Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:31:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004164.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_SRR6004164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:31:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,394,328
Mapped reads	2,642,755 / 77.86%
Unmapped reads	751,573 / 22.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,817 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	172,759 / 5.09%
Duplication rate	5.24%
Clipped reads	1,496,933 / 44.1%

2.2. ACGT Content

Number/percentage of A's	44,796,176 / 26.42%
Number/percentage of C's	30,899,752 / 18.22%
Number/percentage of T's	54,454,875 / 32.12%
Number/percentage of G's	39,383,575 / 23.23%
Number/percentage of N's	21,530 / 0.01%
GC Percentage	41.45%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.473

2.4. Mapping Quality

Mean Mapping Quality	43.93

2.5. Mismatches and indels

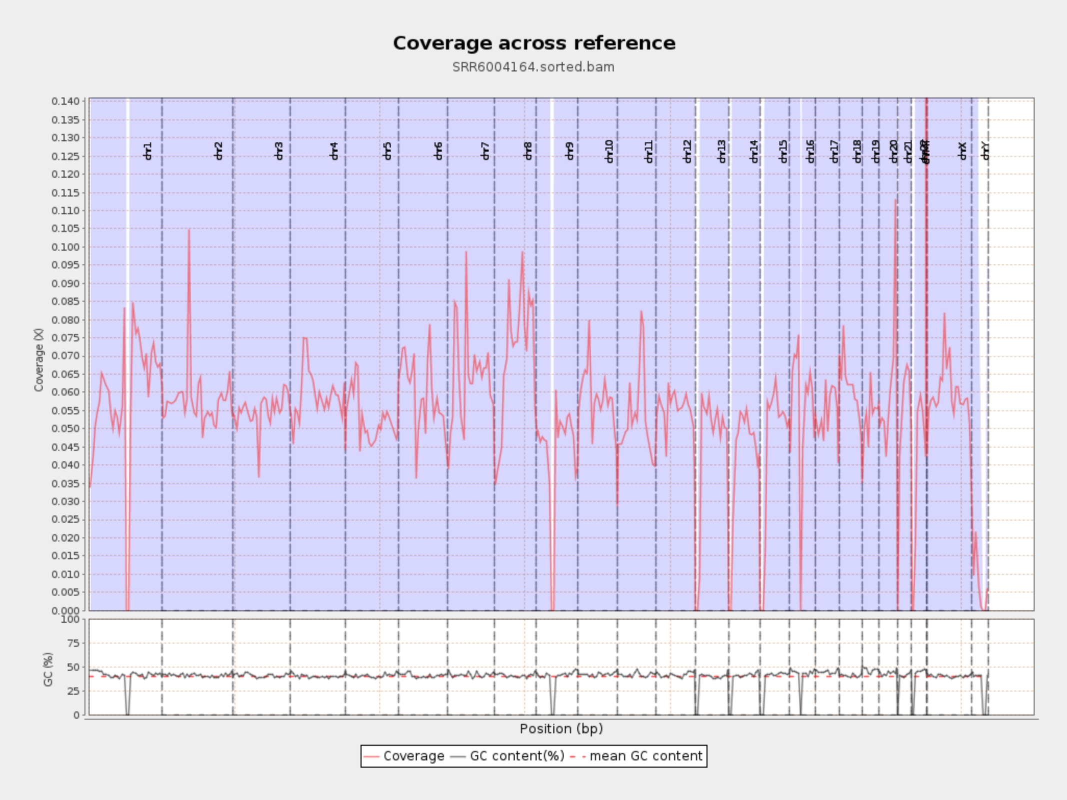
General error rate	1.08%
Mismatches	1,807,613
Insertions	15,060
Mapped reads with at least one insertion	0.56%
Deletions	61,259
Mapped reads with at least one deletion	2.29%
Homopolymer indels	46.81%

2.6. Chromosome stats

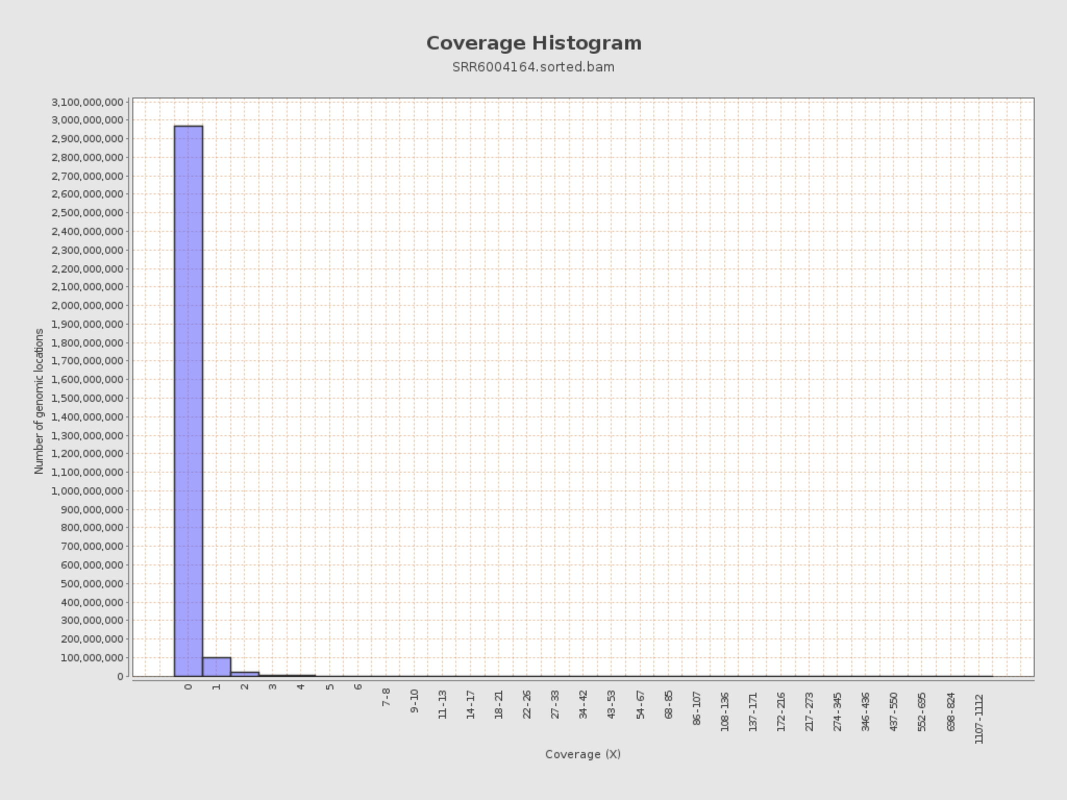
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14593106	0.0585	0.708
chr2	243199373	14169943	0.0583	0.6636
chr3	198022430	10903935	0.0551	0.3027
chr4	191154276	11324155	0.0592	0.3301
chr5	180915260	9555900	0.0528	0.297
chr6	171115067	10193002	0.0596	0.365
chr7	159138663	10324708	0.0649	0.7517

chr8	146364022	10209615	0.0698	0.5428
chr9	141213431	6079331	0.0431	0.4447
chr10	135534747	8001474	0.059	0.401
chr11	135006516	7141807	0.0529	0.484
chr12	133851895	7442003	0.0556	0.3079
chr13	115169878	5087300	0.0442	0.2724
chr14	107349540	4425352	0.0412	0.2944
chr15	102531392	4613993	0.045	0.2828
chr16	90354753	5047200	0.0559	0.3359
chr17	81195210	4406675	0.0543	0.3429
chr18	78077248	4831762	0.0619	0.8486
chr19	59128983	3166989	0.0536	0.5083
chr20	63025520	3918330	0.0622	0.339
chr21	48129895	2506228	0.0521	0.3155
chr22	51304566	1900230	0.037	0.2463
chrMT	16571	111974	6.7572	6.0834
chrX	155270560	9245033	0.0595	0.3609
chrY	59373566	456618	0.0077	0.1603

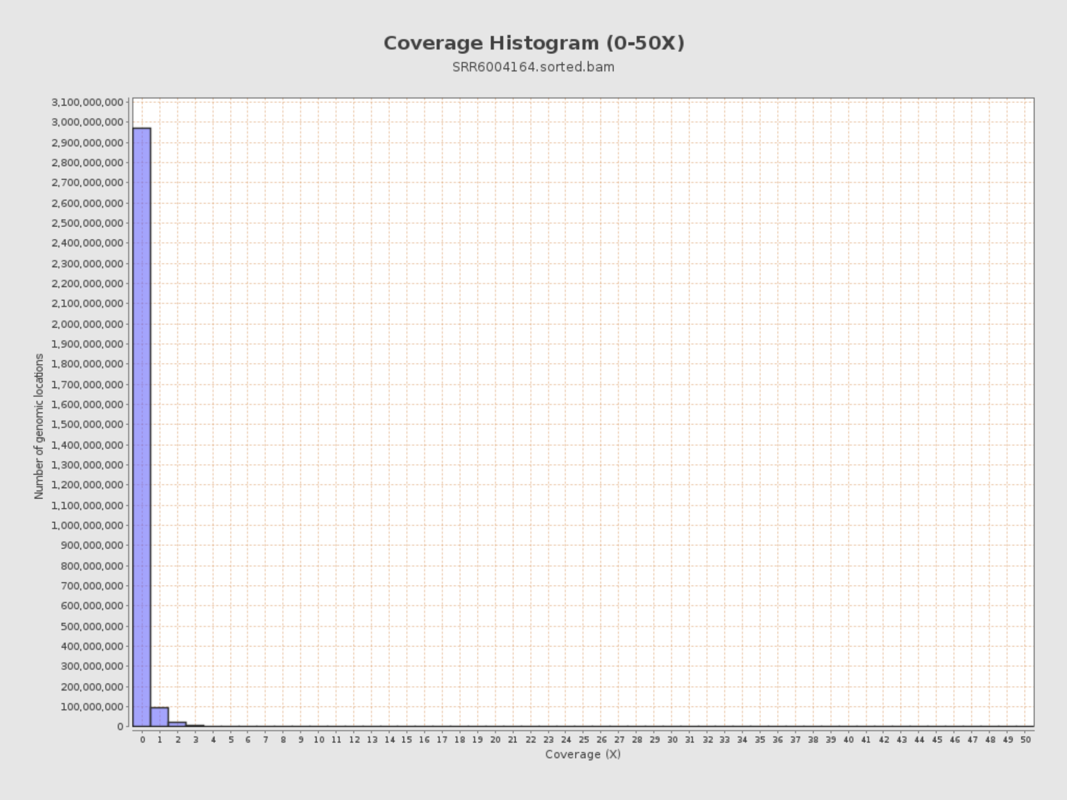
3. Results : Coverage across reference



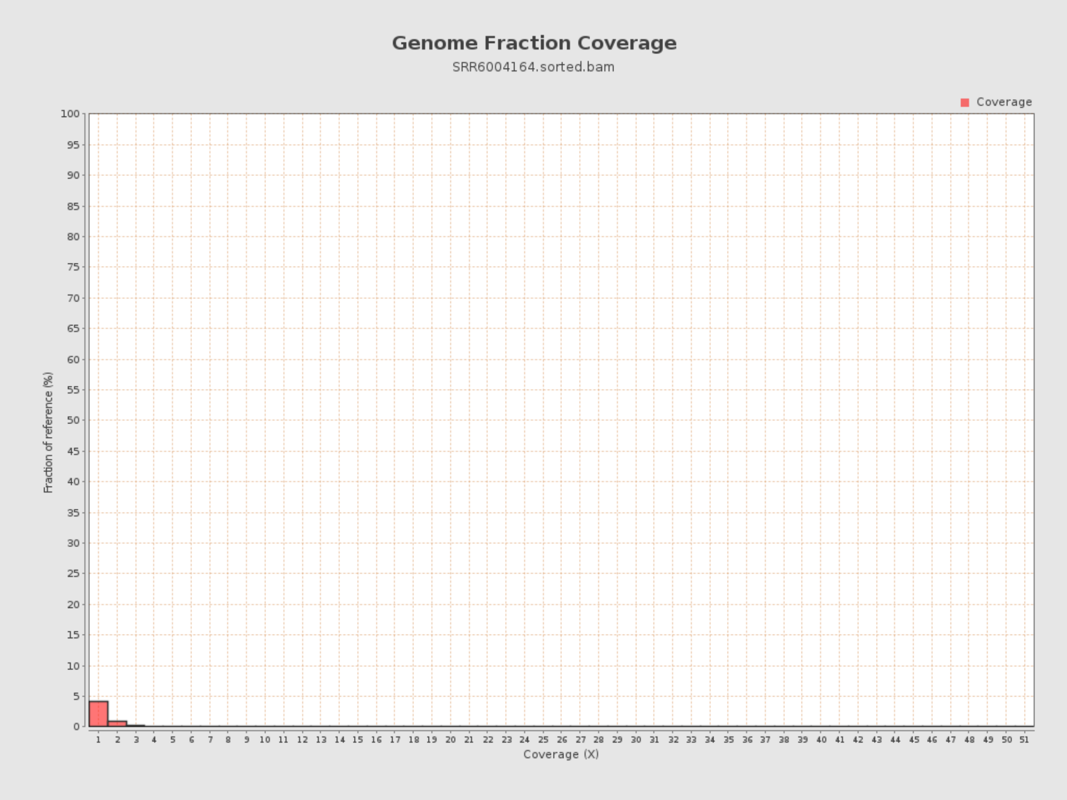
4. Results : Coverage Histogram



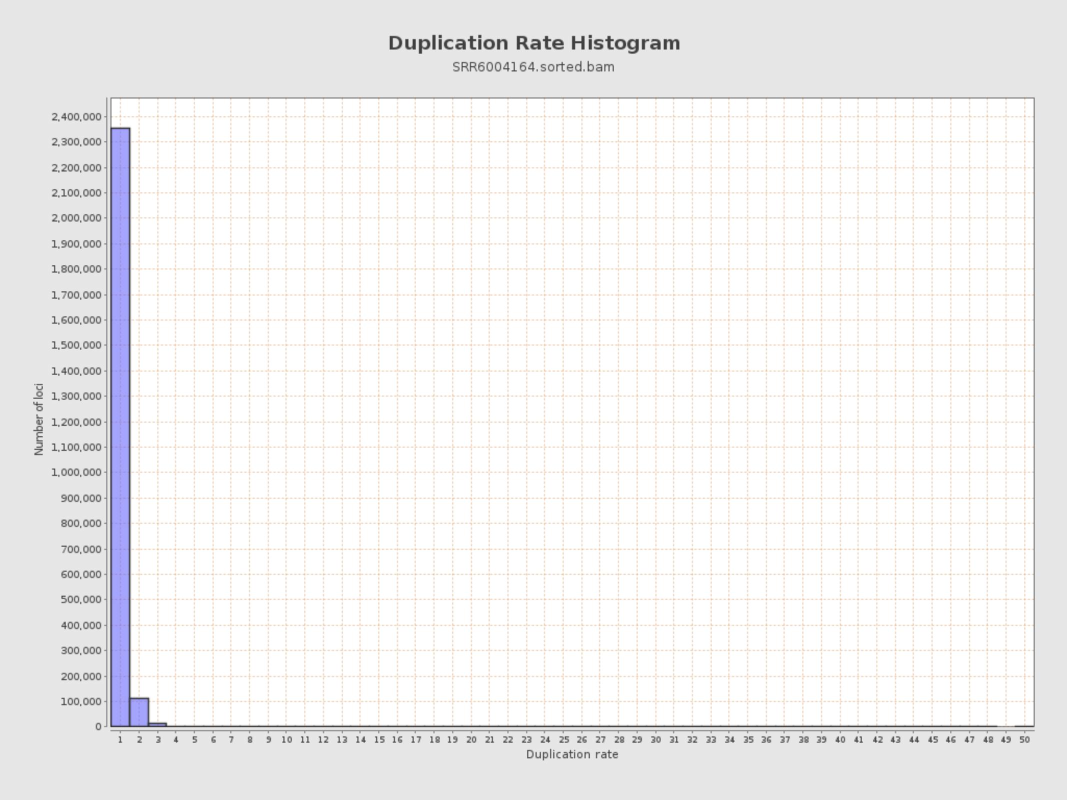
5. Results : Coverage Histogram (0-50X)



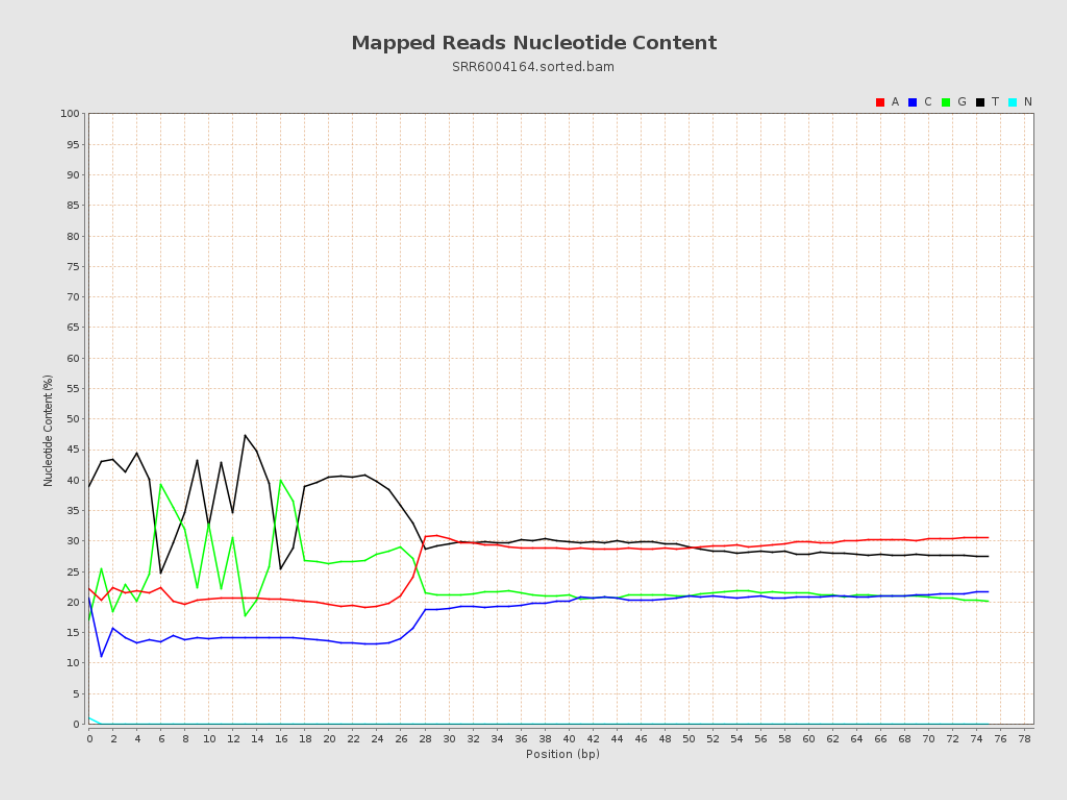
6. Results : Genome Fraction Coverage



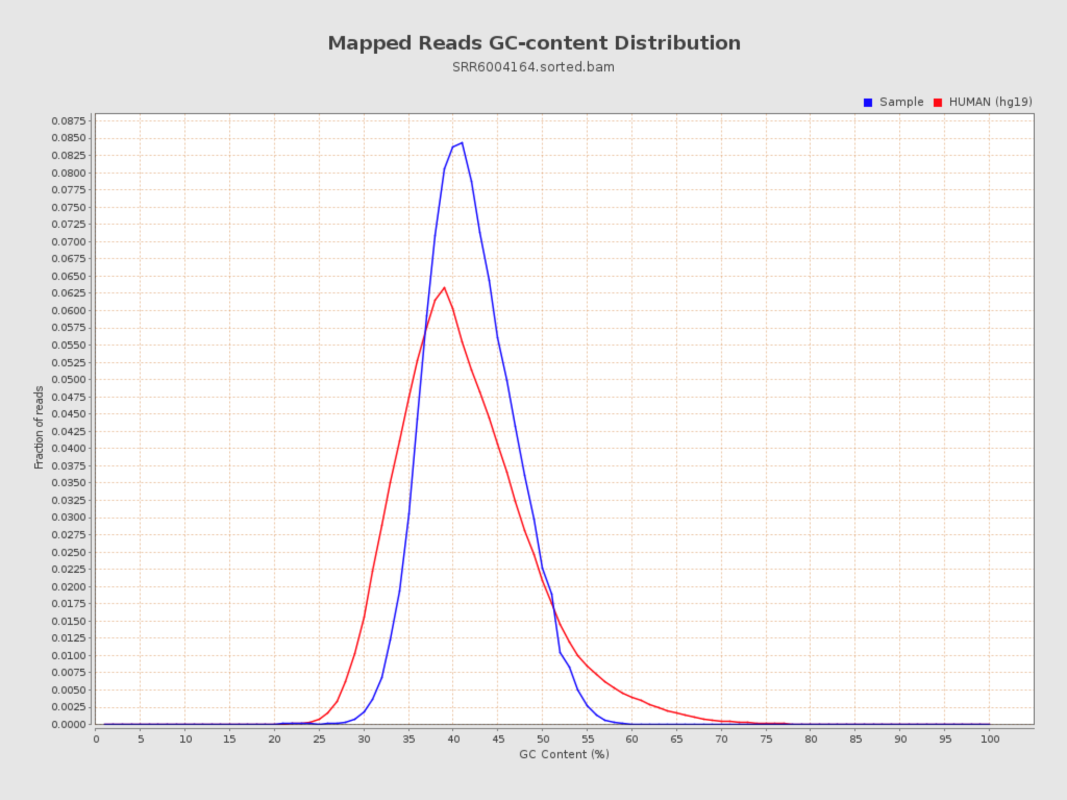
7. Results : Duplication Rate Histogram



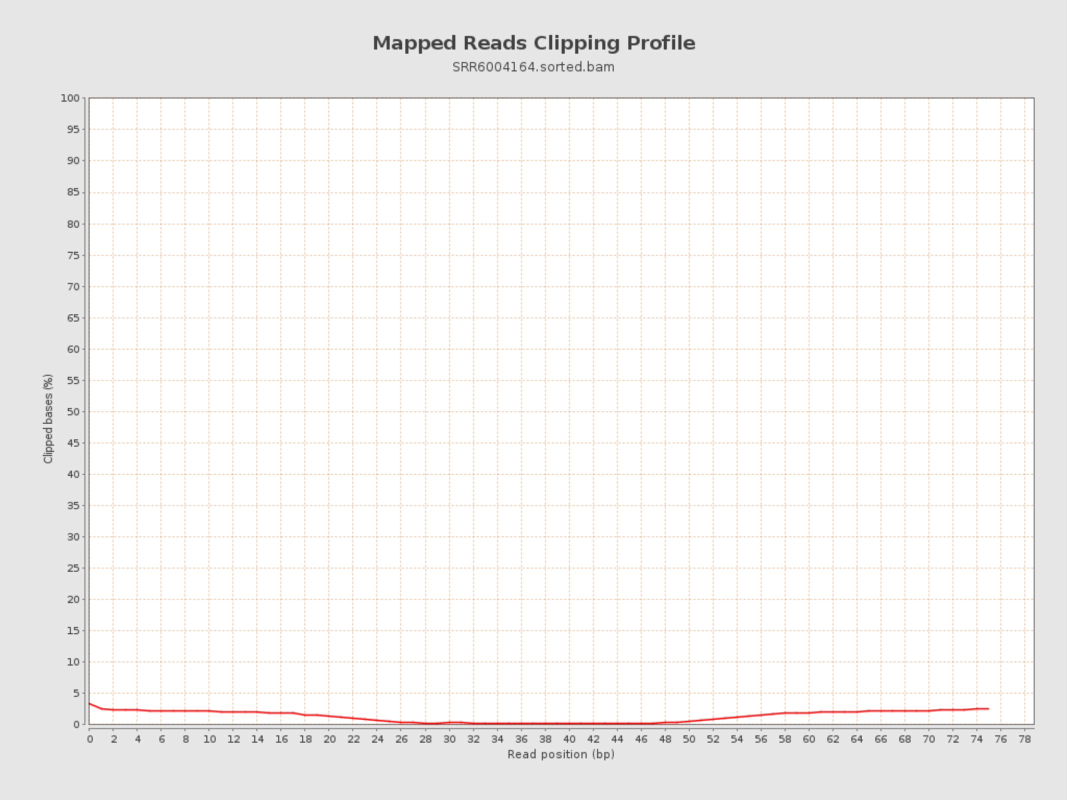
8. Results : Mapped Reads Nucleotide Content



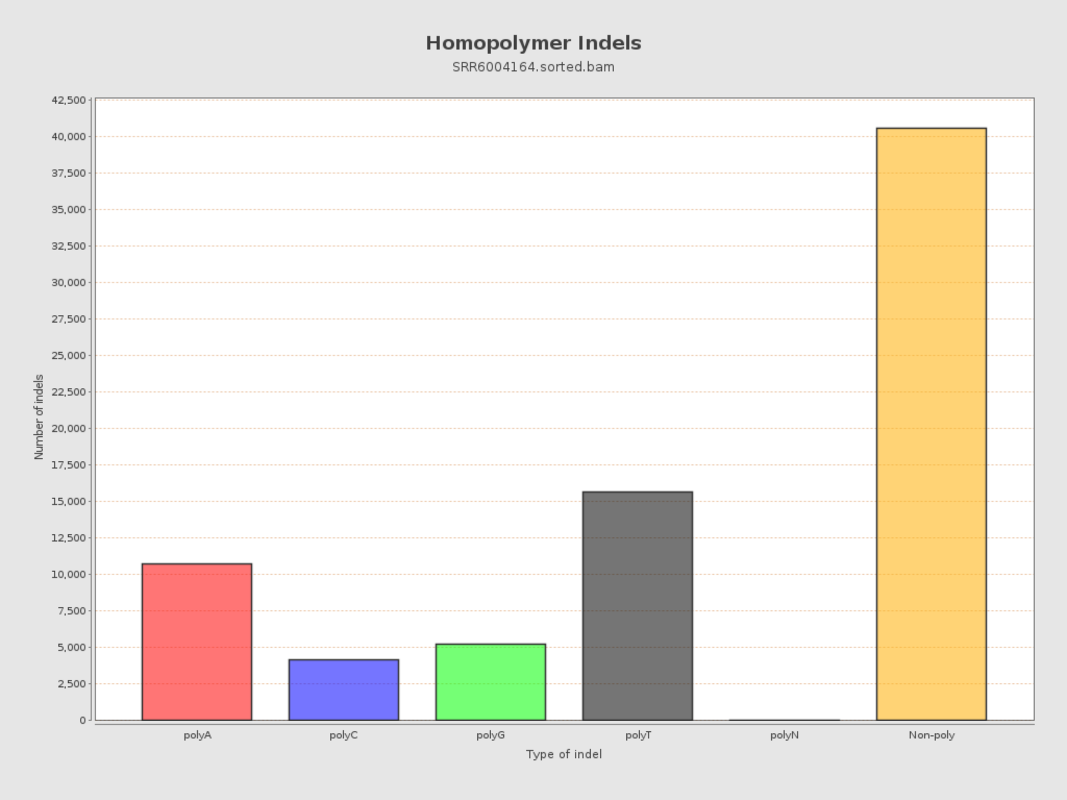
9. Results : Mapped Reads GC-content Distribution



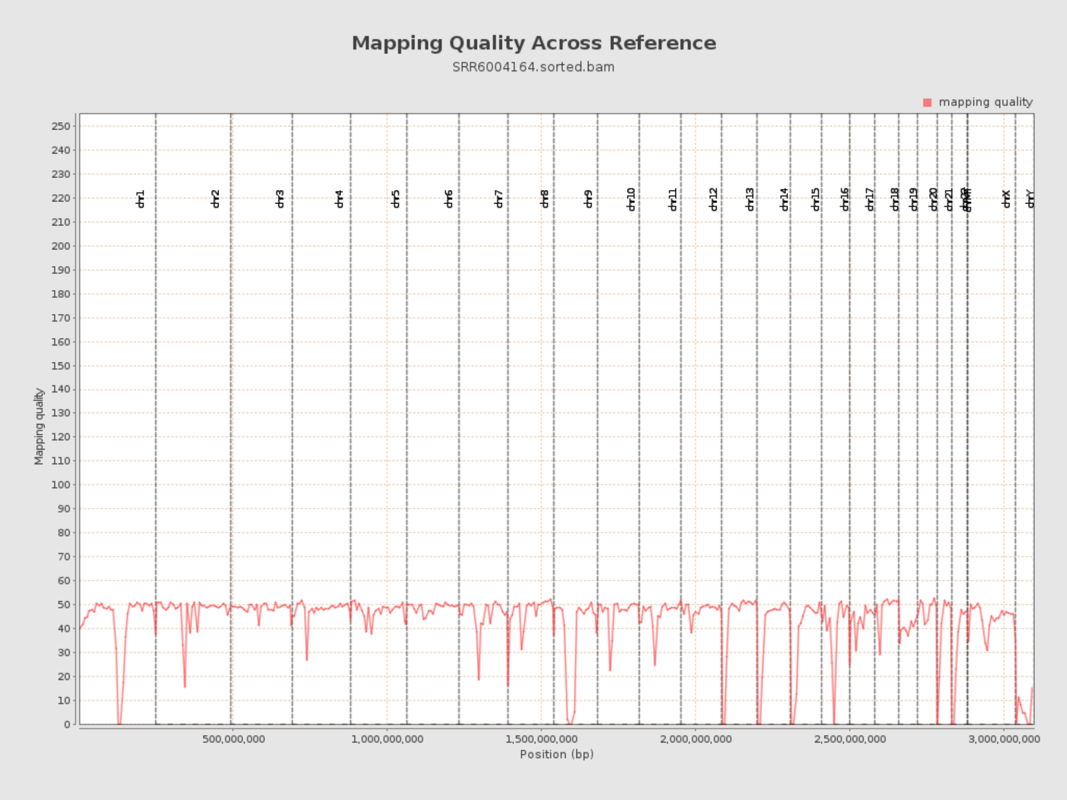
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram