Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:30:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081963.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_SRR3081963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:30:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,904,656
Mapped reads	2,638,643 / 90.84%
Unmapped reads	266,013 / 9.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,785 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	142,639 / 4.91%
Duplication rate	4.37%
Clipped reads	1,132,054 / 38.97%

2.2. ACGT Content

Number/percentage of A's	48,825,138 / 27.62%
Number/percentage of C's	32,725,477 / 18.51%
Number/percentage of T's	55,768,556 / 31.54%
Number/percentage of G's	39,463,429 / 22.32%
Number/percentage of N's	22,281 / 0.01%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.4524

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

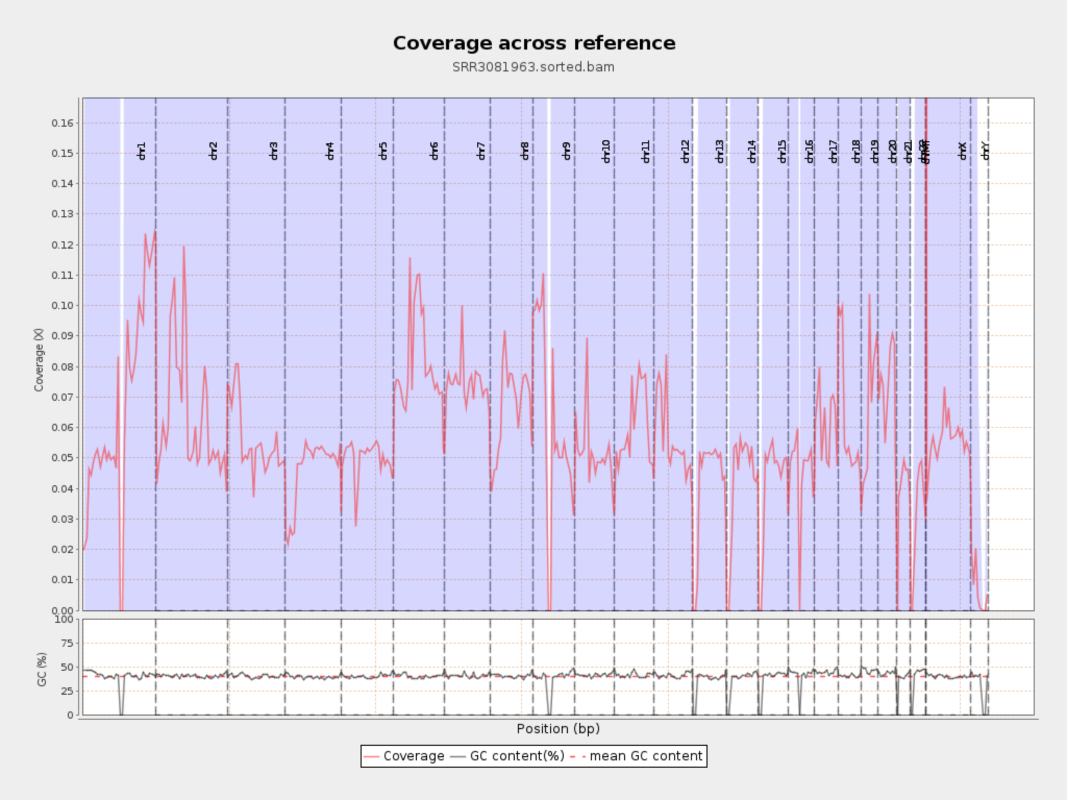
General error rate	0.77%
Mismatches	1,338,835
Insertions	12,293
Mapped reads with at least one insertion	0.46%
Deletions	35,337
Mapped reads with at least one deletion	1.32%
Homopolymer indels	48.28%

2.6. Chromosome stats

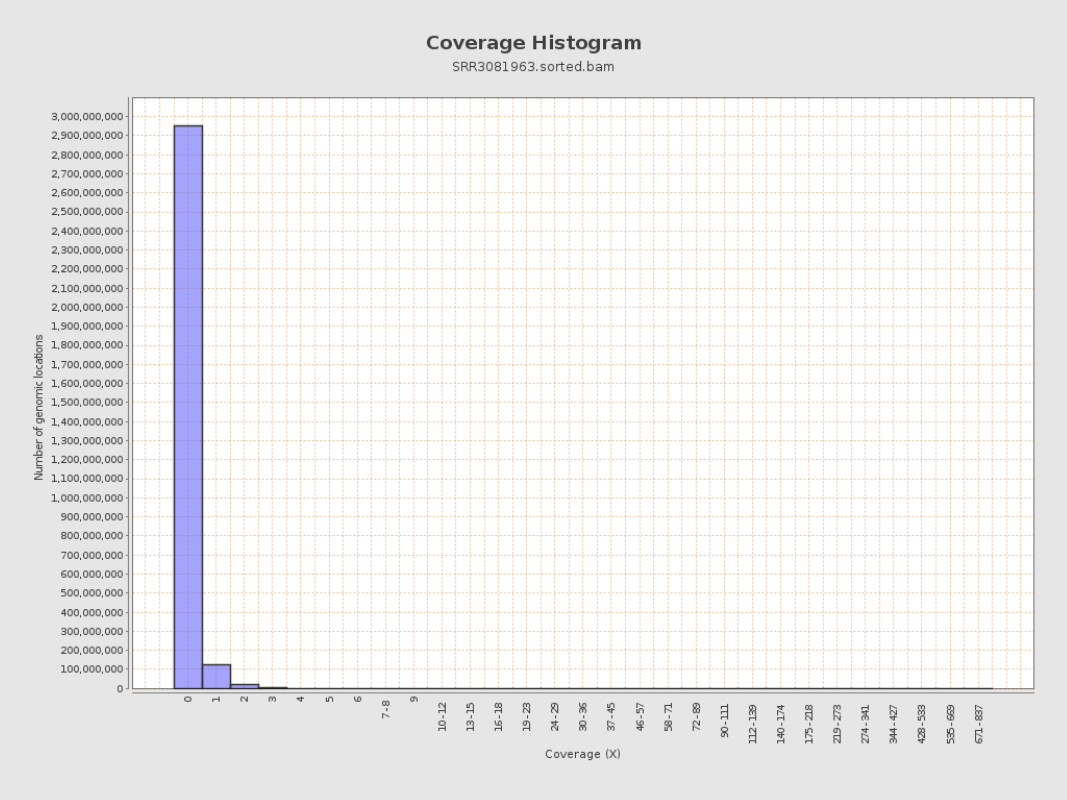
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16669877	0.0669	0.7737
chr2	243199373	15552145	0.0639	0.613
chr3	198022430	11143047	0.0563	0.2745
chr4	191154276	8840546	0.0462	0.266
chr5	180915260	8977416	0.0496	0.2589
chr6	171115067	14016530	0.0819	0.4234
chr7	159138663	11817104	0.0743	0.5809

chr8	146364022	9814593	0.0671	0.614
chr9	141213431	8688284	0.0615	0.4769
chr10	135534747	7075496	0.0522	0.4329
chr11	135006516	8149301	0.0604	0.3681
chr12	133851895	7581791	0.0566	0.2849
chr13	115169878	4764818	0.0414	0.2379
chr14	107349540	4574134	0.0426	0.2684
chr15	102531392	4124801	0.0402	0.2364
chr16	90354753	3978532	0.044	0.2733
chr17	81195210	5057020	0.0623	0.3275
chr18	78077248	4842602	0.062	0.7175
chr19	59128983	3950953	0.0668	0.5974
chr20	63025520	4719331	0.0749	0.3234
chr21	48129895	1885864	0.0392	0.2576
chr22	51304566	1563546	0.0305	0.2003
chrMT	16571	20041	1.2094	1.2254
chrX	155270560	8658424	0.0558	0.3182
chrY	59373566	401497	0.0068	0.146

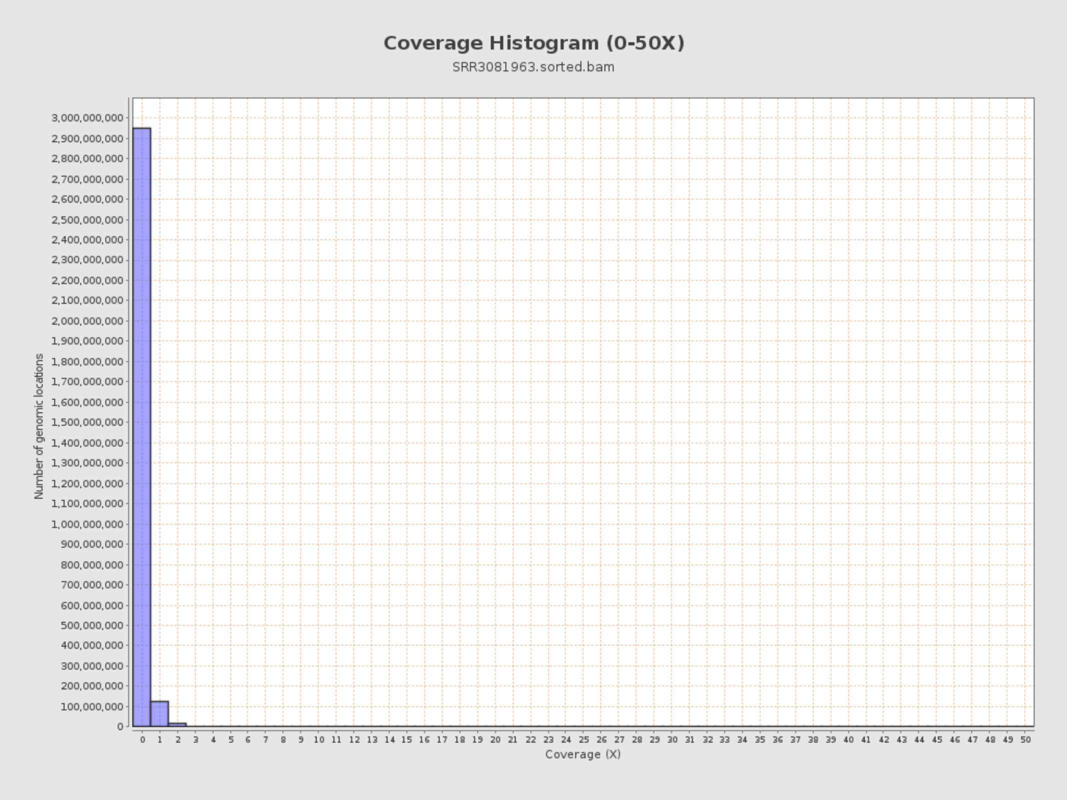
3. Results : Coverage across reference



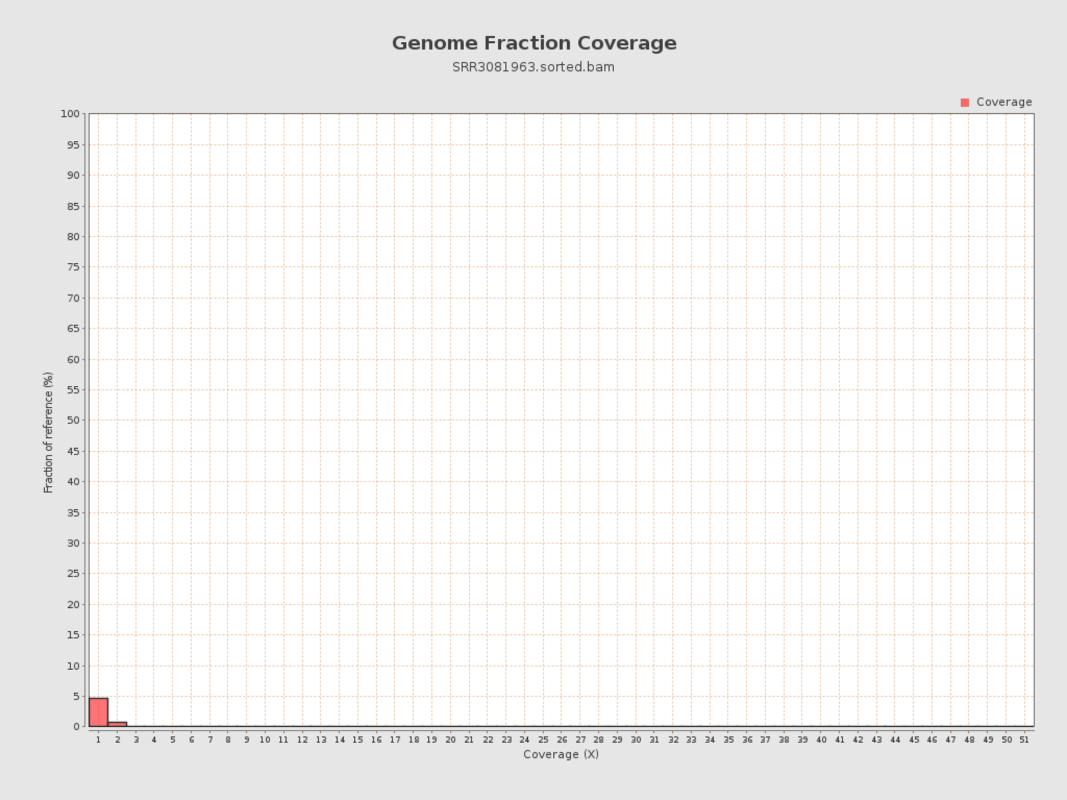
4. Results : Coverage Histogram



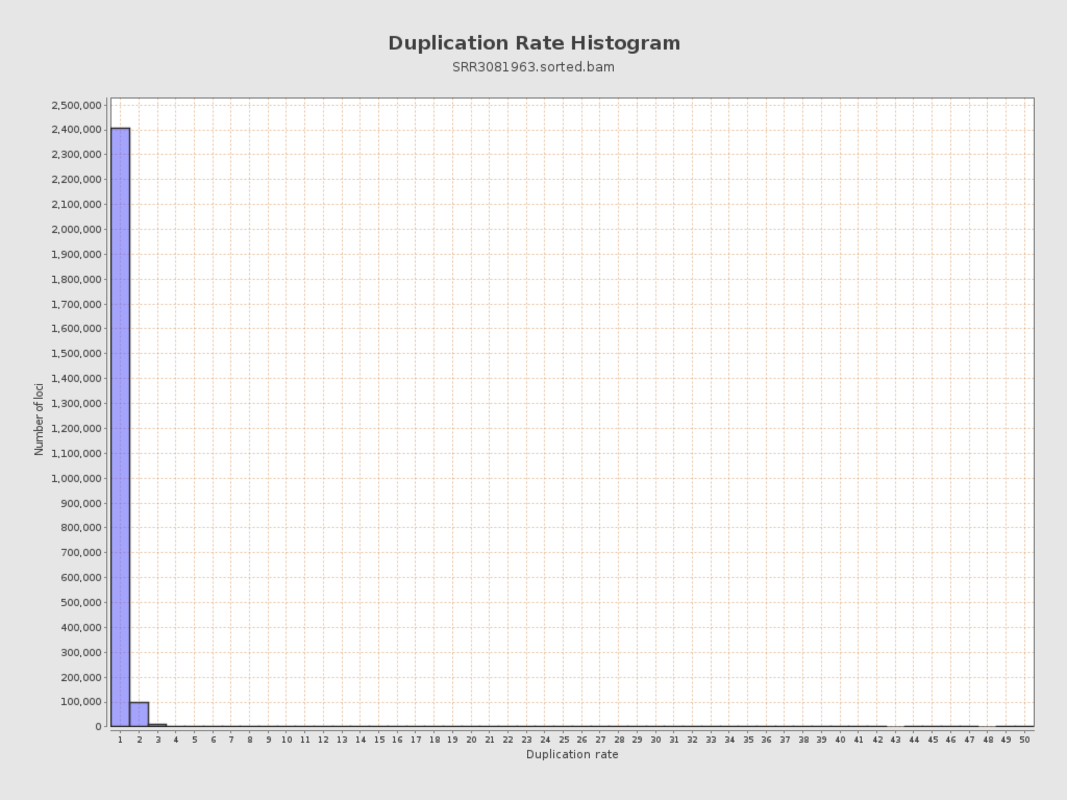
5. Results : Coverage Histogram (0-50X)



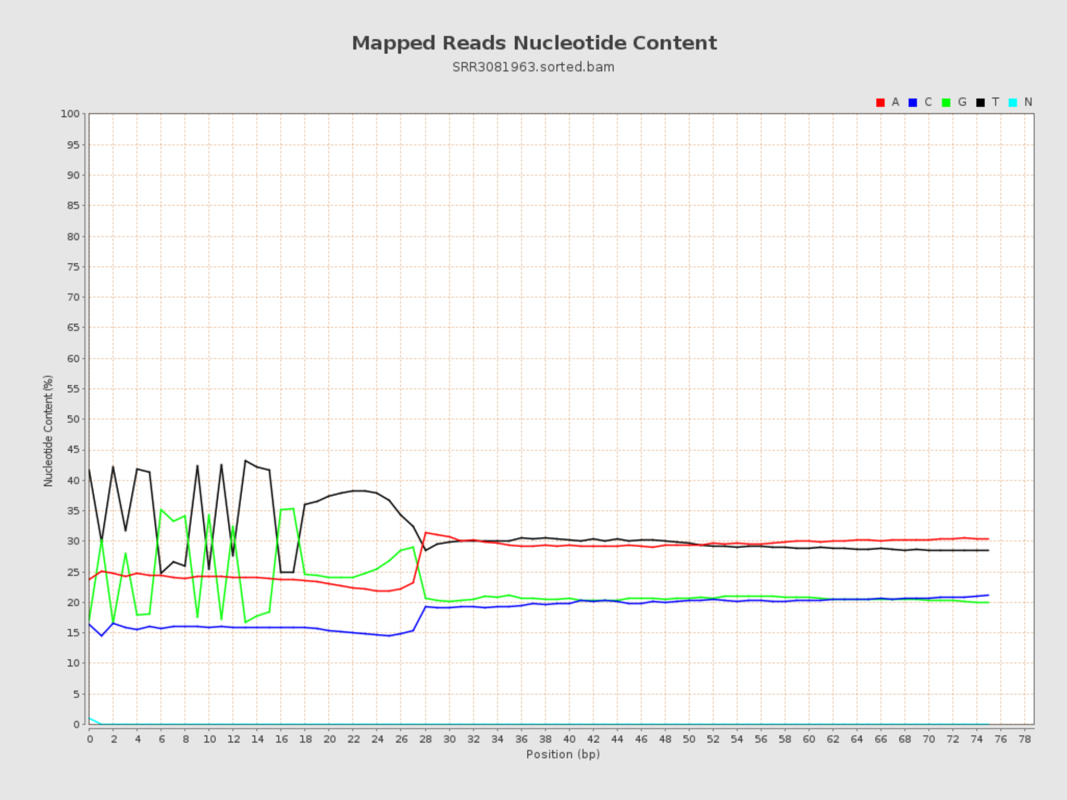
6. Results : Genome Fraction Coverage



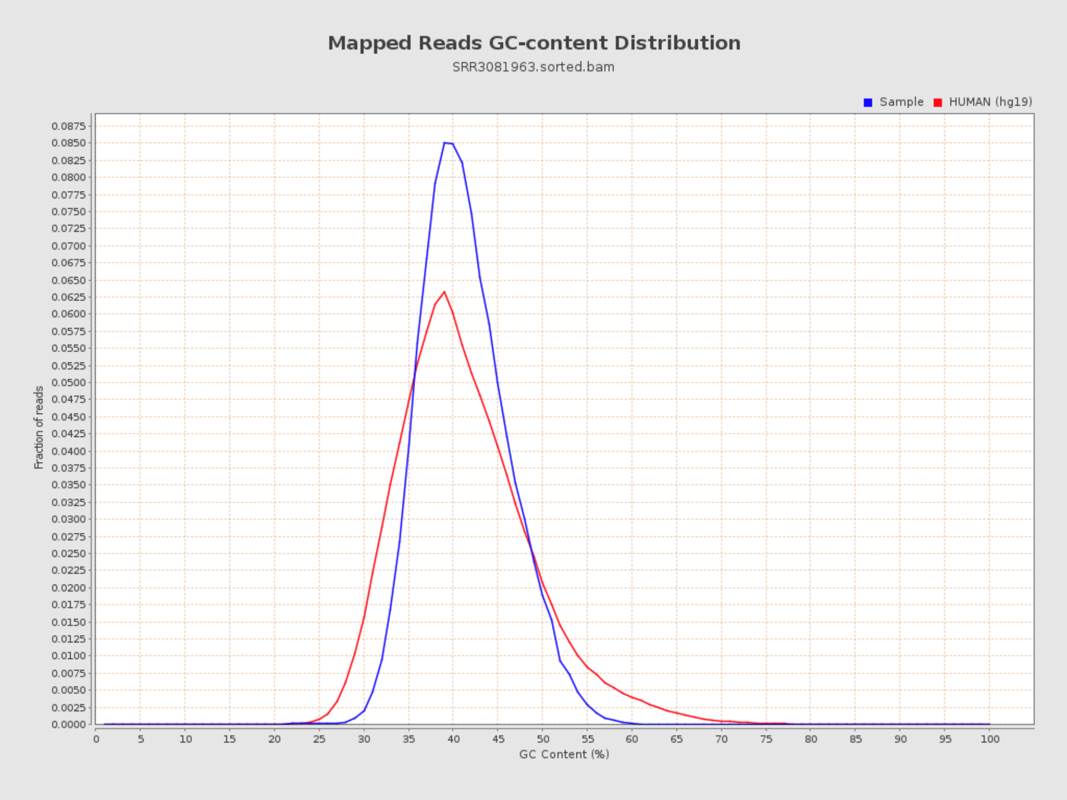
7. Results : Duplication Rate Histogram



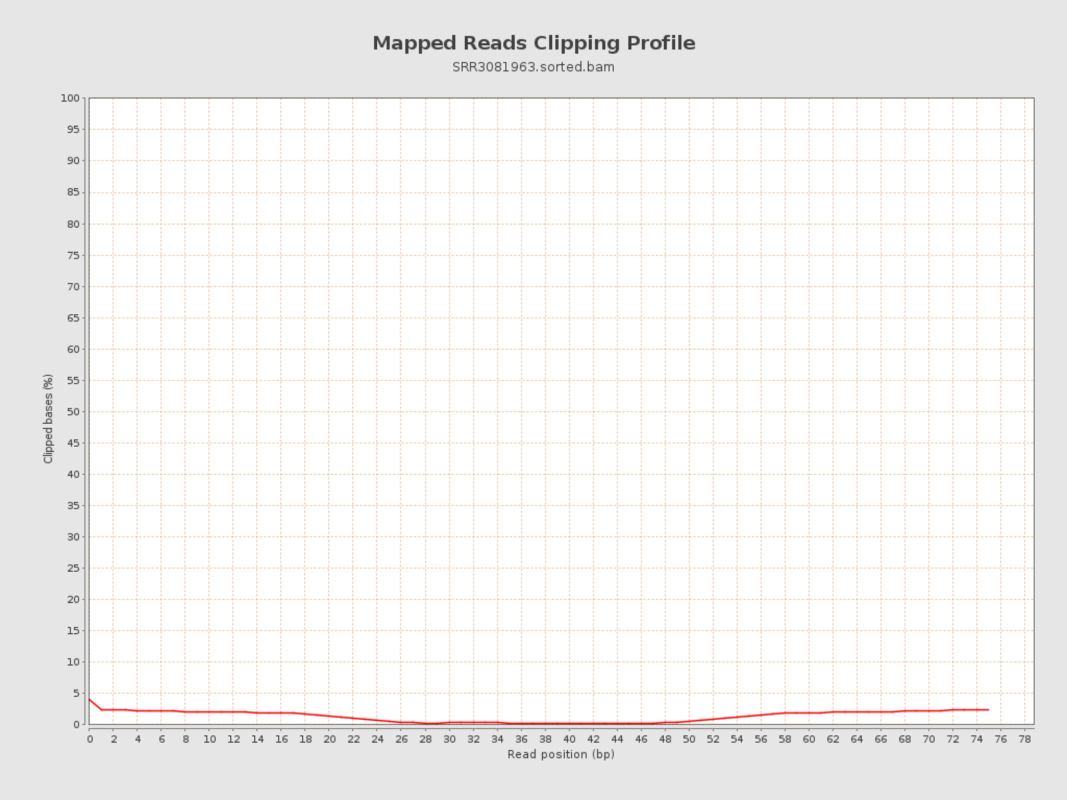
8. Results : Mapped Reads Nucleotide Content



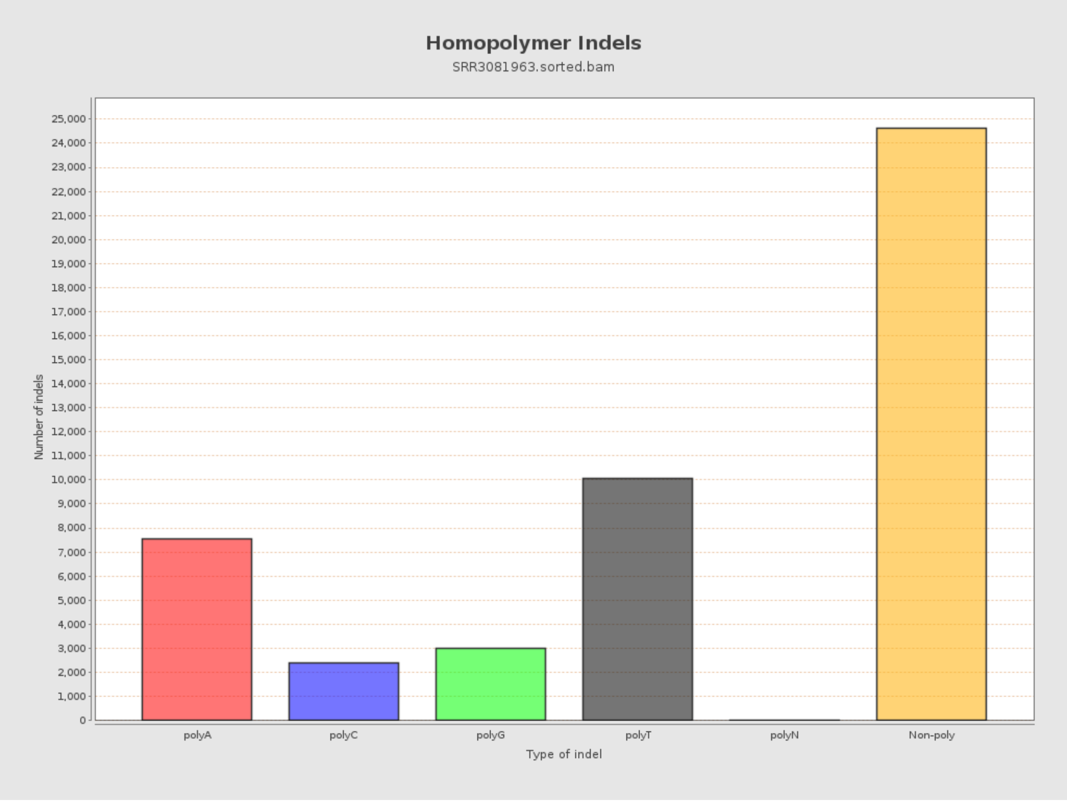
9. Results : Mapped Reads GC-content Distribution



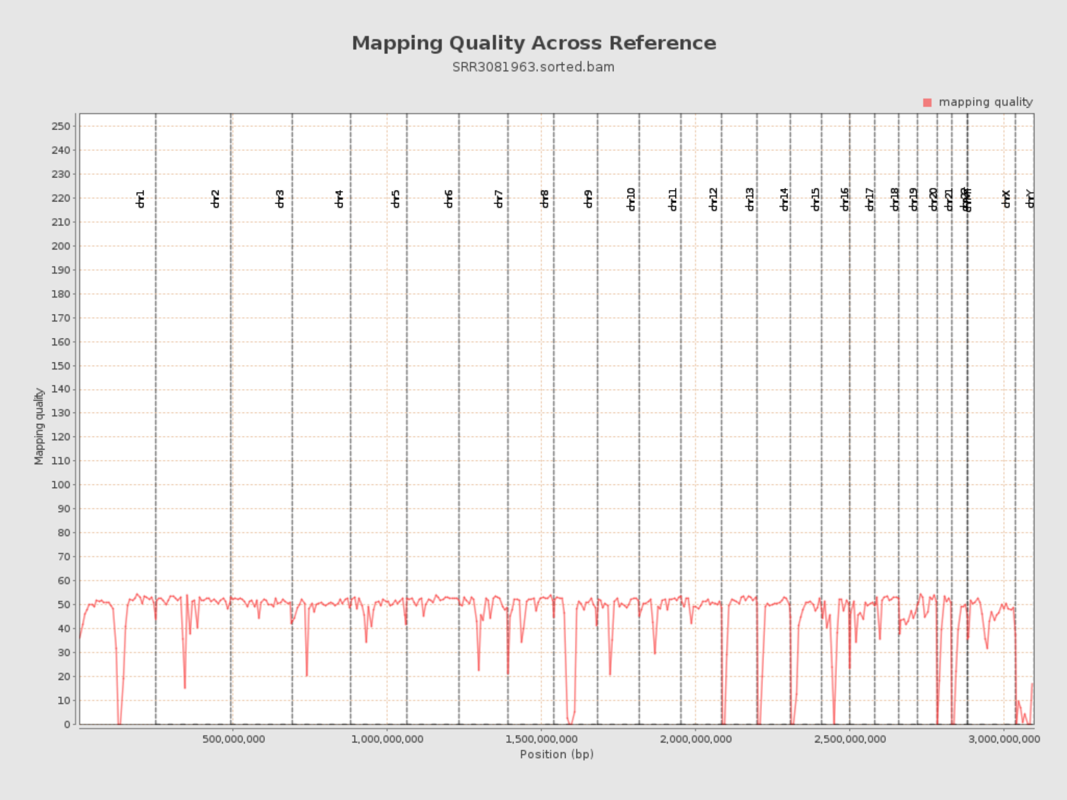
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram