Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:26:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081962.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_SRR3081962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081962.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:26:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,130,415
Mapped reads	2,835,545 / 90.58%
Unmapped reads	294,870 / 9.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,812 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	158,489 / 5.06%
Duplication rate	4.49%
Clipped reads	1,205,681 / 38.52%

2.2. ACGT Content

Number/percentage of A's	52,912,938 / 27.84%
Number/percentage of C's	35,032,674 / 18.43%
Number/percentage of T's	60,098,675 / 31.62%
Number/percentage of G's	41,973,128 / 22.09%
Number/percentage of N's	23,885 / 0.01%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0614

Standard Deviation	0.4934

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

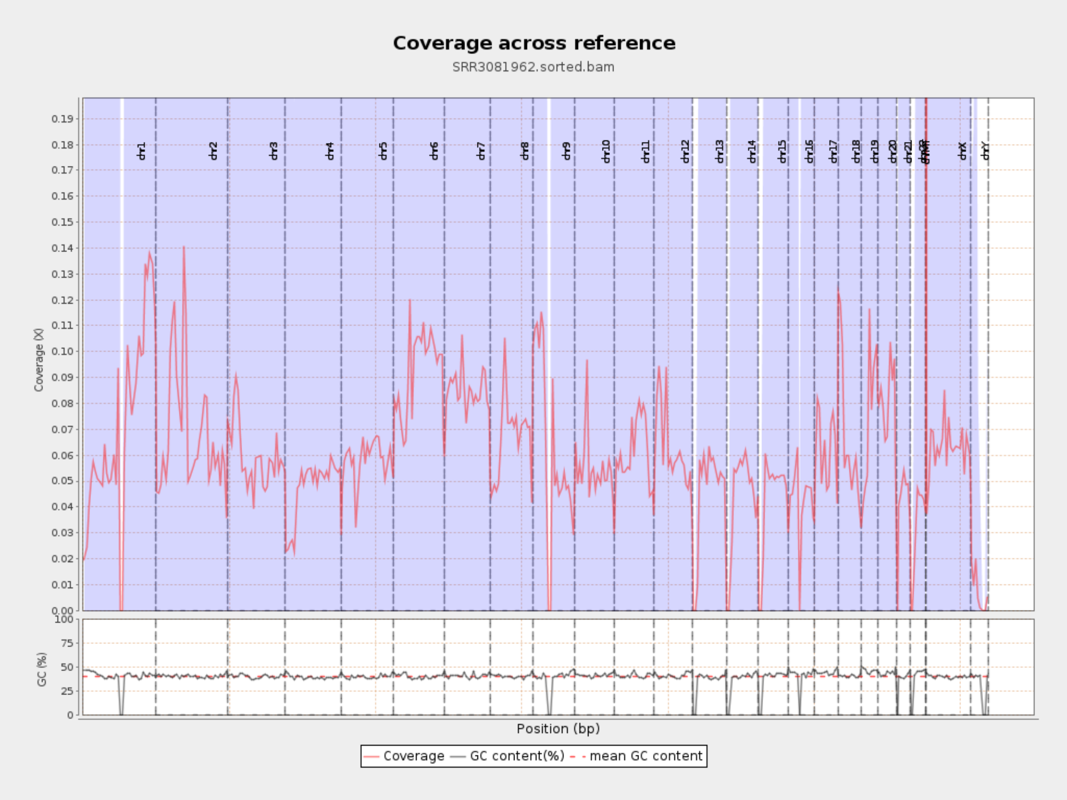
General error rate	0.78%
Mismatches	1,466,123
Insertions	13,596
Mapped reads with at least one insertion	0.48%
Deletions	41,055
Mapped reads with at least one deletion	1.43%
Homopolymer indels	48.42%

2.6. Chromosome stats

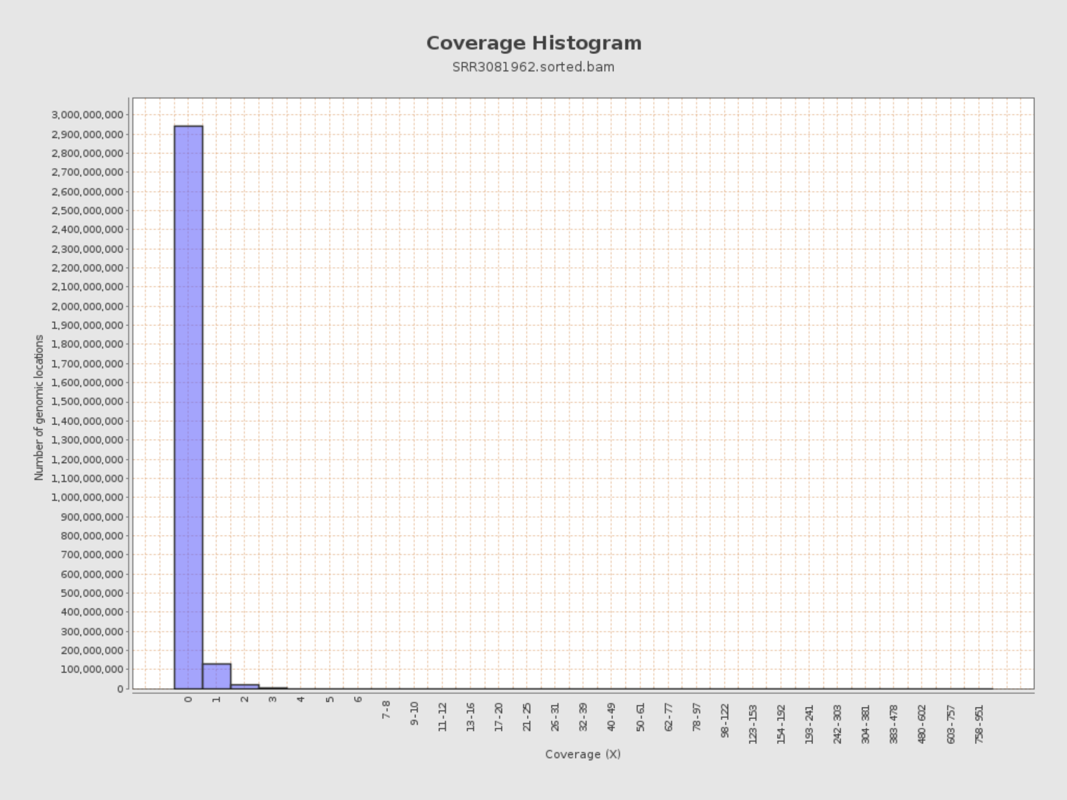
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17723139	0.0711	0.8892
chr2	243199373	16865118	0.0693	0.7273
chr3	198022430	11796159	0.0596	0.2848
chr4	191154276	9059735	0.0474	0.2687
chr5	180915260	10436668	0.0577	0.2811
chr6	171115067	15999533	0.0935	0.4431
chr7	159138663	13464204	0.0846	0.6278

chr8	146364022	9785220	0.0669	0.5781
chr9	141213431	8820056	0.0625	0.5085
chr10	135534747	7467109	0.0551	0.4342
chr11	135006516	8334419	0.0617	0.4018
chr12	133851895	8398921	0.0627	0.2994
chr13	115169878	5238059	0.0455	0.2511
chr14	107349540	4708702	0.0439	0.2678
chr15	102531392	4354966	0.0425	0.2472
chr16	90354753	3740661	0.0414	0.2706
chr17	81195210	5117992	0.063	0.3245
chr18	78077248	5273306	0.0675	0.7566
chr19	59128983	4384720	0.0742	0.6503
chr20	63025520	5177090	0.0821	0.3452
chr21	48129895	1996579	0.0415	0.2621
chr22	51304566	1601187	0.0312	0.2039
chrMT	16571	216695	13.0768	7.6064
chrX	155270560	9742196	0.0627	0.3381
chrY	59373566	410860	0.0069	0.145

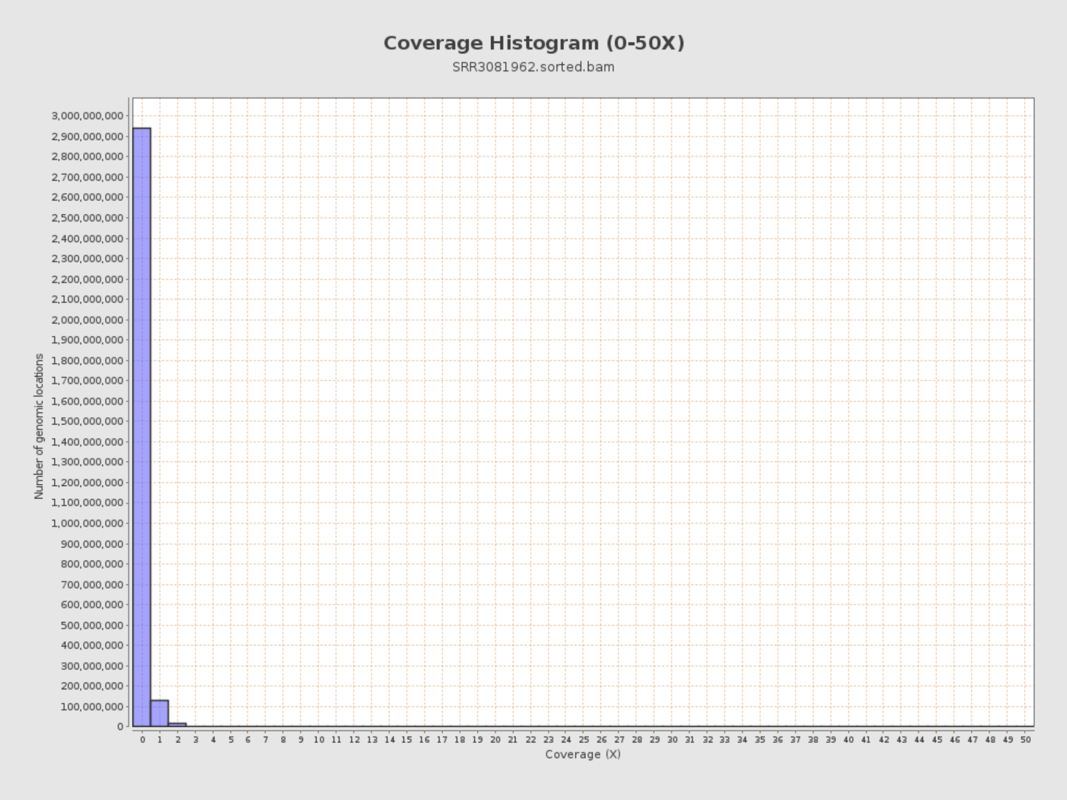
3. Results : Coverage across reference



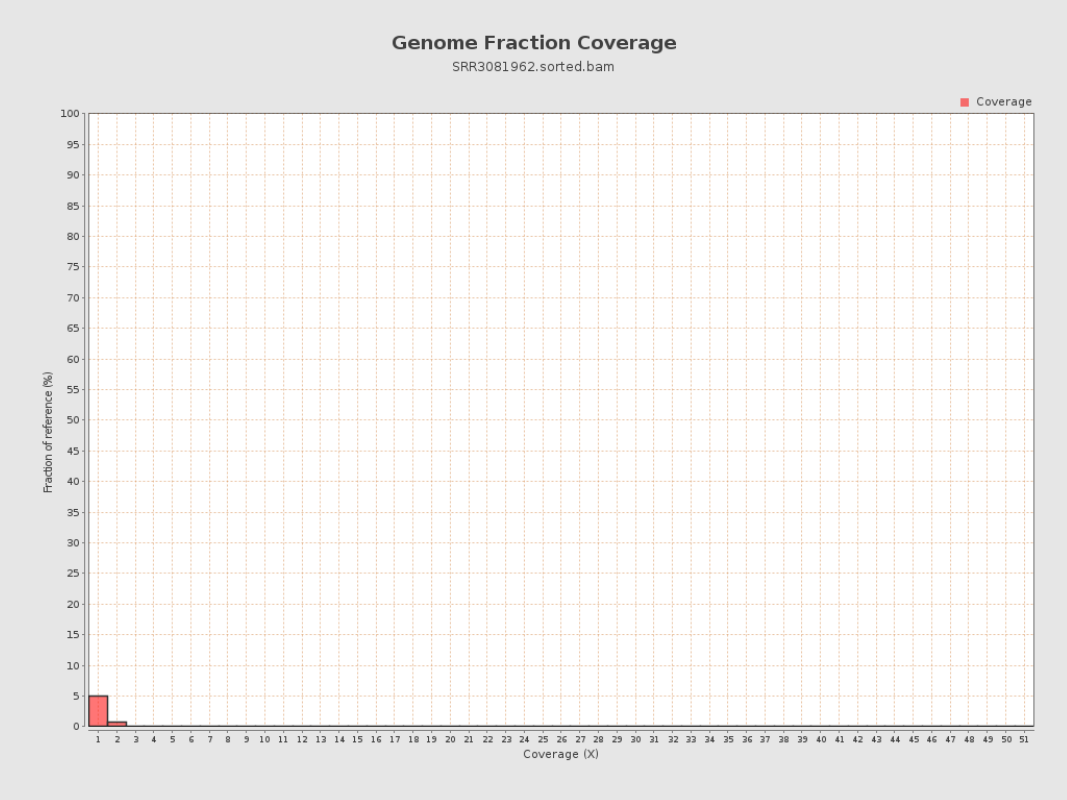
4. Results : Coverage Histogram



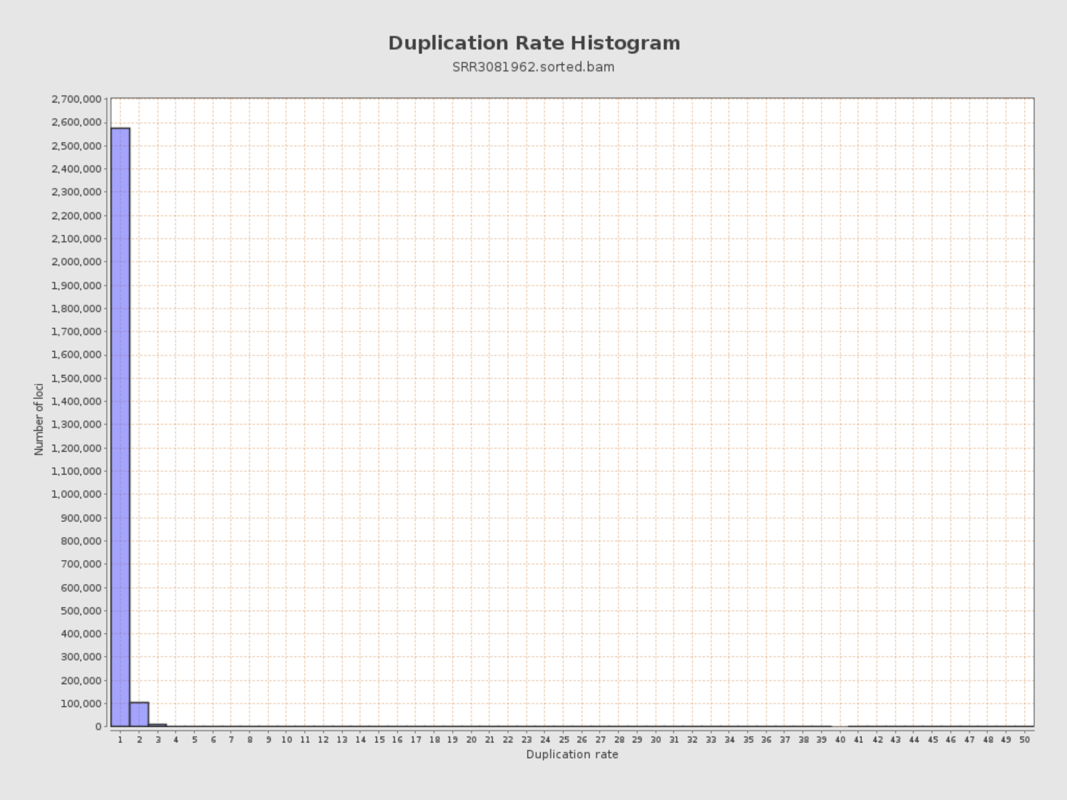
5. Results : Coverage Histogram (0-50X)



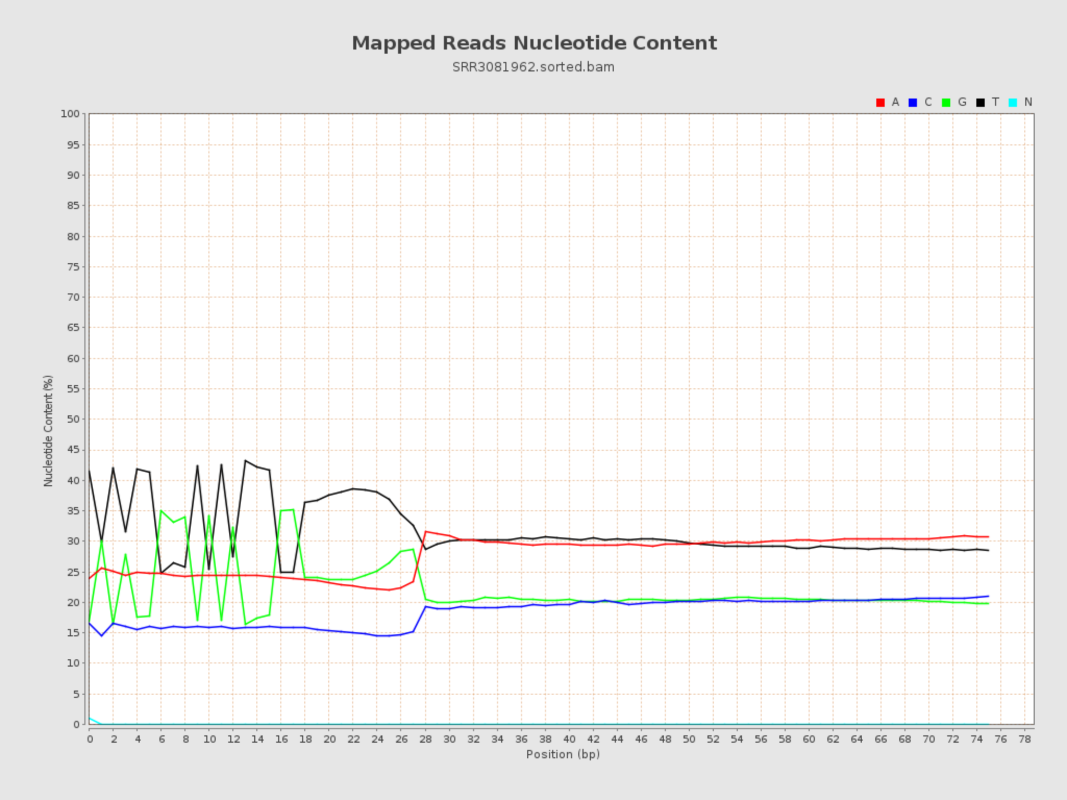
6. Results : Genome Fraction Coverage



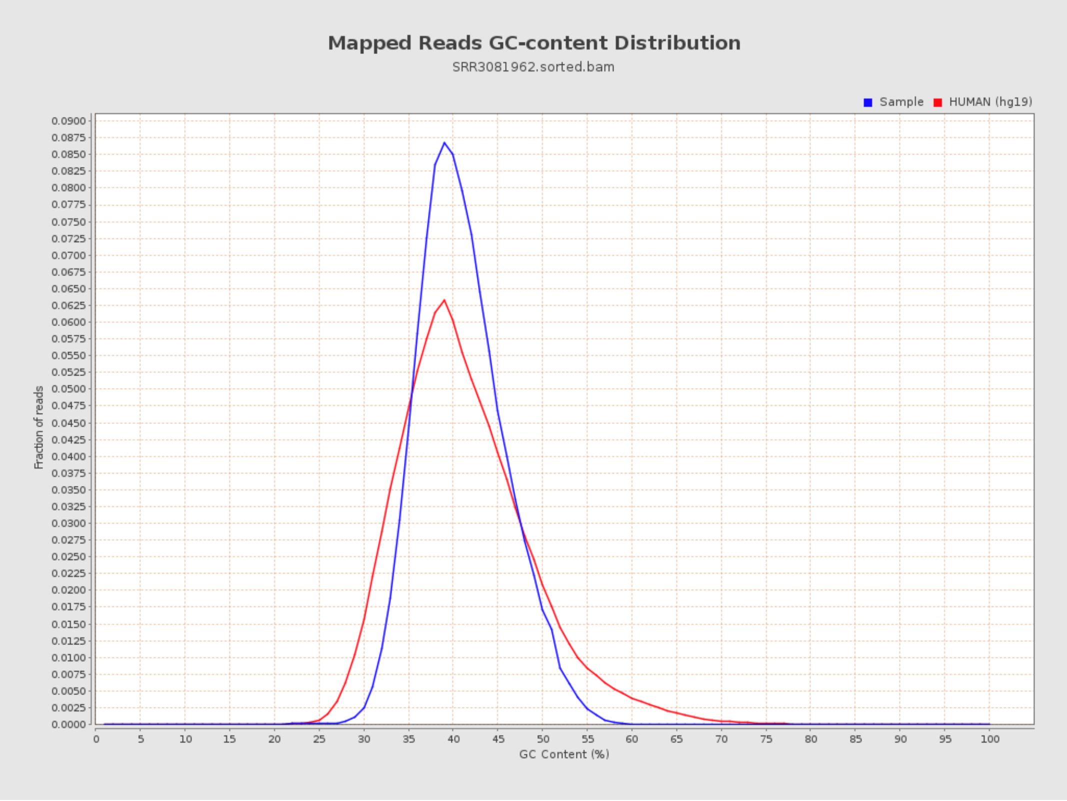
7. Results : Duplication Rate Histogram



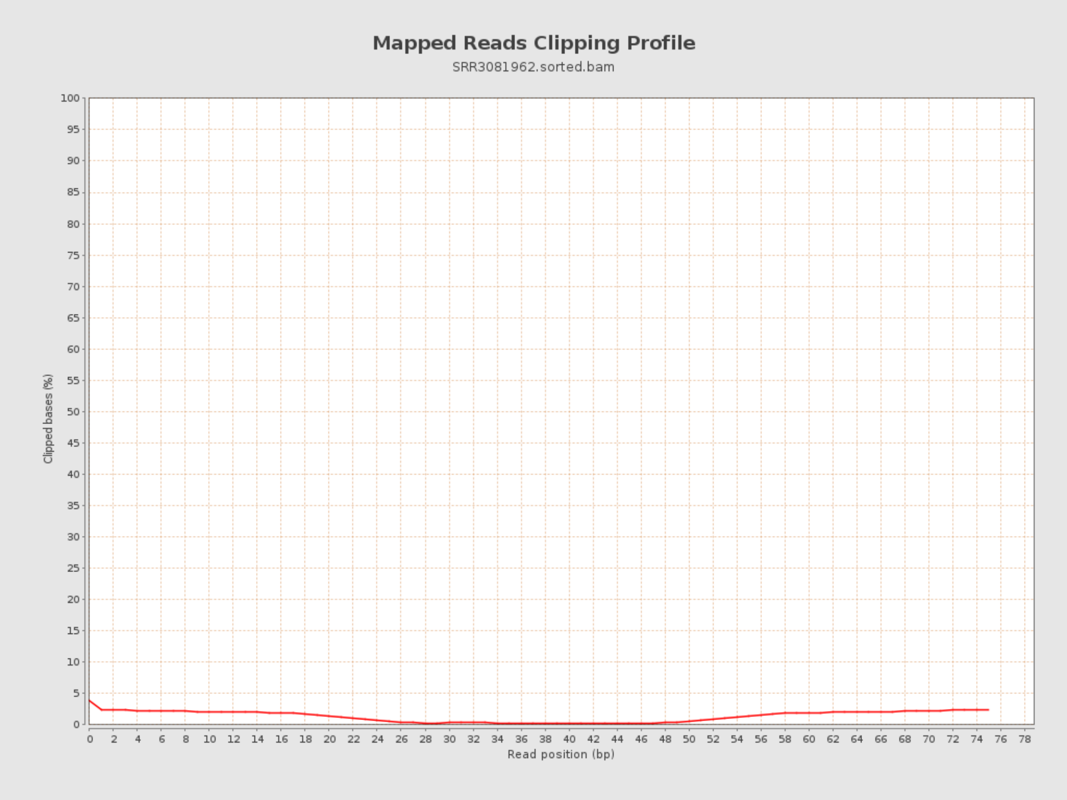
8. Results : Mapped Reads Nucleotide Content



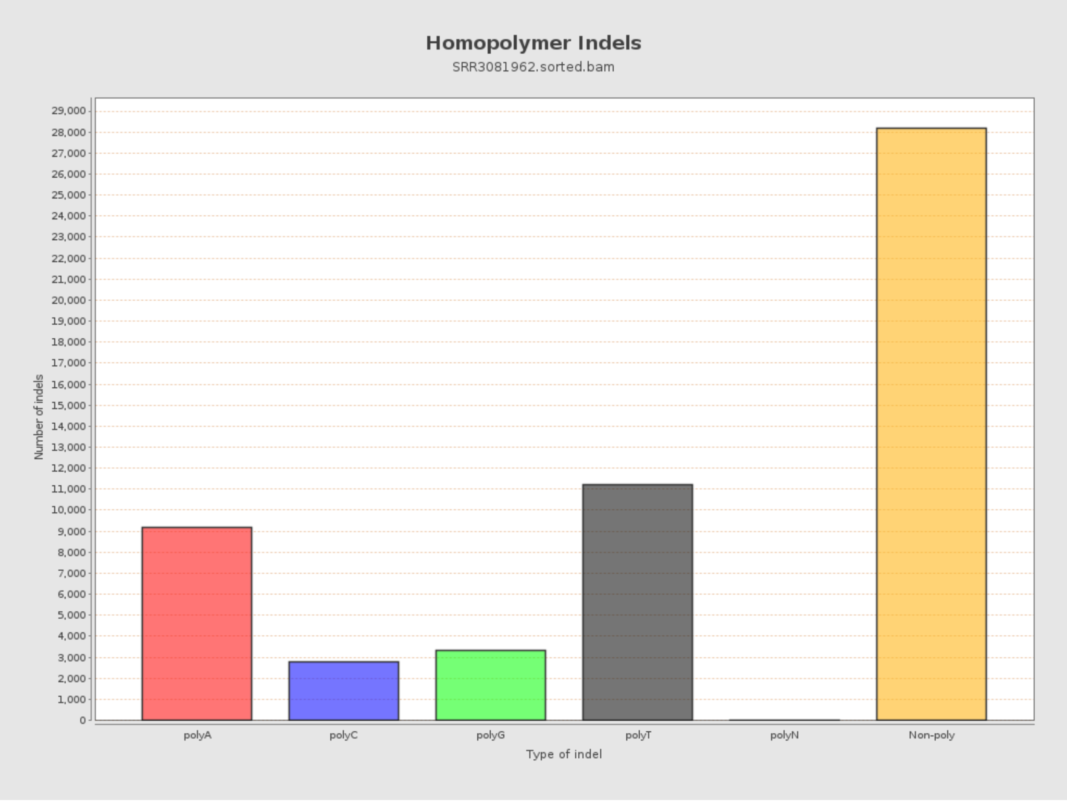
9. Results : Mapped Reads GC-content Distribution



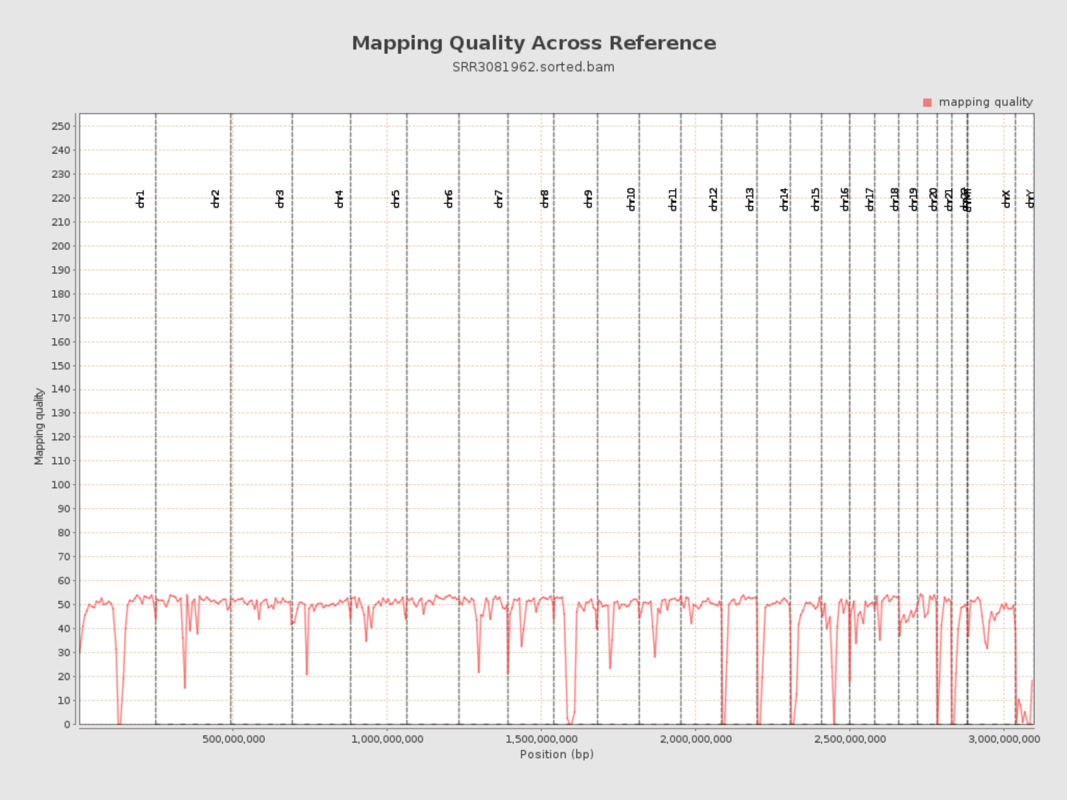
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram