Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:22:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083765.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_SRR3083765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083765.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:22:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083765.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,228,777
Mapped reads	2,005,738 / 62.12%
Unmapped reads	1,223,039 / 37.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,678 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	77,764 / 2.41%
Duplication rate	3.23%
Clipped reads	1,109,180 / 34.35%

2.2. ACGT Content

Number/percentage of A's	35,578,794 / 28.12%
Number/percentage of C's	23,841,805 / 18.84%
Number/percentage of T's	38,893,705 / 30.74%
Number/percentage of G's	28,203,161 / 22.29%
Number/percentage of N's	1,412 / 0%
GC Percentage	41.14%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.299

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

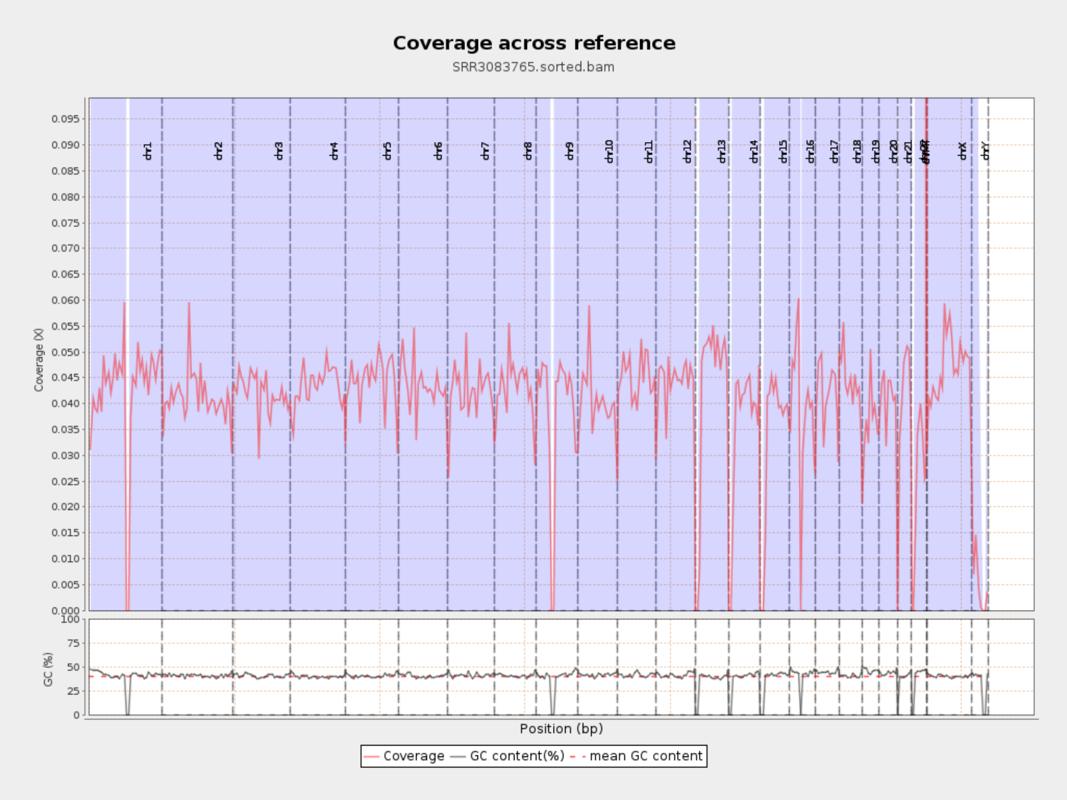
General error rate	0.82%
Mismatches	1,025,842
Insertions	9,249
Mapped reads with at least one insertion	0.46%
Deletions	26,156
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.62%

2.6. Chromosome stats

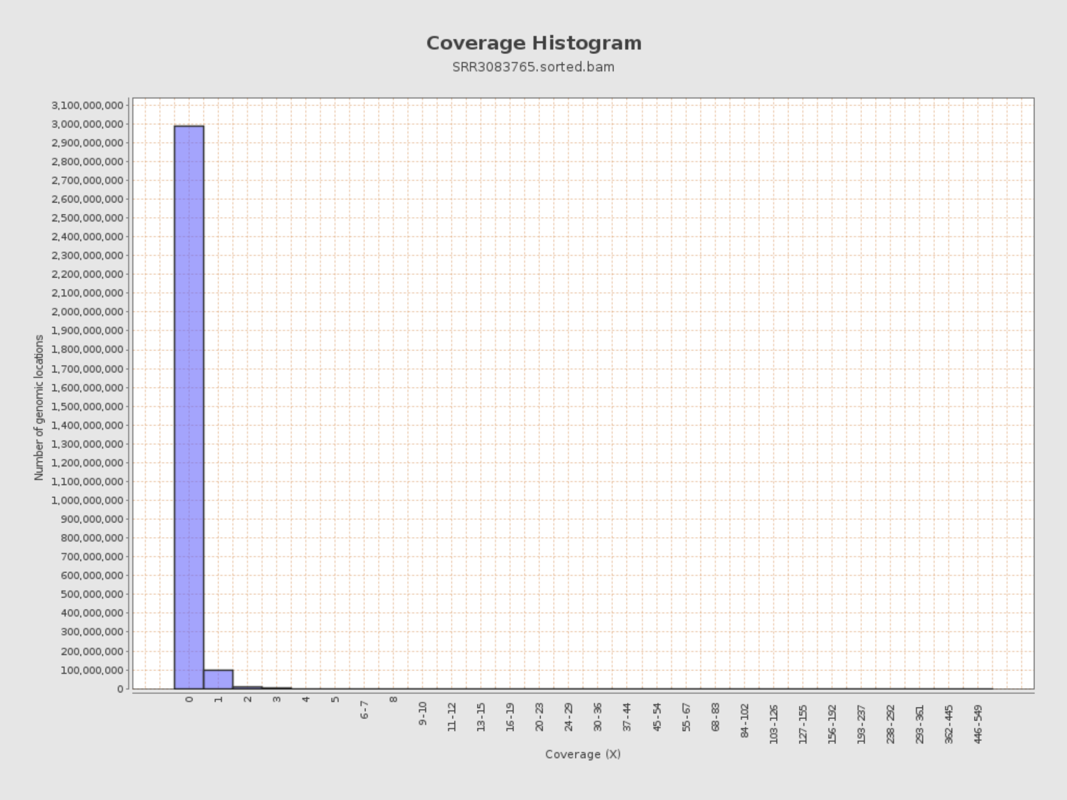
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10539830	0.0423	0.443
chr2	243199373	10030210	0.0412	0.3711
chr3	198022430	8350874	0.0422	0.2286
chr4	191154276	8299622	0.0434	0.2378
chr5	180915260	8075004	0.0446	0.2352
chr6	171115067	7431729	0.0434	0.2712
chr7	159138663	6800366	0.0427	0.3261

chr8	146364022	6303692	0.0431	0.2931
chr9	141213431	5429854	0.0385	0.2816
chr10	135534747	5516560	0.0407	0.3119
chr11	135006516	6072672	0.045	0.2863
chr12	133851895	5901747	0.0441	0.2353
chr13	115169878	4836959	0.042	0.2309
chr14	107349540	3707738	0.0345	0.2194
chr15	102531392	3392578	0.0331	0.2046
chr16	90354753	3519930	0.039	0.2433
chr17	81195210	3381652	0.0416	0.2474
chr18	78077248	3478192	0.0445	0.5741
chr19	59128983	2166200	0.0366	0.3353
chr20	63025520	2565718	0.0407	0.2342
chr21	48129895	1892006	0.0393	0.229
chr22	51304566	1194882	0.0233	0.1688
chrMT	16571	97728	5.8975	4.2949
chrX	155270560	7264374	0.0468	0.2646
chrY	59373566	310436	0.0052	0.1077

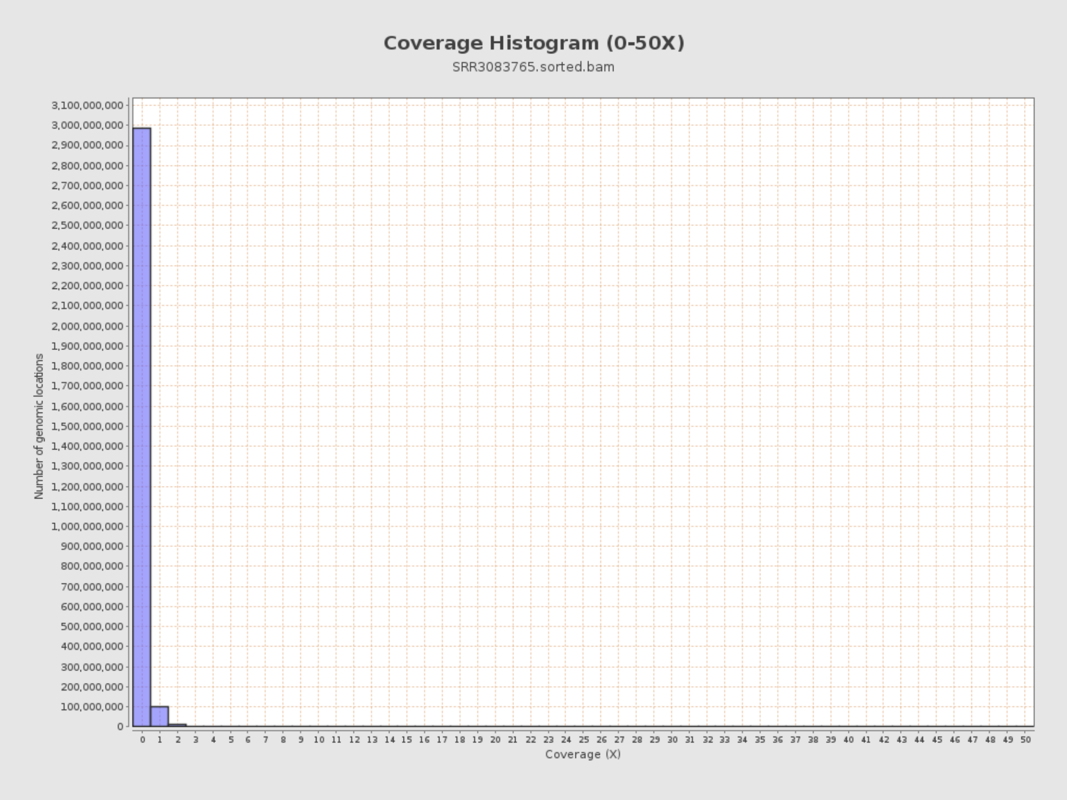
3. Results : Coverage across reference



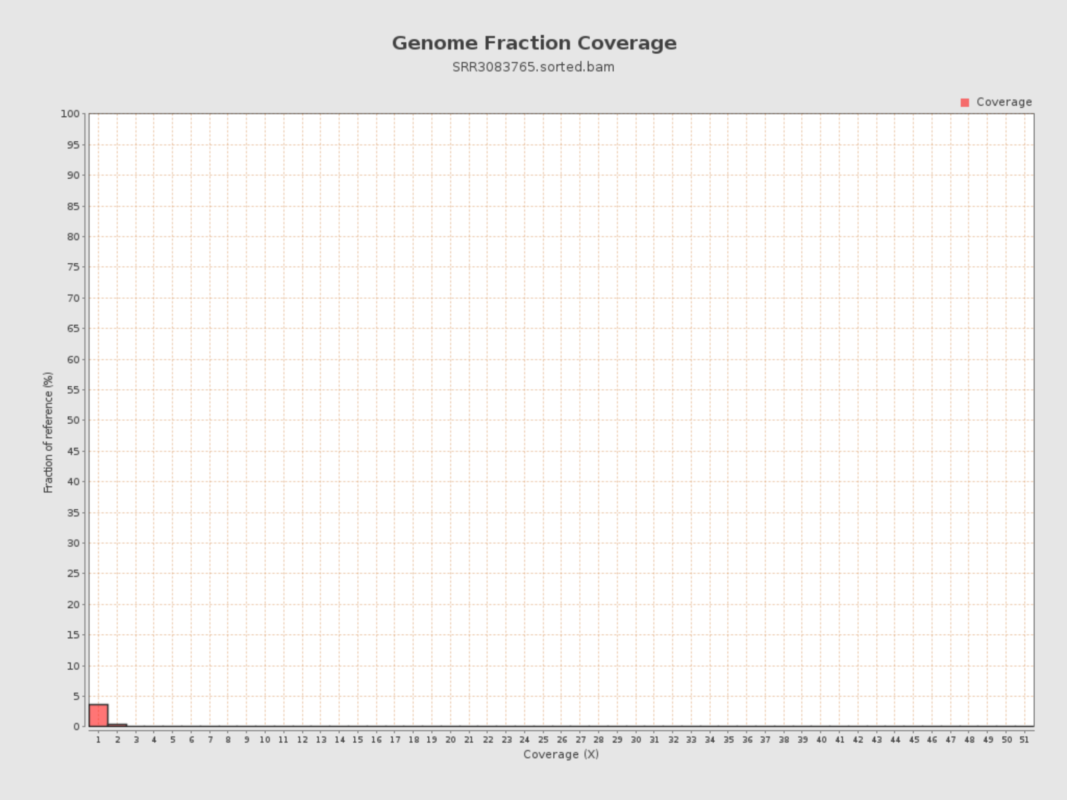
4. Results : Coverage Histogram



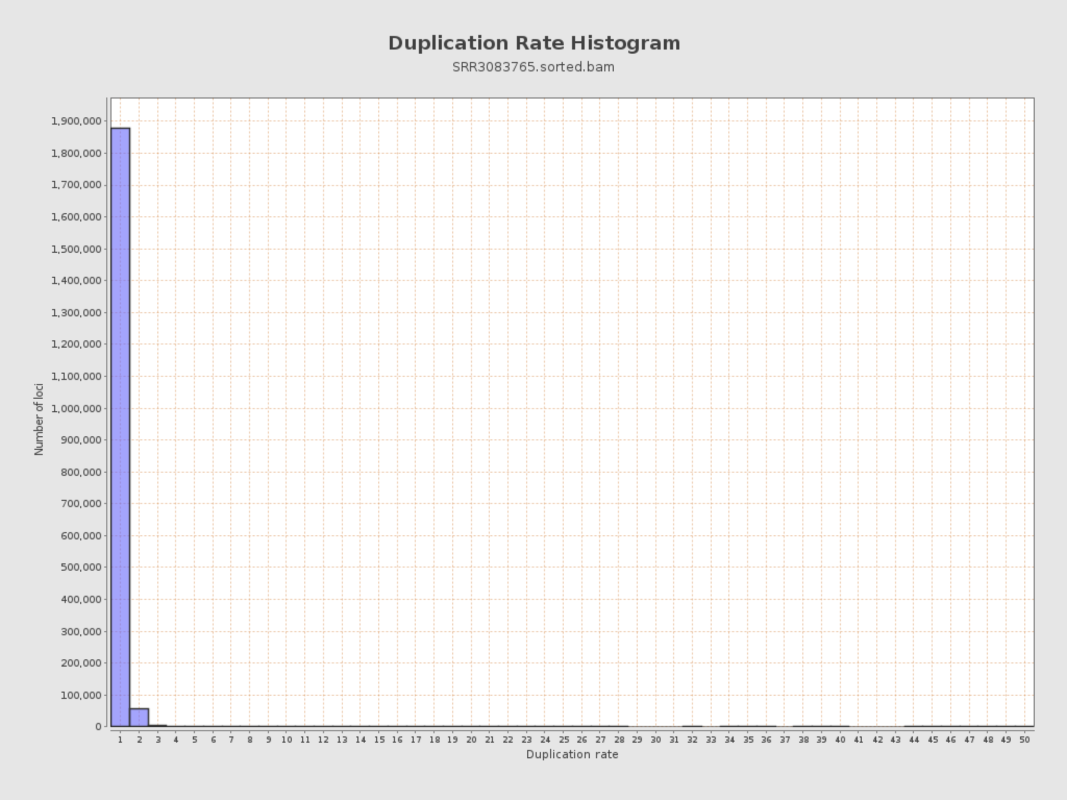
5. Results : Coverage Histogram (0-50X)



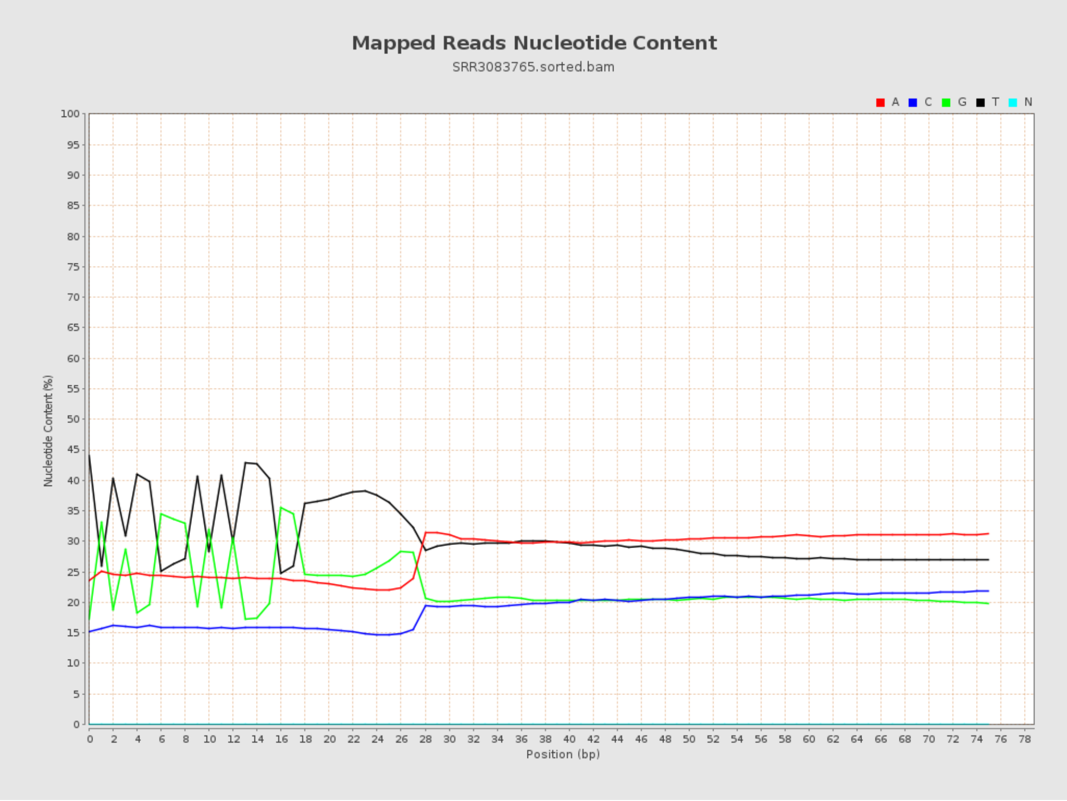
6. Results : Genome Fraction Coverage



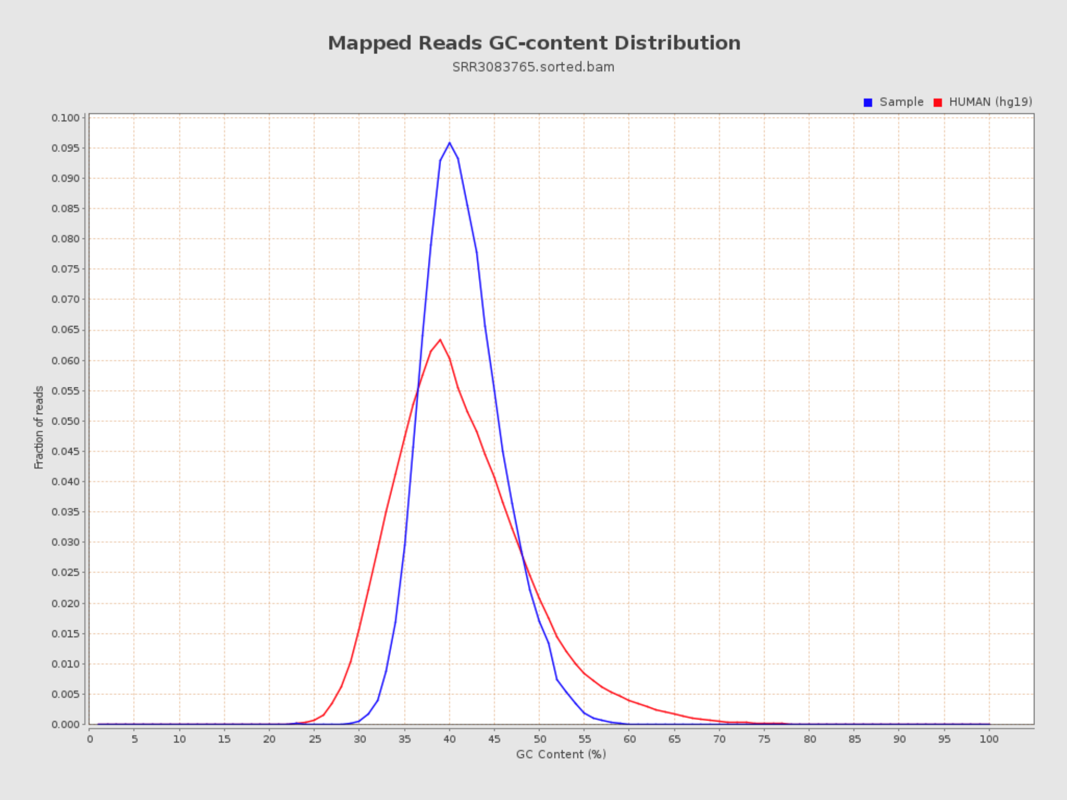
7. Results : Duplication Rate Histogram



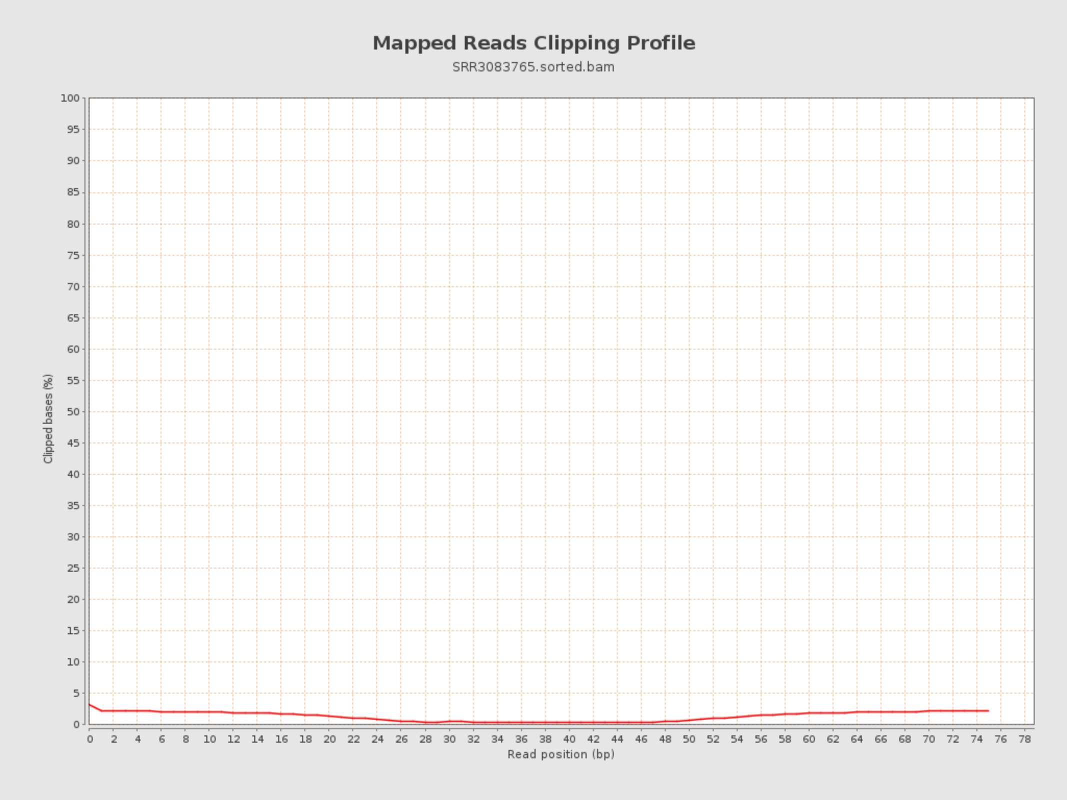
8. Results : Mapped Reads Nucleotide Content



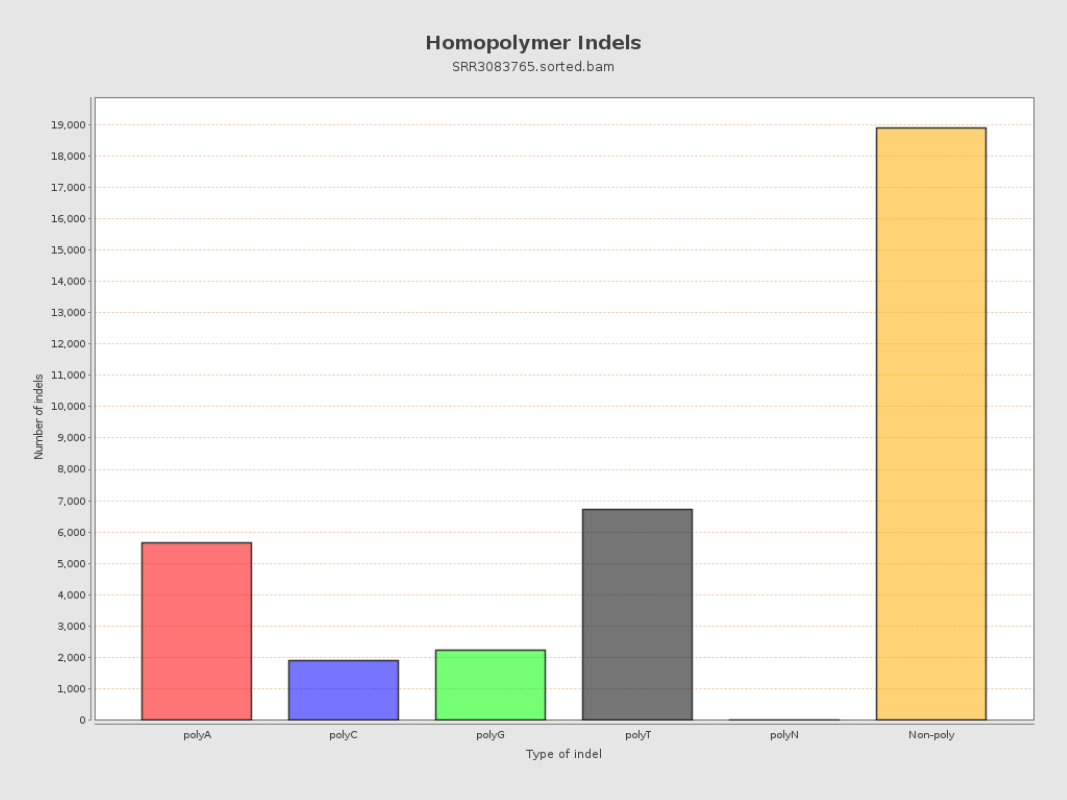
9. Results : Mapped Reads GC-content Distribution



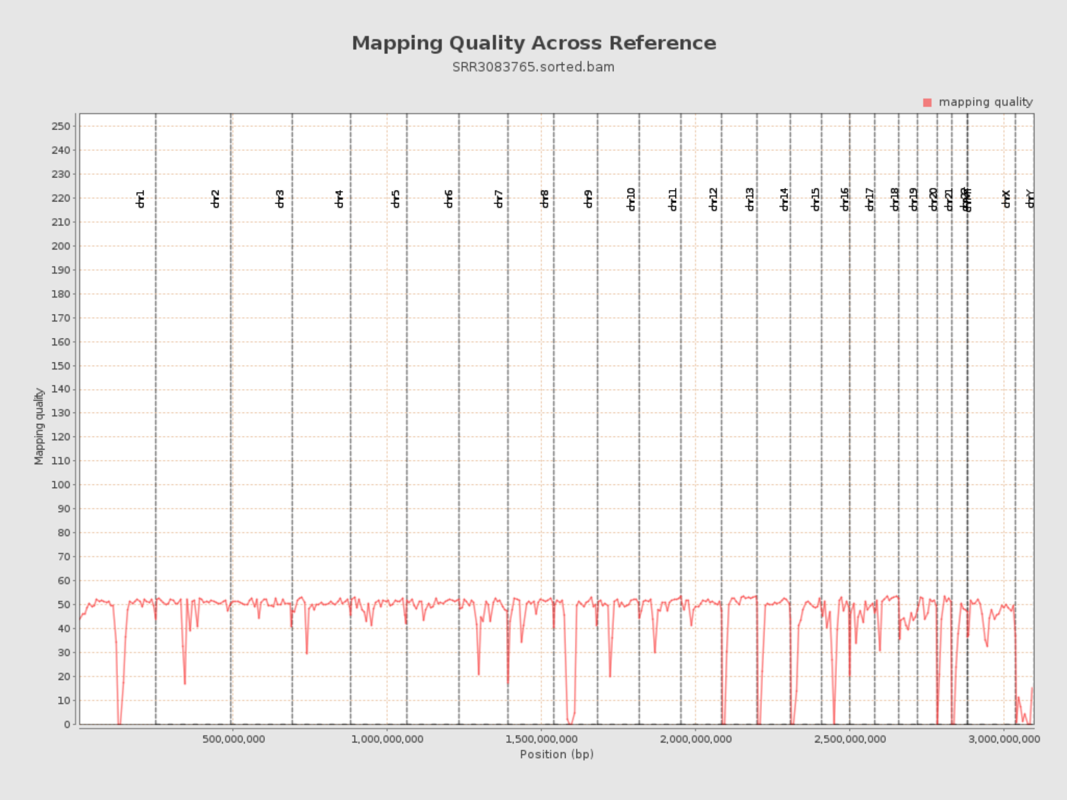
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram