Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:40:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084266.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_SRR3084266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:40:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,216,440
Mapped reads	1,824,322 / 82.31%
Unmapped reads	392,118 / 17.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,090 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	62,173 / 2.81%
Duplication rate	2.82%
Clipped reads	1,006,279 / 45.4%

2.2. ACGT Content

Number/percentage of A's	33,588,836 / 28.86%
Number/percentage of C's	21,720,351 / 18.67%
Number/percentage of T's	35,643,895 / 30.63%
Number/percentage of G's	25,414,629 / 21.84%
Number/percentage of N's	1,236 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.2793

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

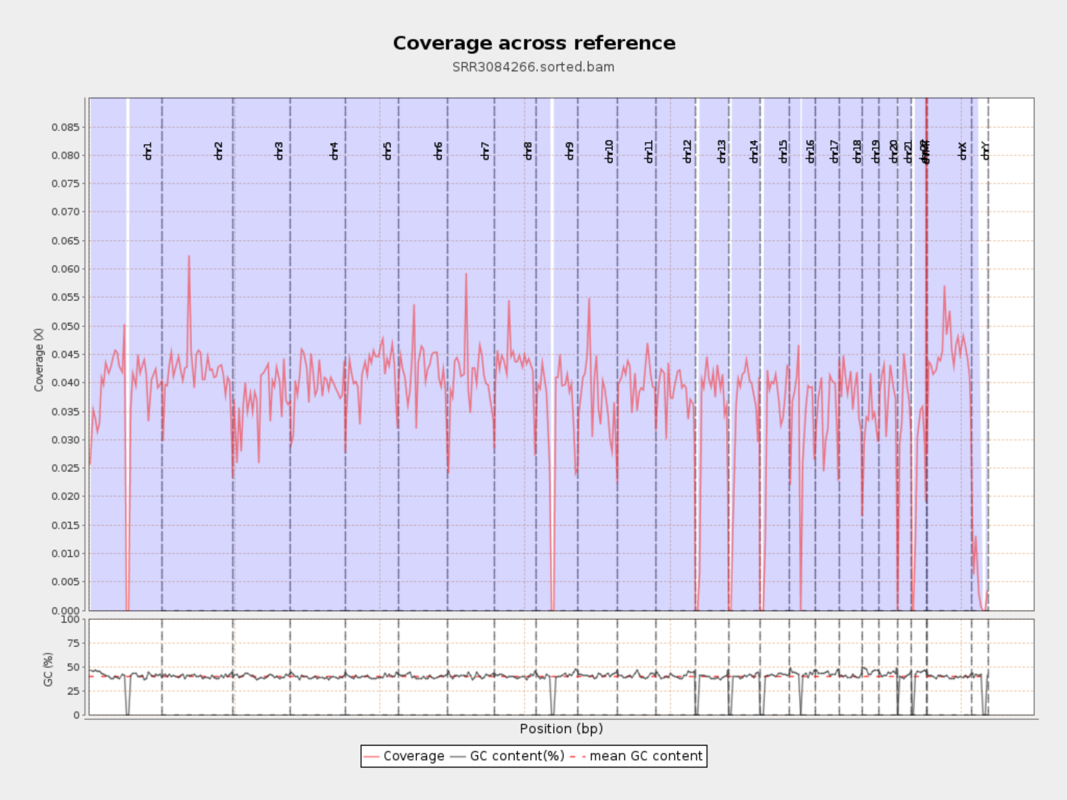
General error rate	0.85%
Mismatches	970,056
Insertions	9,052
Mapped reads with at least one insertion	0.49%
Deletions	25,071
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.46%

2.6. Chromosome stats

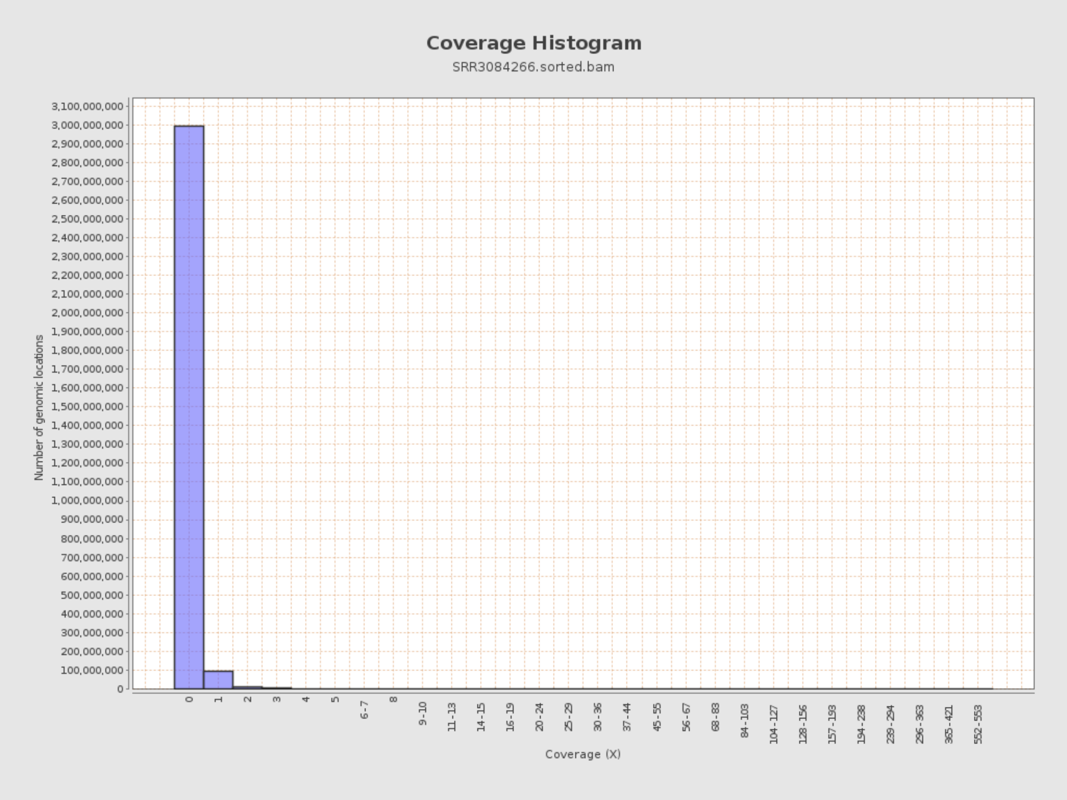
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9409094	0.0377	0.379
chr2	243199373	10286951	0.0423	0.3651
chr3	198022430	7319563	0.037	0.2132
chr4	191154276	7610751	0.0398	0.2257
chr5	180915260	7606864	0.042	0.227
chr6	171115067	7203161	0.0421	0.2588
chr7	159138663	6538968	0.0411	0.3502

chr8	146364022	6353929	0.0434	0.301
chr9	141213431	4784597	0.0339	0.2728
chr10	135534747	5113597	0.0377	0.2767
chr11	135006516	5420559	0.0402	0.2564
chr12	133851895	5146742	0.0385	0.2183
chr13	115169878	3792606	0.0329	0.2014
chr14	107349540	3468662	0.0323	0.2112
chr15	102531392	3209786	0.0313	0.2003
chr16	90354753	2973389	0.0329	0.2208
chr17	81195210	2783750	0.0343	0.22
chr18	78077248	3048025	0.039	0.5133
chr19	59128983	1950383	0.033	0.2959
chr20	63025520	2391364	0.0379	0.2226
chr21	48129895	1575890	0.0327	0.2075
chr22	51304566	1142144	0.0223	0.1636
chrMT	16571	5562	0.3356	0.6486
chrX	155270560	6994965	0.0451	0.2524
chrY	59373566	277045	0.0047	0.093

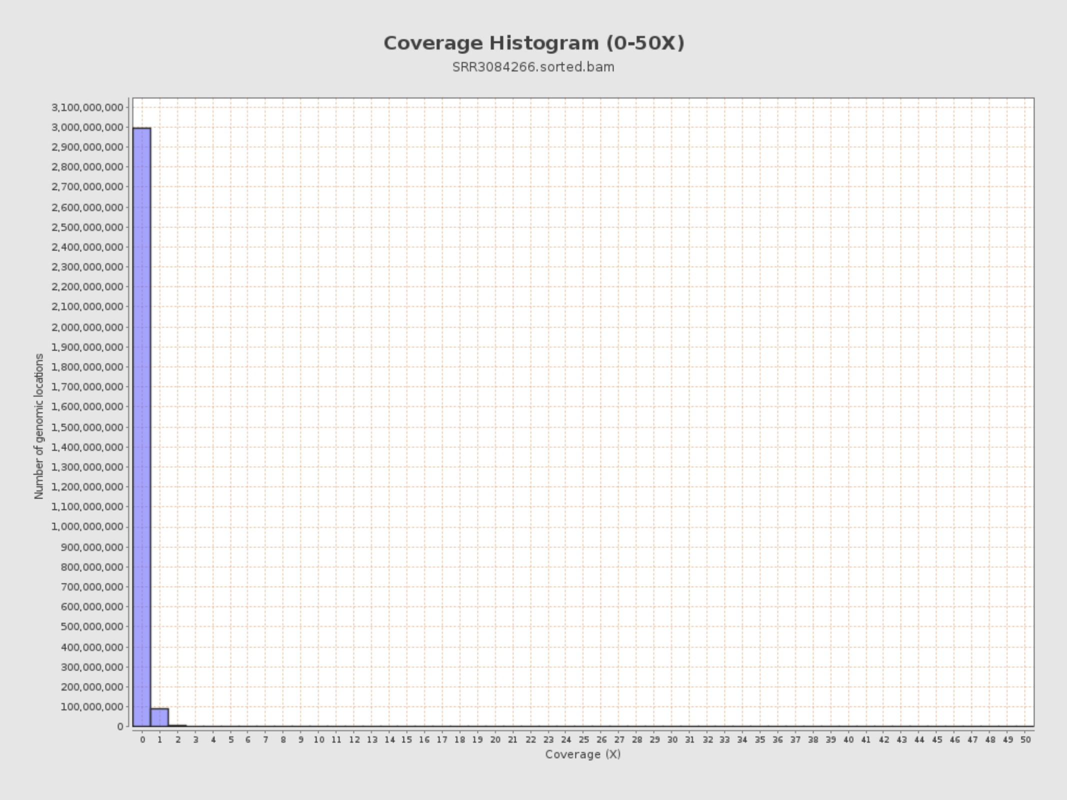
3. Results : Coverage across reference



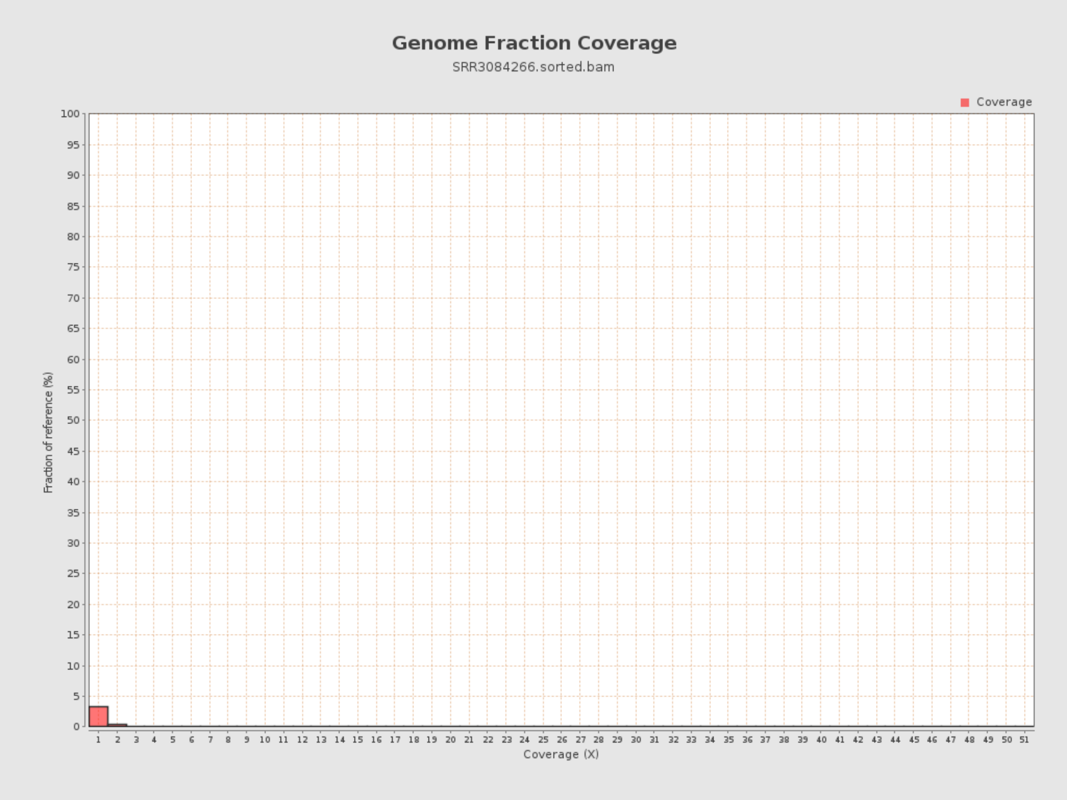
4. Results : Coverage Histogram



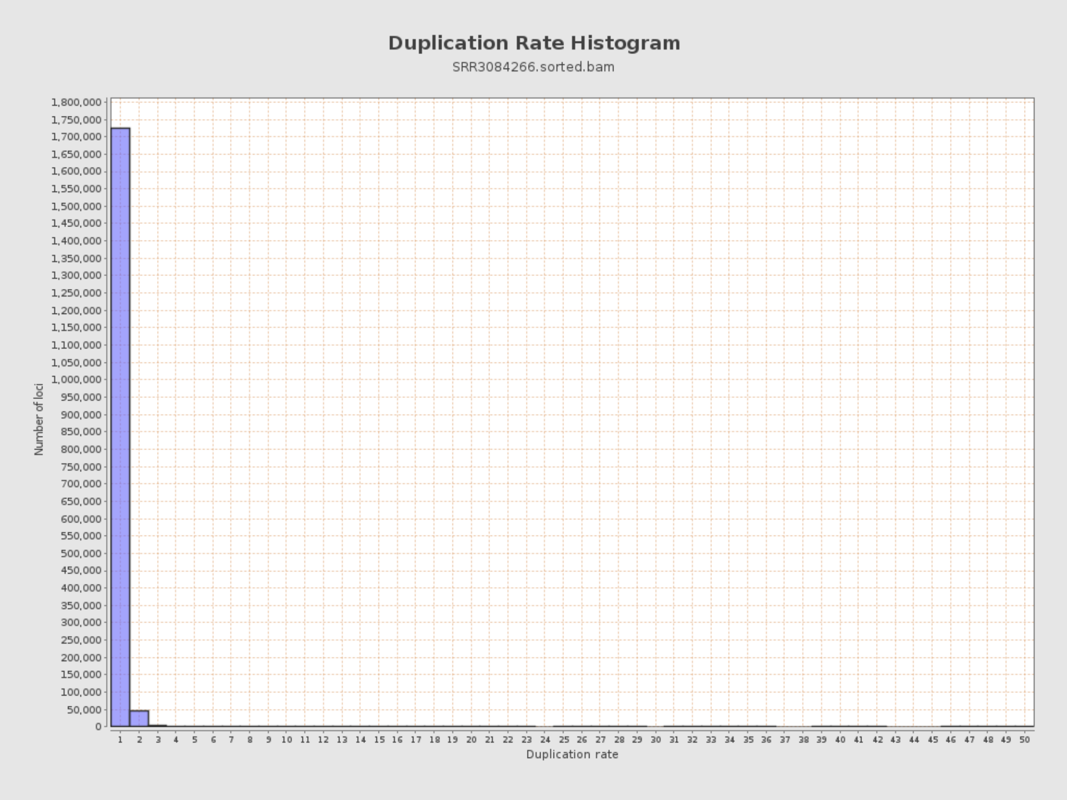
5. Results : Coverage Histogram (0-50X)



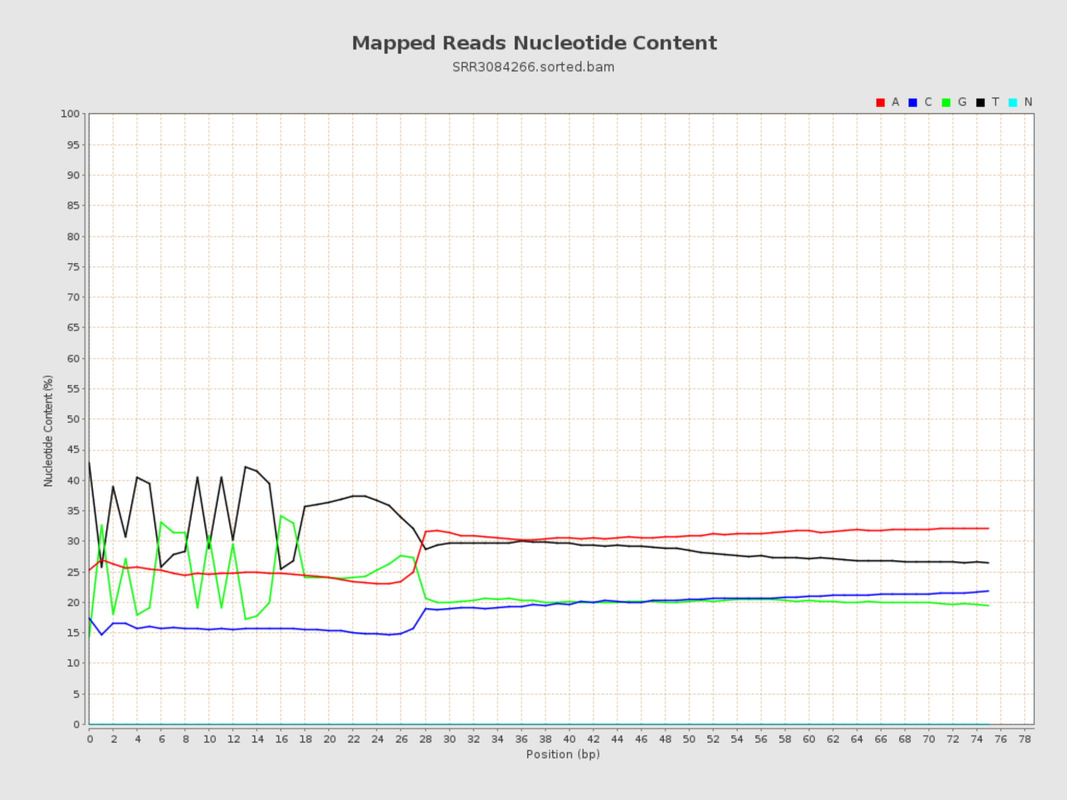
6. Results : Genome Fraction Coverage



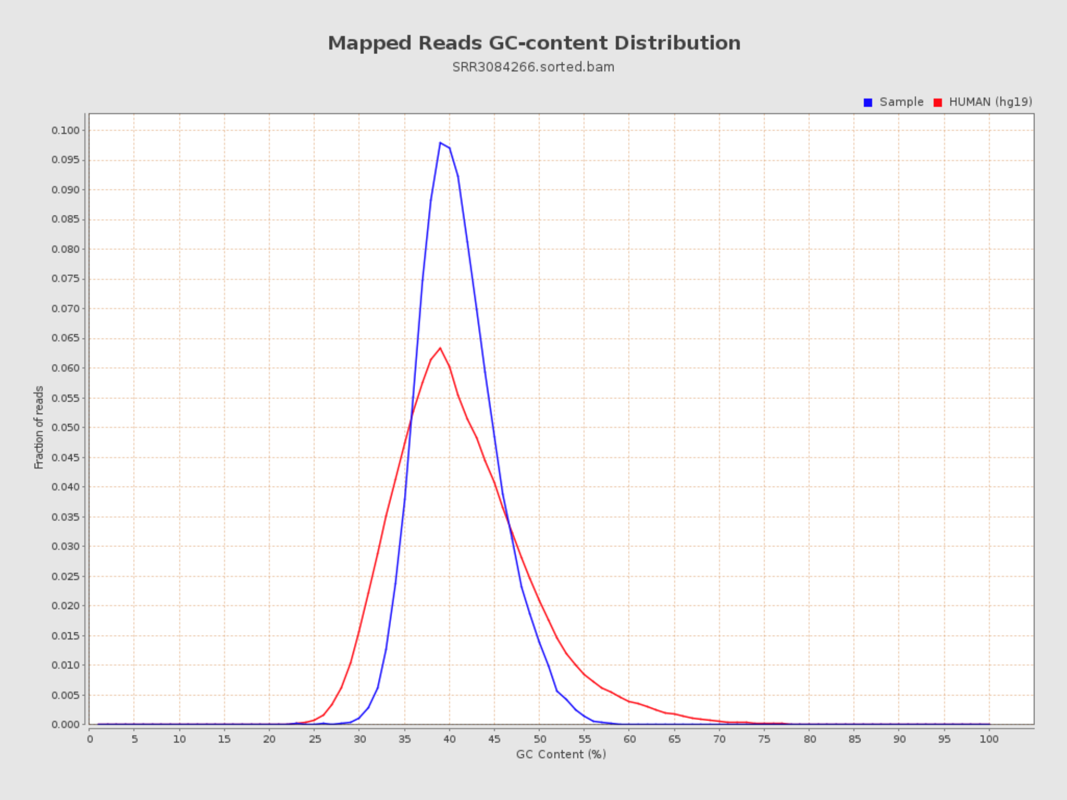
7. Results : Duplication Rate Histogram



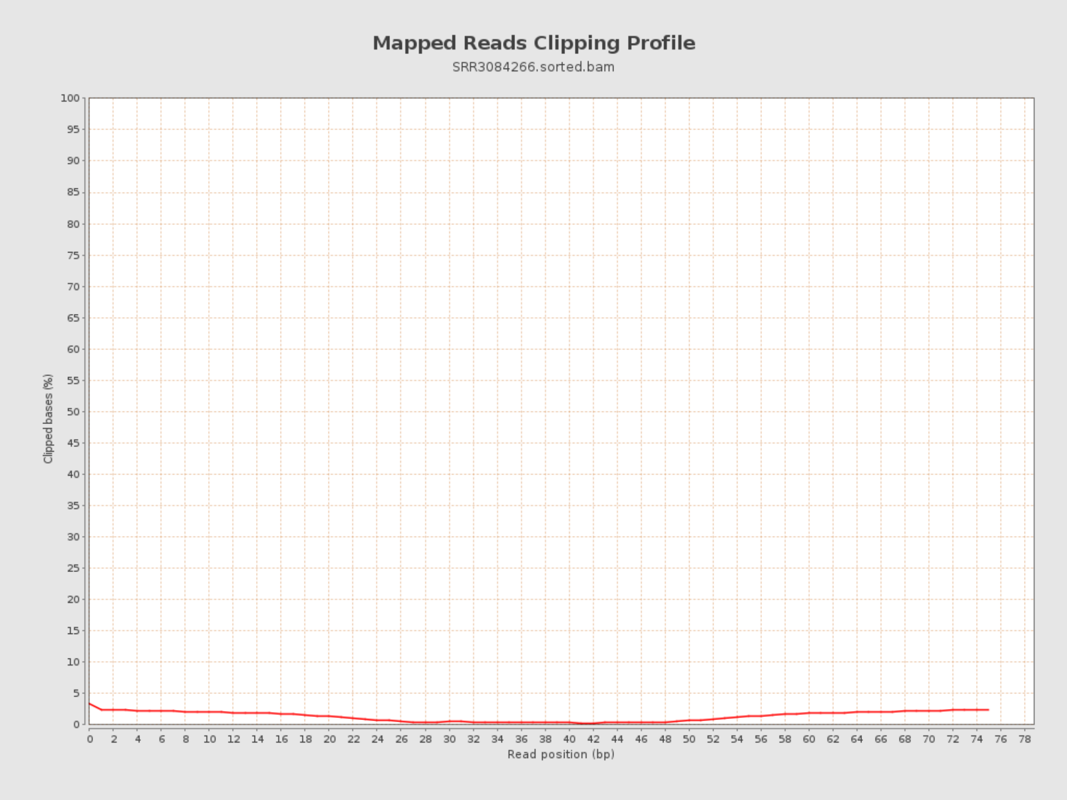
8. Results : Mapped Reads Nucleotide Content



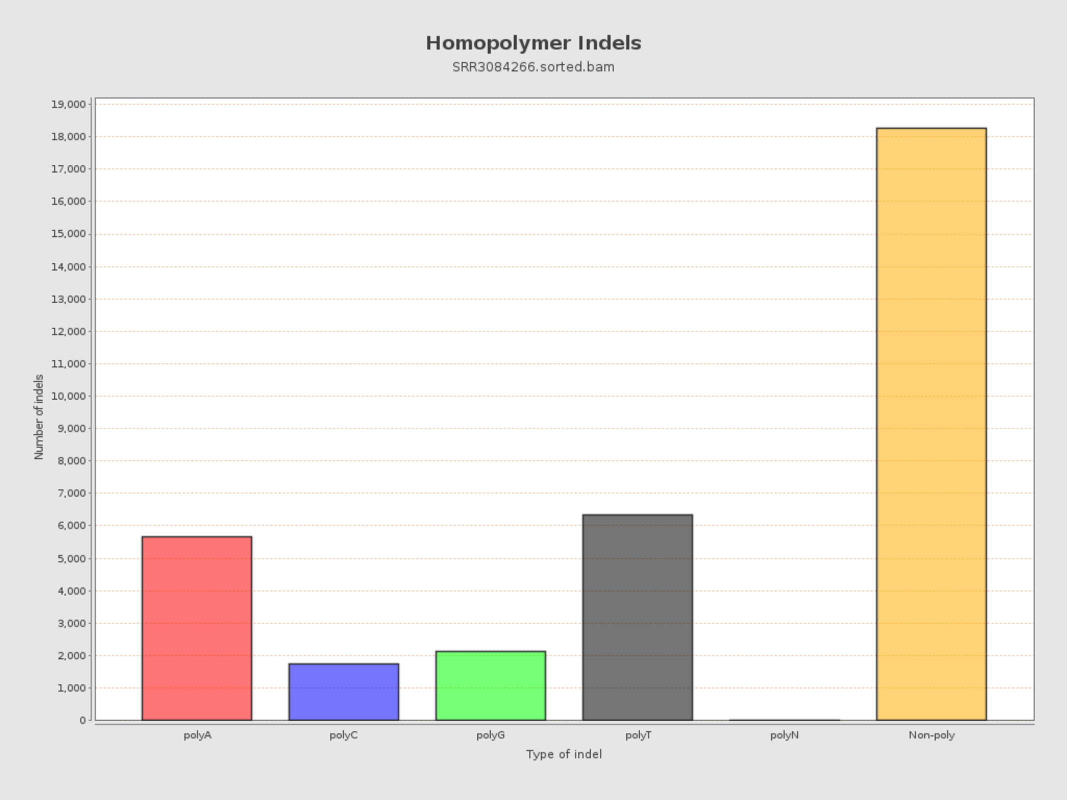
9. Results : Mapped Reads GC-content Distribution



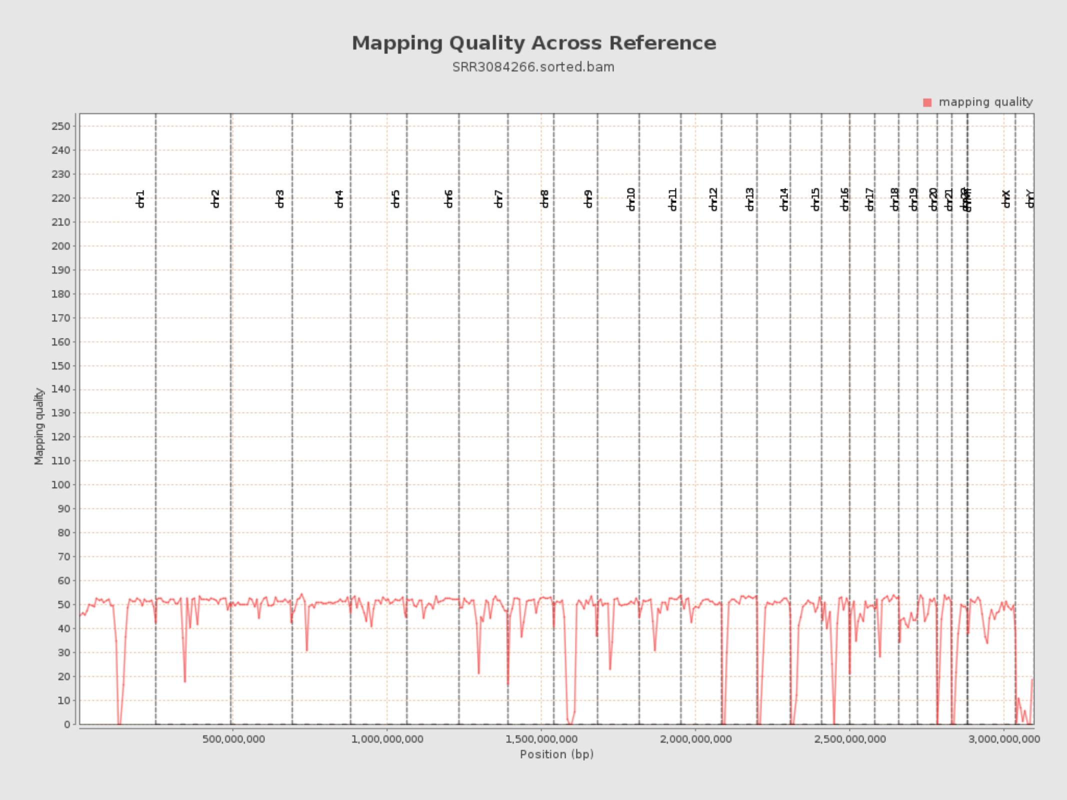
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram