0.5062
chr12	133851895	7075614	0.0529	0.3141
chr13	115169878	7492097	0.0651	0.3272
chr14	107349540	8717456	0.0812	1.8714
chr15	102531392	8186288	0.0798	0.3639
chr16	90354753	7771257	0.086	0.4548
chr17	81195210	4576507	0.0564	0.3421
chr18	78077248	7651960	0.098	0.718
chr19	59128983	6222632	0.1052	0.7977
chr20	63025520	5872964	0.0932	0.4211
chr21	48129895	3623528	0.0753	0.3958
chr22	51304566	1818949	0.0355	0.2496
chrMT	16571	53397	3.2223	3.0267
chrX	155270560	16248971	0.1046	0.4526
chrY	59373566	823263	0.0139	0.2433

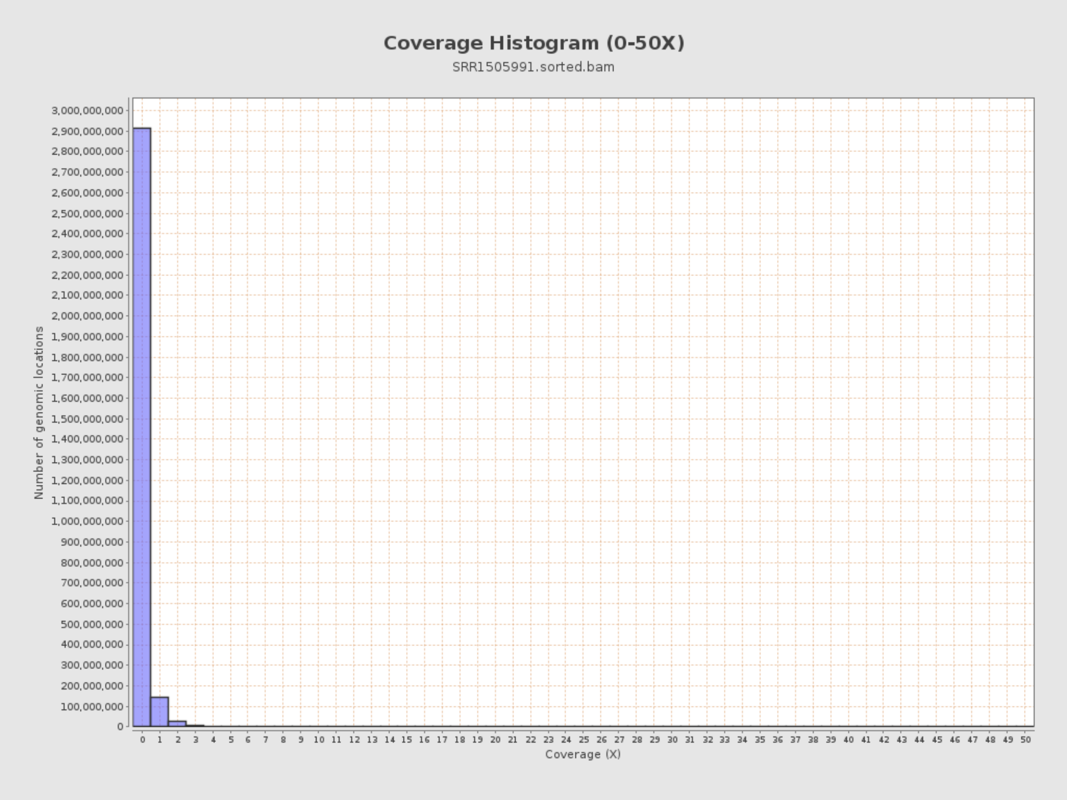
3. Results : Coverage across reference



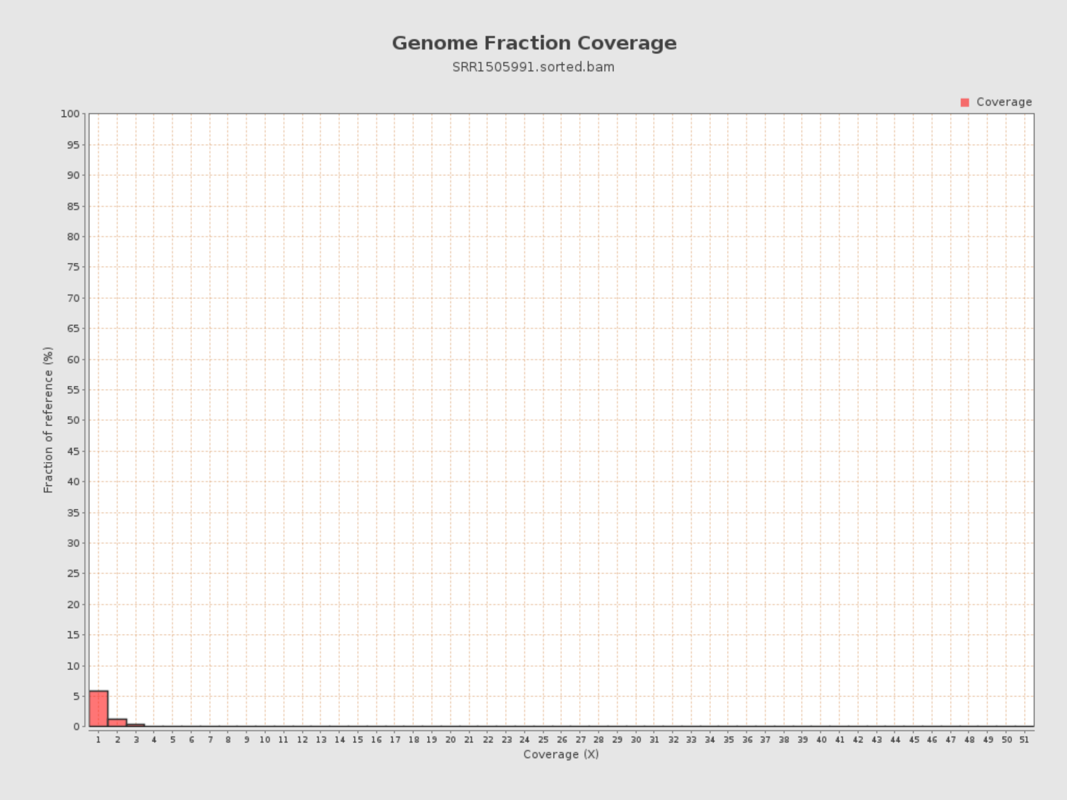
4. Results : Coverage Histogram



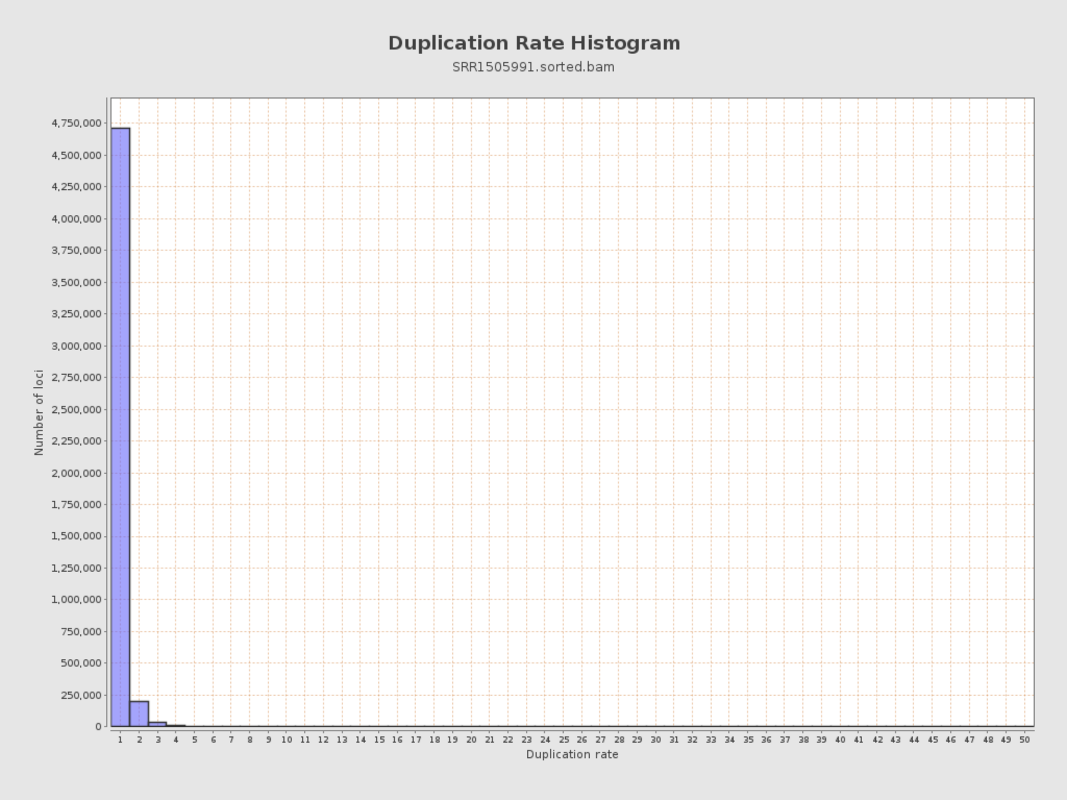
5. Results : Coverage Histogram (0-50X)



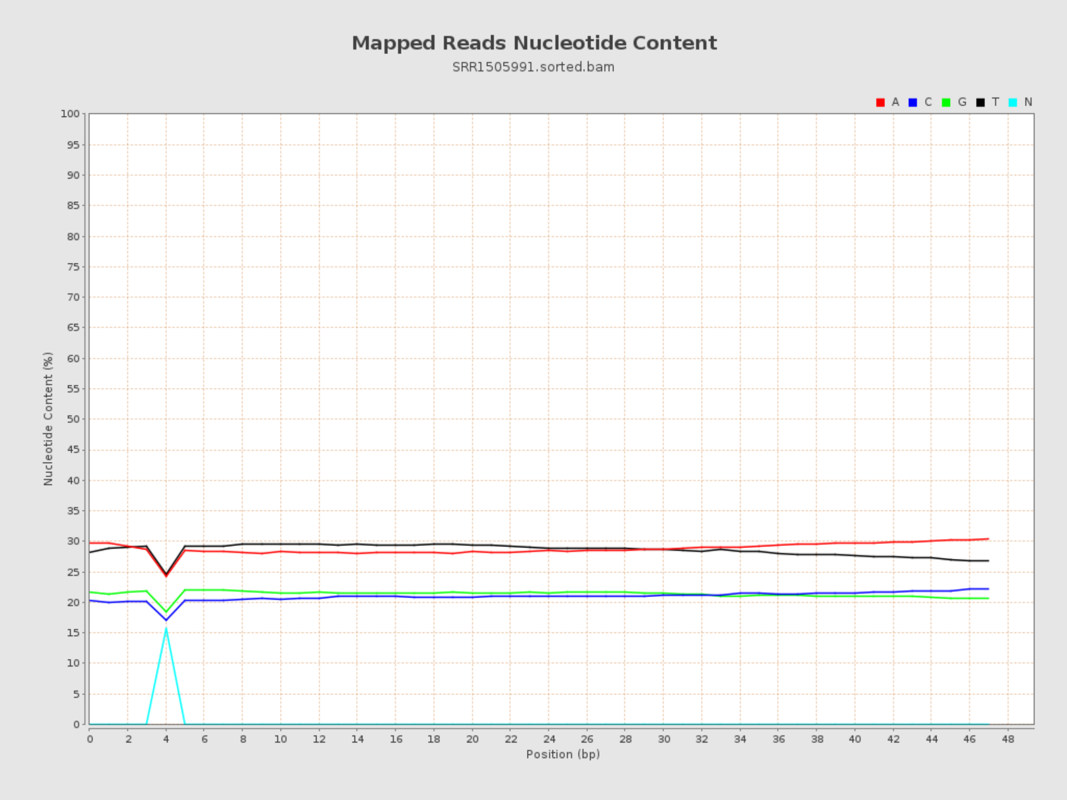
6. Results : Genome Fraction Coverage



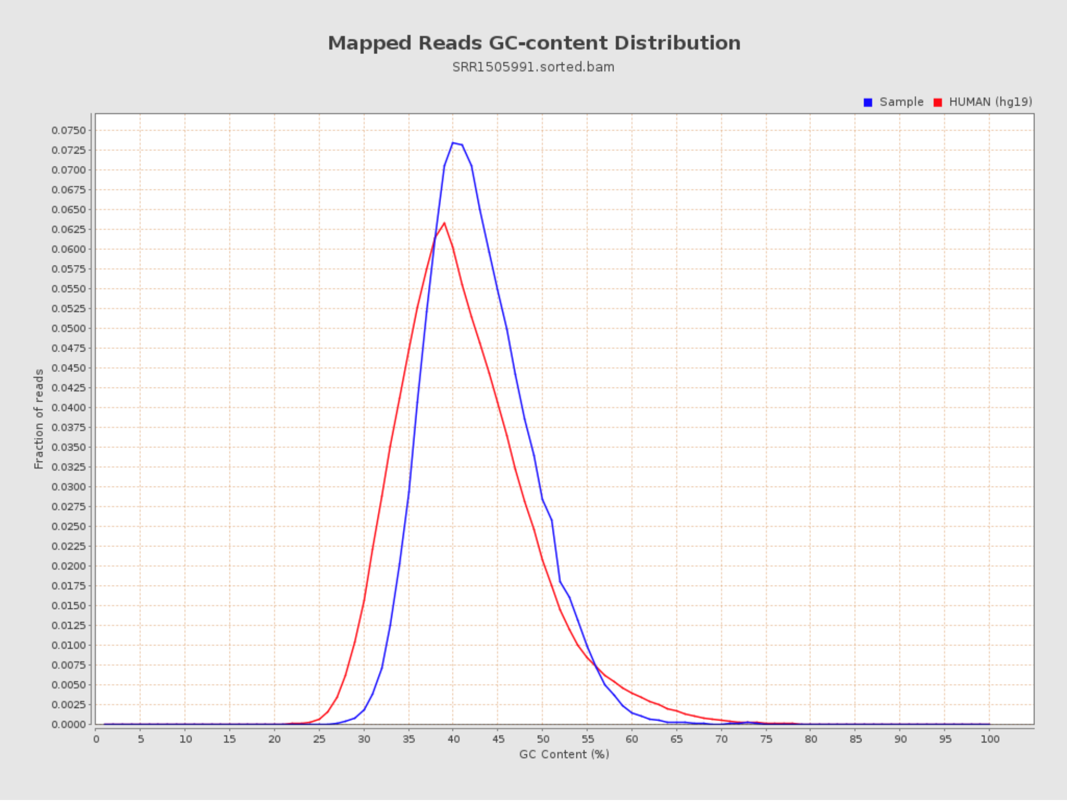
7. Results : Duplication Rate Histogram



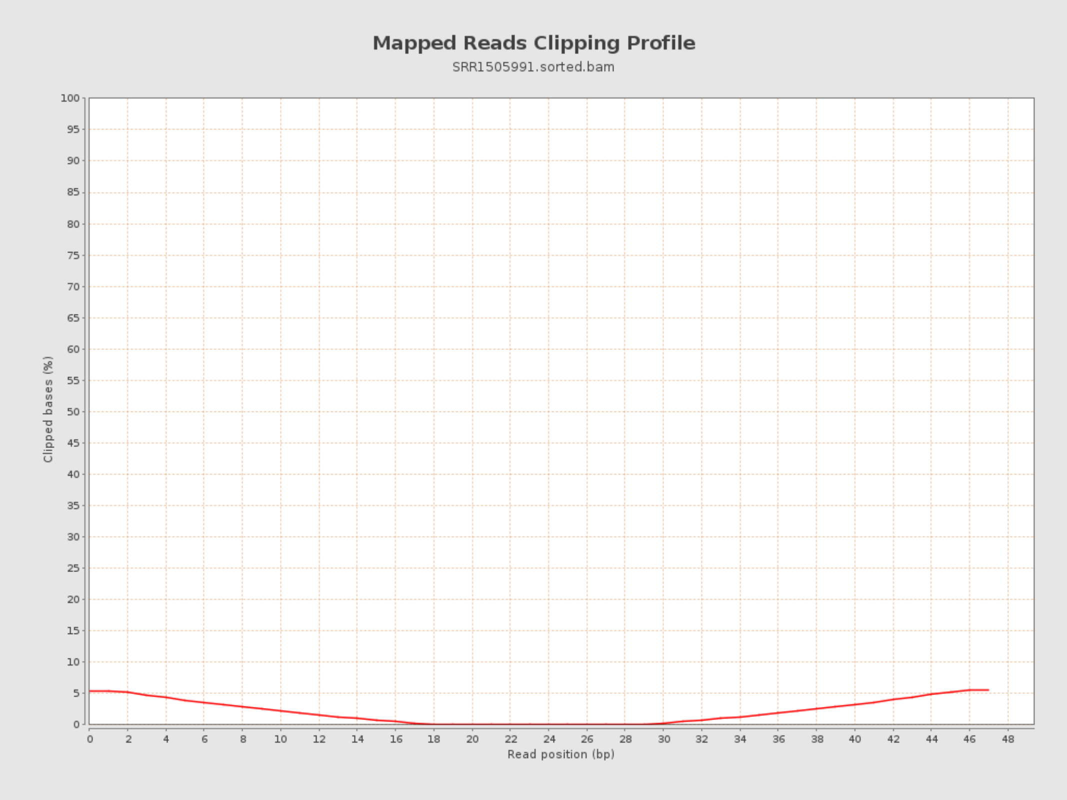
8. Results : Mapped Reads Nucleotide Content



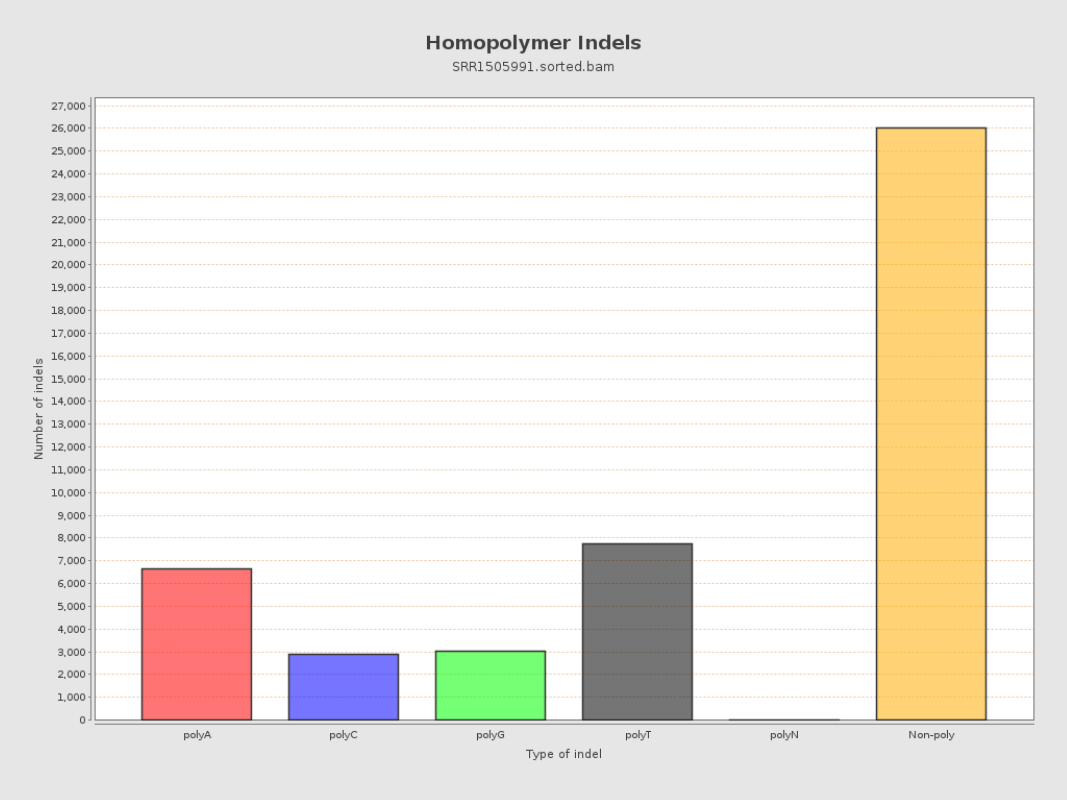
9. Results : Mapped Reads GC-content Distribution



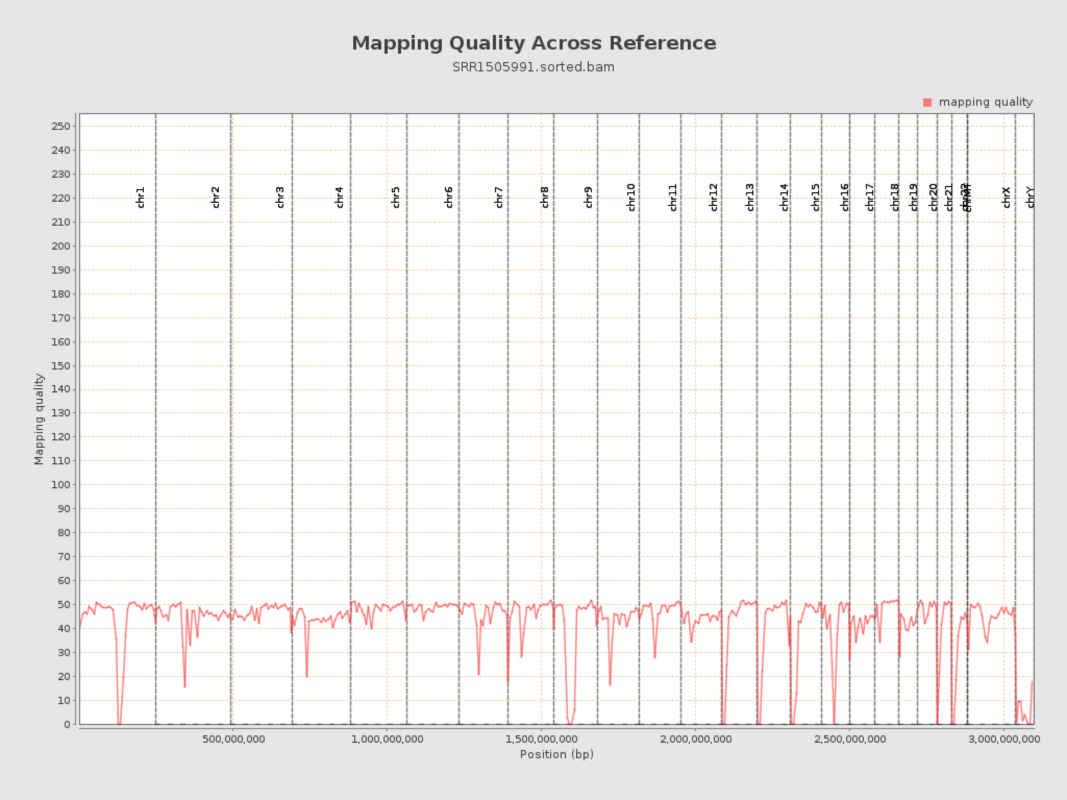
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram